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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in
the Fetal liver and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_FETAL_LIVER.txt,
25 created 24 January 2001, having 25,630,231 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known a priori with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only a priori biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of
25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
5 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
10 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a
15 plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,674 - 25,129, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in
accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 25,130 - 37,156, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

15 Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e^{-30}$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e^{-30}$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

30 Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by
5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture
10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying
15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the
20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or
30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about
35 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

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As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without

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such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome- 25 derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

 Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

 For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query -
including information on identical sequences and
information on nonidentical sequences that have diffuse or
focal regions of sequence homology to the query sequence -
5 can then be passed directly to process 500, or used to
inform analyses subsequently undertaken in process 200,
process 300, or process 400.

Experimental data, whether obtained by physical
or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data
itself, a process colloquially termed "annotation". Such
annotation can be done using any technique that usefully
relates the functional information to the sequence, as, for
example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or
relational database, by linking to external databases, or
by a combination thereof. Such database techniques are
well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or
displayed 800.

The methods and apparatus of the present
invention rapidly produce functional information from
genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence
annotation produces a need for methods of displaying the
information in meaningful ways.

FIG. 3 shows visual display 80 presenting a
single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic
works of Piet Mondrian, visual display 80 is alternatively
described herein as a "Mondrian".

Each of the visual elements of display 80 is
aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence
5 is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the
10 sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored
15 electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of
20 a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user
25 specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or
30 alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene
35 name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be

20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among

25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of

30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode
5 protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in
10 one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

15 Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray
20 hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently
25 available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
30 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health
35 problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, Prog. Liver Dis. 5 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy 10 findings were very similar, but there were wide differences between families.

Kalra et al., Hum. Hered. 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The 15 hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., New Eng. J. Med. 307:271-277 (1982) described 4 white American sibs who died between 20 ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

25 Cloninger, Science 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both 30 men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and 35 antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL), low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation).

Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary schlerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

 The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

 Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements
5 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10 The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
15 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
20 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
25 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
30 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
35 amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a
5 hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

10 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
15 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

20 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 – 25,129, respectively, for probe SEQ ID NOS. 1 – 12,673. The minimum amount of ORF required to be
25 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 – 25,129 individually by routine experimentation using standard high stringency
30 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
35 poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
15 for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
15 GRAIL uses a neural network, GENEFINDER uses a hidden
Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

20 The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

ORFs predicted by any two of the three programs
("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

15

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution
5 containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,
10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference
20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,
25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

 The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

 To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

 Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present
5 in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

10 Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the
15 observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes
20 from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

25 For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria,
30 approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

35 Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Expressed Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 12,673) and probe exon (SEQ ID NOs.: 12,674 – 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single-exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Fetal liver.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
475	13108	26600	4.41				
922	13635	26053	9.9				
1083	13688		2.9				
1345	13940	28462	10.32				
1650	14248	26782	2.59				
1678	14270	26803	5.03				
1763	14363	26899	1.73				
1785	14375	26919	0.99				
1792	14382	26927	9.24				
1935	14519	27075	1.21				
2021	14603	27188	3.24				
2210	14786	27360	4.38				
2318	14890	27485	2.04				
2607	15169	27735	0.89				
2607	15169	27735	0.89				
3220	15832	28311	1.65				
3498	16101	28678	1.22				
3568	16170	28652	10.28				
3617	16220		0.8				
3718	16319	28787	0.97				
4020	16618		0.84				
4275	16861	29310	1.53				
4348	16935	29376	8.4				
4368	16955	29386	0.74				
4368	16955	29397	0.74				
4430	17016		1.3				
4862	17537	29879	1.04				
5007	17580		0.69				
5054	17627	30071	0.61				
5197	17762	30187	5.95				
5212	17777	30198	1.32				
5462	18097	30415	2.1				
5462	18097	30416	2.1				
5815	18244		5.64				

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	18408		9.03				
5859	18244		4.85				
5910	18532	31257	0.84				
5915	18537	31262	3.18				
6173	24759	31552	1.41				
6200	18810	31579	1.65				
6548	19146		1.28				
6668	19264	32067	1				
6668	19264	32068	1				
7179	19711	32559	1.13				
7179	19711	32560	1.13				
7441	19965	32831	1.4				
7441	19965	32832	1.4				
8005	20547	33451	1.65				
8422	20982	33878	1.45				
8794	21333	34257	0.57				
8794	21333	34258	0.57				
9453	21979	34931	4.84				
9881	22180	35155	0.78				
9795	22294	35277	1.19				
9936	22431	35408	1.03				
10214	22709	35702	0.48				
10214	22709	35703	0.48				
10326	22820	35815	0.65				
10326	22820	35816	0.65				
10563	23088		3.06				
10725	24789	36268	2.48				
10908	23425		2.99				
11238	23769	36827	2.73				
11336	23034	36043	1.87				
11336	23034	36044	1.87				
11374	23826		2.59				
12117	24376		2.19				
12439	24576	30914	1.8				

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	18813	31583	14.37	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 16, 16, 17 and 18
7948	20490	33400	1.65	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9658	22157	35128	0.47	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9658	22157	35129	0.47	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7073	19845	32483	0.8	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7073	19845	32484	0.8	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10319	22813	35808	1.22	9.6E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
10319	22813	35809	1.22	9.6E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2889	15247	27814	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	15247	27815	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2890	15568	28040	3.18	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8042	20584	33481	0.96	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8833	21471	34380	3.48	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5600	18134	30543	2.82	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5600	18134	30544	2.82	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9351	21865	P08241	0.9	9.0E+00	P08241	SWISSPROT	RHODOPSIN
6186	18788	31864	6.12	8.9E+00	BE971808.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834592 3'
6517	19117	31907	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6517	19117	31908	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
486	13098	25580	1.88	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
8378	20315	33217	3.8	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumin-like protease (see2a)
11048	23561		2.47	8.0E+00	P41820	SWISSPROT	BREFELIN A RESISTANCE PROTEIN
8092	20633		0.78	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7384	19810		1.95	7.5E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8302	20843	33764	1.34	7.3E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8302	20843	33765	1.34	7.3E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5888	18589	31324	3.35	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4285508 5'
8888	21227	34147	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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8688	21227	34148	2.63	7.4E+00	P04828	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3008	15822	28098	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3008	16622	28100	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7097	19688	32507	0.7	7.2E+00	BE17090.1	EST_HUMAN	RCO-HT0813-200300-031-407 HT0813 Homo sapiens cDNA
7203	19734	32585	1.22	7.1E+00	P28186	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7203	19734	32586	1.22	7.1E+00	P28186	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9516	22016		7.96	7.1E+00	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11263	23791	36848	3.2	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
8892	23388	36387	3.36	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11226	23637	36678	1.87	7.0E+00	O22489	SWISSPROT	WD-40 REPEAT PROTEIN MSJ3
8226	20766	33684	4.06	6.9E+00	P35878	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10263	22748	35736	1.2	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
7848	20391	33293	1.38	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Sceres melanocyte 2NBHM Homo sapiens cDNA IMAGE:291860 5'
7848	20391	33294	1.38	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Sceres melanocyte 2NBHM Homo sapiens cDNA IMAGE:291860 5'
9080	21597		1.13	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10110	22605	35596	3.85	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5488	18122		0.59	6.6E+00	Q98028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9886	22481	35465	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9896	22481	35466	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11008	23522		2.13	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9108	21844	34584	7.21	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP32; COAT PROTEIN GP33]
10206	22701	35695	0.49	6.5E+00	BE869001.1	EST_HUMAN	801878435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680969 5'
9857	22158	35127	1.11	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
10455	22949	35958	0.53	6.2E+00	6754821	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7102	19872	32511	1.34	6.0E+00	BE780163.1	EST_HUMAN	601488031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
9730	22228	35205	0.46	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (8/7)
10407	22901	35896	0.8	6.0E+00	AE001892.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10407	22901	35897	0.8	6.0E+00	AE001892.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6843	19238	32042	6.97	5.8E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
3578	18180		1.18	5.8E+00	7681557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7215	19746	32601	0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7215	19746	32602	0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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7570	20087		1.31	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11349	23047	38059	2.68	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
6399	18002	31760	0.73	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10658	23190		1.94	5.5E+00	AF176426.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11348	23048	38058	3.79	5.5E+00	P11890	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
11578	24024		2.08	5.6E+00	AL161671.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
7009	19507	32326	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7009	19507	32327	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7369	19895		0.72	5.4E+00	Q69436	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
7811	20364		1.58	5.4E+00	Q91082	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8734	21273	34193	0.78	5.4E+00	P40379	SWISSPROT	REPT PROTEIN
8734	21273	34194	0.78	5.4E+00	P40379	SWISSPROT	REPT PROTEIN
9949	22444	35423	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
8949	22444	35424	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4899	17474	29830	1.52	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6614	19211		0.67	5.3E+00	P41779	SWISSPROT	HOMEBOX PROTEIN CEH-20
8024	20666		3.71	5.3E+00	P64098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8914	21452		0.62	5.3E+00	AB034980.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5655	18282		1.04	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0891-270400-186-109 HT0891 Homo sapiens cDNA
10274	22769		0.78	5.2E+00	AF248070.1	NT	Drosophila orientalis R18 retrotransposable element reverse transcriptase gene, partial cds
11074	23586		2.1	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03G IN CHROMOSOME 1
8892	21430	34354	0.88	5.1E+00	O16005	SWISSPROT	RHODOPSIN
9739	22237	35217	0.97	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6430	19033	31817	0.85	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4124114 5'
10088	22591		0.69	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131508 5'
10327	22821	35817	3.37	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11170	23677	36723	13.64	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/182
10131	22626		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4135	16727		12.06	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8095	20638	33547	0.85	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-p10 GN0042 Homo sapiens cDNA
8478	21017		4.86	4.8E+00	AW1750087.1	EST_HUMAN	PMD-BT0547-310100-002-604 BT0547 Homo sapiens cDNA

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311	12866	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
312	12968	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3312	15923	28389	1.08	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C80
9124	21659	34601	1.09	4.6E+00	BE848437.1	EST_HUMAN	7689g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292088 3' similar to TR:O75140 O75140
9124	21659	34602	1.09	4.6E+00	BE848437.1	EST_HUMAN	KIAA0645 PROTEIN; contains element PTR5 repetitive element;
10280	22786		0.77	4.6E+00	AF240786.1	NT	7689g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292088 3' similar to TR:O75140 O75140
11474	23924	36994	1.89	4.5E+00	AE001044.1	NT	KIAA0645 PROTEIN; contains element PTR5 repetitive element;
11598	24039	37108	1.67	4.5E+00	BF69894.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3076	15891	28184	1.53	4.4E+00	BF630893.1	EST_HUMAN	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3076	15891	28185	1.53	4.4E+00	BF630893.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
6349	18954		1.8	4.4E+00	X13414.1	NT	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6268	18874		0.82	4.3E+00	AF058679.1	NT	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
7484	19896	32851	2.36	4.3E+00	Y13402.1	NT	Murine I gene for MHC class II (Ia) associated invariant chain
7611	20124	33001	0.84	4.3E+00	AE001222.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
10741	23266	36282	8.92	4.3E+00	AF240786.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
5708	18334		3.21	4.2E+00	P18444	SWISSPROT	Trepennia pallidum section 38 of 87 of the complete genome
5780	18405	31121	1.46	4.2E+00	P51826	SWISSPROT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
6869	19603	32435	1.86	4.2E+00	P13983	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
6869	19603	32436	1.86	4.2E+00	P13983	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
8880	21428	34353	4.95	4.2E+00	A180913.1	EST_HUMAN	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9832	22330	35312	2.07	4.2E+00	P31388	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
7168	18698	32545	0.81	4.1E+00	BE253668.1	EST_HUMAN	w67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
7284	19792	32648	1.7	4.1E+00	BF247939.1	EST_HUMAN	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
7657	20189	33058	8.1	4.1E+00	O23810	SWISSPROT	60111072F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33351534 5'
7759	20287	33163	4.03	4.1E+00	P28964	SWISSPROT	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4086758 5'
7759	20287	33164	4.03	4.1E+00	P28964	SWISSPROT	YY1 PROTEIN PRECURSOR
7857	20399	33306	2.78	4.1E+00	U57503.1	NT	GENE 68 PROTEIN
8459	21885	34938	0.63	4.1E+00	P11253	SWISSPROT	GENE 68 PROTEIN
9590	22090	35054	2.26	4.1E+00	BF692425.1	EST_HUMAN	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
							50S RIBOSOMAL PROTEIN L4
							602247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:433208 5'

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10208	22703		0.5	4.1E+00	P48414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
10499	22893	36003	0.62	4.1E+00	O84242	SWISSPROT	3-OXOACYL-JACYL-CARRIER-PROTEIN SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
10765	23289		2.97	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVL1
10851	23372		13.84	4.1E+00	BE86880.1	EST_HUMAN	601607510FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808031 5'
3599	18203		0.82	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5650	19515	32336	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5650	19515	32337	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7017	19515	32338	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7017	19515	32337	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7240	19769	32625	1.34	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10070	22565	35560	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10158	22653	35647	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10158	22653	35648	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11423	23974	36937	3.99	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11423	23974	36938	3.99	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3550	18154	28636	4.79	3.9E+00	X64518.1	NT	N.labacum chitinase gene 50 for class I chitinase C
4413	18998		0.74	3.9E+00	AF055488.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5839	18463	31186	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5839	18463	31187	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6746	18039	32145	0.71	3.9E+00	AF298209.1	NT	Dictyostellium discoideum non-L TR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6792	18083	32198	0.72	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
6855	18532	32357	4.12	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7388	18923	32787	6.09	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPW4-beta-1) gene, exon 2

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8269	20900	33718	2.16	3.9E+00	X65985.1	NT	Xlaevis mRNA for M4 muscarinic receptor
11289	23007	36014	3.27	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11291	23743	36900	1.62	3.9E+00	AA691489.1	EST_HUMAN	nt18a12.e1 NCJ_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2668	16217		1.1	3.8E+00	AE001582.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
6826	19126	31918	0.78	3.8E+00	Q57830	SWISSPROT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
8371	20911	33831	1.06	3.8E+00	D44725.1	EST_HUMAN	HYPOTHETICAL PROTEIN MJ0386
9710	22208		0.55	3.8E+00	A1360981.1	NT	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
4092	16697	28144	13.66	3.7E+00	AL181839.2	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NGTC7864
7218	19749		0.79	3.7E+00	AL445065.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
						NT	Thermoplasma acidophilum complete genome; segment 3/5
						NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
8842	21181		0.53	3.7E+00	4503950	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
9108	21841	34581	0.88	3.7E+00	U43541.1	NT	602120551F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36881	3.11	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36882	3.11	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4277748 5'
11767	24159		1.28	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
619	13248	25719	2.6	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 6'
4817	17492		0.99	3.6E+00	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
8487	21026	33942	0.78	3.6E+00	D12387.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8487	21026	33943	0.78	3.6E+00	D12387.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8879	21118	34038	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8579	21118	34039	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
10793	23259		4.32	3.6E+00	M69795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3284	15895	28373	1.08	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6151	18784		1.08	3.5E+00	L42888.1	NT	y940c08.t1 Soares Infant brain T1N1B Homo sapiens cDNA clone IMAGE:34940 5'
6360	18984	31742	0.92	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8421	20981		0.55	3.5E+00	P24557	SWISSPROT	z986b04.s1 Straligene HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8862	21500	34421	0.88	3.5E+00	AA180988.1	EST_HUMAN	z986b04.s1 Straligene HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8862	21500	34422	0.88	3.5E+00	AA180988.1	EST_HUMAN	z986b04.s1 Straligene HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9414	21923	34872	1.12	3.5E+00	AL181553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1659	14151	28883	4.49	3.4E+00	AF254577.1	NT	Brassica napus RP85d mRNA, complete cds
2812	15174	27742	1.02	3.4E+00	AL18278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7397	19922	32786	2.85	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7890	20198	33088	0.88	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8611	21150		0.89	3.4E+00	U85408.1	NT	Human alternatively spliced poliovirus channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
8003	21540	34470	0.7	3.4E+00	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9040	21577	34508	0.5	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 8
10185	22850	38855	3.61	3.4E+00	AF013187.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11408	23857	38922	1.98	3.4E+00	L77670.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
6218	18828	31601	0.9	3.3E+00	Q08889	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31602	0.9	3.3E+00	Q08889	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7834	20376	33281	0.88	3.3E+00	AF111186.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	22855	35847	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	22855	35848	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
628	13158	25640	1.72	3.2E+00	X98422.1	NT	D. rerio xp-50 POU gene
4098	13158	25640	0.7	3.2E+00	X98422.1	NT	D. rerio xp-50 POU gene
4836	17413	28888	1.24	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5757	18383	31085	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5757	18383	31086	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5787	18412	31129	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6448	19049	31834	1.88	3.2E+00	P18831	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6448	19049	31835	1.88	3.2E+00	P18831	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7601	20114	32891	0.84	3.2E+00	P04276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7760	20258	33154	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7750	20258	33155	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8980	21498	34927	4.84	3.2E+00	P13081	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9449	21975	34927	1.52	3.2E+00	M38383.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
10047	22542	35539	1.91	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC8 gene for guanidyl cyclase C, complete cds
11727	24193		4.08	3.2E+00	L39386.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
6035	18654	31386	2.24	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.6 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7421	18845	32810	0.97	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7711	20220		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus peptidylase (pelE) gene, complete cds
8538	21077	33995	4.27	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 5'DEIODINASE) (DIO1) (TYPE 1 D1) (5D1)
8538	21077	33998	4.27	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 5'DEIODINASE) (DIO1) (TYPE 1 D1) (8D1)
9183	21780		3.77	3.1E+00	Q14967	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9249	21776	34728	0.52	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9810	22303	35292	0.75	3.1E+00	7624758	NT	Chlorella vulgaris chloroplast, complete genome
9899	22396		0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F82C9.6 IN CHROMOSOME III
10239	22734	35728	4.7	3.1E+00	P49385	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
11338	23036		2.91	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11355	23809		7.48	3.1E+00	S56860.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, POC7-MZ1, mRNA, 2871 nt]
12490	24619		1.38	3.1E+00	U77663.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds
5641	18173	30588	1.88	3.0E+00	X63098.1	NT	S. aureus genes encoding Sau981 DNA methyltransferase and Sau981 restriction endonuclease
6873	19289	32073	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6873	19289	32074	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7209	19740		10.44	3.0E+00	P18403	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7247	19776		0.77	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8838	21377		1.33	3.0E+00	X67838.1	NT	B. napus DNA for mycelinase
10185	22690	35983	0.83	3.0E+00	Q68805	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10527	23084	36075	1.82	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
10888	23409	38428	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409						RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409	38427	7.04	3.0E+00	P51842	SWISSPROT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
2055	14638	27207	2.32	2.9E+00	AE002225.2	NT	Bonaparita pedicularis mitochondrial DNA for 16S ribosomal RNA
6224	18533		0.88	2.9E+00	AB026033.1	NT	F. pringii gdcA gene for P-protein of the glycine cleavage system
6989	19487	32309	3.74	2.9E+00	Z36879.1	NT	
7262	19780	32844	4.37	2.9E+00	Q14314	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
7262	19790	32646	4.37	2.8E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7479	20001	32868	6.04	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7809	20382	33260	0.87	2.8E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7809	20382	33261	0.87	2.8E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8041	20563	33490	0.89	2.8E+00	BF344171.1	EST_HUMAN	602017413F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4163058 5'
1504	14096	28634	4.87	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1875	14287		3.45	2.8E+00	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7348	18874	32740	4.88	2.8E+00	8383724	NT	Mus musculus endomucin (LOC53423), mRNA
9531	22031		0.57	2.8E+00	BE568182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10569	19874	32740	1.88	2.8E+00	8383724	NT	Mus musculus endomucin (LOC53423), mRNA
251	12911	25394	9.31	2.7E+00	66793008	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
251	12911	25395	9.31	2.7E+00	66793008	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
6740	18398	31073	1.2	2.7E+00	L14006.1	NT	Homo sapiens apcA polymorphism Kringle IV gene, exons 1 and 2
8098	20628		0.8	2.7E+00	U15947.1	NT	Iporoba purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8898	21436		1.68	2.7E+00	AL116459.1	NT	Bethyda cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9353	20292	33191	0.63	2.7E+00	AW088101.1	EST_HUMAN	xc88612X1 NCL CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:U17733
10364	22898		1.48	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4781	17362	28812	4.97	2.6E+00	AF068749.1	NT	CM0-BT0281-031198-087-p04 BT0281 Homo sapiens cDNA
5738	18382	31068	1.94	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5738	18382	31069	1.94	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5892	18812		2.42	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7689	20198		5.98	2.6E+00	AF235602.1	NT	Mycobacterium fortitum furA II gene
8003	20545	33447	1.08	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing Inositol 5-phosphatase (SHIP) gene, exons 16 through 27, and complete cds
8003	20545	33448	1.08	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
9576	22076	35039	3.02	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
10257	22762		1.51	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10807	23428	36443	1.69	2.6E+00	AF143676.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12390	24898		2.78	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1513	14105	28640	2.29	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1513	14105	28641	2.28	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1513	14105	28641	2.28	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5981	18601	31334	1.71	2.5E+00	P13486	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5981	18601	31336	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5986	18601	31334	1.39	2.6E+00	P13486	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5986	18601	31336	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6826	19416	32234	0.73	2.6E+00	D3032.1	NT	Vibrio cholerae cba gene and cbaB gene for cholera toxin, complete cds
7736	20244	33136	1.06	2.9E+00	AW949158.1	EST_HUMAN	QV4-F70005-110500-205-007 F70005 Homo sapiens cDNA
9032	21568	34468	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9766	22264	35247	0.88	2.6E+00	BE287758.1	EST_HUMAN	601176778F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531080 5'
11724	24131		1.66	2.5E+00	AF289885.1	NT	Mus musculus EIF4H gene, partial cds; LMK1 gene, complete cds; and ELN gene, partial cds
3047	16663	28144	0.8	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' and
5033	17607	30052	6.78	2.4E+00	4603352	NT	Homo sapiens double C2-like domain, alpha (DOC2A) mRNA
6161	18774	31538	4.02	2.4E+00	P02843	SWISSPROT	VITELLOGENIN1 PRECURSOR (YOLK PROTEIN 1)
8082	20624	33536	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8082	20624	33537	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8183	20604		2.33	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8585	21124		1.62	2.4E+00	AW876126.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
8762	21301	34222	8.16	2.4E+00	P24081	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9951	22446	35427	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9951	22446	35428	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10017	22512	35504	1.62	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
10141	22636		7.38	2.4E+00	P08099	SWISSPROT	XYLOSE KINASE (XYLOKINASE)
10225	22720	35710	1.63	2.4E+00	BE328702.1	EST_HUMAN	hr6306.x1 NCLCGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10225	22720	35711	1.63	2.4E+00	BE328702.1	EST_HUMAN	hr6306.x1 NCLCGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10483	22977	35886	1.27	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
10958	23473	36498	1.68	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
11237	23768	36826	2.27	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1298	13890	26413	11.15	2.3E+00	Z48724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4189	18786		1.65	2.3E+00	AJ401081.1	NT	Bos taurus partial cyto gene for cytochrome b
6000	18620		0.91	2.3E+00	N86245.1	EST_HUMAN	J7940F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7477	18999	32864	2.54	2.3E+00	8678554	NT	PROLYCABOXYPEPTIDASE
7593	25120		4.61	2.3E+00	P07189	SWISSPROT	Rattus norvegicus ATPase, Cav++ transporting, ubiquitous (Atp2a3), mRNA
7758	20264	33159	1.06	2.3E+00	X60265.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
							M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9036	21575	34505	0.83	2.3E+00	9635317	NT	Polyturus ornithipirnis mitochondrion, complete genome
9097	21633	34572	1.79	2.3E+00	Q11127	SWISSPROT	ALPHA(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10681	23213	36224	2	2.3E+00	Q07076	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
11612	24055	37119	2.92	2.3E+00	BF541987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
11612	24055	37120	2.62	2.3E+00	BF541987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
11950	24278	31020	7.31	2.3E+00	BE885237.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
4089	16685	29143	91.07	2.2E+00	AF020528.1	NT	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4403	16888	29432	4.6	2.2E+00	D67071.1	NT	Magnaporthe oryzae Class IV chitin synthase (chs4) gene, complete cds
4403	16888	29433	4.5	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							Rat gene for regucalcin, exon1 (non-coding exon)
5545	18177	30591	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5545	18177	30592	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
6016	18635	31373	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022+08 CT0254 Homo sapiens cDNA
6016	18635	31374	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022+08 CT0254 Homo sapiens cDNA
6212	18822	31593	9.1	2.2E+00	BE250383.1	EST_HUMAN	600843401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2969777 3'
6495	18096	31880	4.32	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6709	19303	32107	3.04	2.2E+00	P61459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7037	18057		3.58	2.2E+00	AA584574.1	EST_HUMAN	nr5502.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058378 3'
7358	18884	32747	0.9	2.2E+00	AA137027.1	EST_HUMAN	zn97704.11 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7602	20115	32892	25.23	2.2E+00	AA446012.1	EST_HUMAN	zn05g10.11 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
8046	20588	33494	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8046	20588	33495	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9265	21791		12.17	2.2E+00	BE741878.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9488	24783		2.57	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
9986	22461	35443	1.96	2.2E+00	A1280373.1	EST_HUMAN	qm69b03.x1 Soares placenta_8to6weeks_2NbHP8c9w Homo sapiens cDNA clone IMAGE:1893985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9886	22481	35444	1.98	2.2E+00	A1200373.1	EST_HUMAN	qm98603.x1 Soares_placenta_8to9weeks_2NHP8c8W Homo sapiens cDNA clone IMAGE:1883986 3'
10008	22503	35494	3.7	2.2E+00	BF248782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10363	22847	35841	2.99	2.2E+00	AF183416.1	NT	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
11316	23014	36023	4.01	2.2E+00	P07011	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11482	23932	37003	4.23	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
595	18419	28689	6.28	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3848	18251		0.65	2.1E+00	AW449388.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6281	18889		0.85	2.1E+00	P76367	SWISSPROT	U1-H-B13-aki-e-08-Q-U1.st NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6889	19633	32471	3.38	2.1E+00	O70159	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
7110	19480	32288	5.13	2.1E+00	N29575.1	EST_HUMAN	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
8434	20974		2.27	2.1E+00	AU123630.1	EST_HUMAN	W08a10.s1 Soares_melanocytes_2NBM Homo sapiens cDNA clone IMAGE:270818 3' similar to gb:M55654
10454	22848		0.58	2.1E+00	Y10284.1	NT	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1238	13836	26352	1.3	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1238	13836	26353	1.3	2.0E+00	AF180527.1	NT	H.sapiens TRAF1 gene, putative promoter region
1380	13973	26501	0.92	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1619	14212		2.89	2.0E+00	P25582	SWISSPROT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
2194	14770	27343	3.69	2.0E+00	Z78279.1	NT	Oryctolagus cuniculus Net-K-ATPase beta 1 subunit mRNA, complete cds
2194	14770	27344	3.69	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
4176	18787	28215	1.9	2.0E+00	AW684486.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
4176	18787	28216	1.9	2.0E+00	AW684486.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
7552	20071		0.77	2.0E+00	P07588	SWISSPROT	h13c05.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872188 3' similar to gb:X01877
7987	20509	33415	3.58	2.0E+00	AB008876.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7987	20509	33416	3.58	2.0E+00	AB008876.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7987	20509	33417	3.58	2.0E+00	AB008876.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
8853	21382	34314	3.52	2.0E+00	F31500.1	EST_HUMAN	GLYCOPROTEINS E1 AND E2
12295	24946	30622	7.77	2.0E+00	5834843	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
5784	18409	31124	6.89	1.9E+00	8754389	NT	Escherichia coli 0157 DNA, map position at 49 min., complete cds
5784	18409	31125	6.89	1.9E+00	8754389	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
6249	18858	31630	1.2	1.9E+00	BE968995.1	EST_HUMAN	HSPD22703 HK3 Homo sapiens cDNA clone s4000117B08
							Gallus gallus mitochondrion, complete genome
							Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
							Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
							601879836F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6780	19353		1.02	1.8E+00	AW845989.1	EST_HUMAN	MR0-CT0083-071089-002-p02 CT0083 Homo sapiens cDNA
6845	19436		2.31	1.8E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8386	20936	33858	2.18	1.8E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8398	20936	33859	2.16	1.8E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8593	21132		2.45	1.8E+00	BF380208.1	EST_HUMAN	GM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8825	21364		1.35	1.8E+00	O81781	SWISSPROT	ARGININE DEIMINASE (ADI)(ARGININE DIHYDROLASE)(AD) ab94404.s1 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
9548	22048	35009	0.8	1.8E+00	AA699126.1	EST_HUMAN	Homo sapiens gag-pro-pol precursor protein gene, partial cds
10456	22950	35959	0.52	1.8E+00	AF249288.1	NT	PROTEIN B8 PRECURSOR
3128	15742	28211	1.88	1.8E+00	P21004	SWISSPROT	Synechococcus sp. PCC7842 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3184	15788	28234	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7842 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15788	28235	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7842 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6027	18846		2.02	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6263	18992	31634	2.02	1.8E+00	BF311989.1	EST_HUMAN	601807854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
6532	19132		1.53	1.8E+00	BF68327.1	EST_HUMAN	602139470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5'
6838	19428	32244	1.35	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7119	19459	32274	1.08	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8080	20602	33512	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8080	20602	33513	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8788	21327	34252	2.12	1.8E+00	O43281	SWISSPROT	EMBRYONAL FN-ASSOCIATED SUBSTRATE (HEFS)
9102	21638	34577	0.63	1.8E+00	R31042.1	EST_HUMAN	YH72508.1 Scars placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9186	21703	34645	0.8	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-148-e03 OT0030 Homo sapiens cDNA
9783	22281	35244	0.87	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22678		3.78	1.8E+00	AF111848.1	NT	Homo sapiens PRO5530 mRNA, complete cds
10447	22841		0.85	1.8E+00	P44326	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE)(CDA)
12075	24915		8.65	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12163	24403		4.98	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
12478	24815	30760	1.38	1.8E+00	BF121412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	13760	28259	2.08	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2311	14893	27488	2.37	1.7E+00	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2411	14879	27554	1.29	1.7E+00	A1141067.1	EST_HUMAN	cd43h05.x1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4568	17141	26589	0.74	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5797	18422	31137	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171269-127-405 BT0282 Homo sapiens cDNA
5797	18422	31139	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171269-127-405 BT0282 Homo sapiens cDNA
6168	18760	31545	3.36	1.7E+00	Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
7270	18768	32654	1.33	1.7E+00	Q93703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7270	18768	32655	1.33	1.7E+00	Q93703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7308	19834	32693	1.63	1.7E+00	P20393	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA)
7796	20339	33247	0.98	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7978	20518	33426	1.34	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
8096	20548	33452	0.57	1.7E+00	BF630630.1	EST_HUMAN	602071917F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4214689 5'
8479	21018	33633	0.61	1.7E+00	AF246513.1	NT	Hippoglossus hippoglossus interferon inducible hb protein (hb) mRNA, complete cds
8582	21101		2.08	1.7E+00	BF508000.1	EST_HUMAN	601894256F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8638	21177	34096	0.49	1.7E+00	X69083.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
8638	21177	34097	0.49	1.7E+00	X69083.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9076	24792	34545	2.25	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9076	24792	34546	2.28	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9524	22024		1.65	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
11497	23917	36865	2.16	1.7E+00	W22424.1	EST_HUMAN	tu82607.x1 NCI_CGAP_Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12030	24320	30963	1.62	1.7E+00	A1678443.1	EST_HUMAN	tu82607.x1 NCI_CGAP_Gaa4 Homo sapiens cDNA clone IMAGE:2267649 3' similar to contains MSR1.11
12558	24659	30873	1.79	1.7E+00	A198573.1	EST_HUMAN	MSR1 repetitive element;
2078	14658	27229	21.82	1.6E+00	AF186339.1	NT	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1
2087	14688	27238	4.3	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2093	14673	27243	1.04	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2323	14894		1.13	1.6E+00	X98373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2886	15604	28084	1.5	1.6E+00	W58426.1	EST_HUMAN	B.napus gene encoding endo-polygalacturonase
4104	16698		7.23	1.6E+00	BF570077.1	EST_HUMAN	z42507.1.r1 Soares_fetal_heart_NihHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D26805 N-ACETYL-LACTOSAMINE SYNTHASE (HUMAN);
							602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310581 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4444	17030	29470	1.11	1.6E+00	AF159827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA8) mRNA, complete cds
4444	17030	29471	1.11	1.6E+00	AF159827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA8) mRNA, complete cds
9148	17715	30148	0.8	1.6E+00	AF076394.1	NT	Utricularia chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
9148	17715	30148	0.8	1.6E+00	AF076394.1	NT	Utricularia chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5993	18813	31347	1.95	1.6E+00	L04808.1	NT	Breathydenio ratio MHC class II DA-beta-2'01 gene, 3' end
6072	18889	31434	0.92	1.6E+00	AF005831.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6598	19183	31998	0.93	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6811	19402	32218	1.07	1.6E+00	AW204881.1	EST_HUMAN	UI-H-812-ahr-b-04-0-U1.s1 NCJ_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:27275113'
7293	19821	32680	2.32	1.6E+00	BE687287.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7973	20515		1.09	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8320	20881	33786	3.24	1.6E+00	AJ287131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SGL & CYP_b genes
8831	21370	34284	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8831	21370	34295	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9381	24790	33221	3.16	1.6E+00	X52048.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9381	24790	33222	3.16	1.6E+00	X52048.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9648	22148	35119	1.34	1.6E+00	T41260.1	EST_HUMAN	ph888_19/1TV Outward Alu-primed hmcDNA library Homo sapiens cDNA clone ph888_19/1TV
10052	22547	35541	0.52	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (IAL), and zinc finger protein (DNZ1) genes, complete cds
10088	22593	35575	0.92	1.6E+00	AW835844.1	EST_HUMAN	QV4-L T0016-080200-100-407 L70016 Homo sapiens cDNA
10088	22593	35576	0.92	1.6E+00	AW835844.1	EST_HUMAN	QV4-L T0016-080200-100-407 L70016 Homo sapiens cDNA
10248	22741	35731	0.49	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10650	23182	38168	1.99	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10688	23216	38228	1.56	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10723	18889	31434	6.41	1.6E+00	AF005831.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
11552	24000	37072	2.92	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
35	12714	25173	4.02	1.5E+00	U53448.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
252	12912	25398	2.17	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 84 of the complete genome
649	13272		1.98	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardin) (Adam15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1880	14544	27101	2.55	1.5E+00	AF27265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptpn) gene, exons 10 and 11 and partial cde
2454	15021	27592	2.13	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2556	15120	27690	1.83	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3172	15021	27592	1.84	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3421	16029	28510	0.7	1.5E+00	AE001845.1	NT	Dracontococcus radiodurans R1 section 82 of 228 of the complete chromosome 1
5903	18525	31250	0.94	1.5E+00	A1855301.1	EST_HUMAN	HKF-1.;
5903	18525	31251	0.94	1.5E+00	A1855301.1	EST_HUMAN	HKF-1.;
6538	19137	31650	2.88	1.5E+00	R17878.1	EST_HUMAN	Y91062.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7182	19714		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3881555 5'
7214	19745	32599	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7383	18608	32774	1.02	1.5E+00	AA889259.1	EST_HUMAN	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
8085	20607	33519	0.85	1.5E+00	BE887446.1	EST_HUMAN	alc28f10.s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1407115 3'
8578	21117	34037	1.1	1.5E+00	K02138.1	NT	601609586F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3911181 5'
8949	21494		0.53	1.5E+00	A8038516.1	NT	Mouse germline IgM chain gene, mu-delta region
9081	21598	34528	0.54	1.5E+00	BF217818.1	EST_HUMAN	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9404	21913	34892	0.9	1.5E+00	R81928.1	EST_HUMAN	601882632F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4085135 5'
9553	22053	35018	1.12	1.5E+00	AW375697.1	EST_HUMAN	Y03101.1 Scores placenta NB21P Homo sapiens cDNA clone IMAGE:147697 5'
9774	22272	35257	5.97	1.5E+00	BF376754.1	EST_HUMAN	QV3-CT0192-281099-008-009 CT0192 Homo sapiens cDNA
9885	22460		1.47	1.5E+00	BF337844.1	EST_HUMAN	RCO-TN0078-150900-034-005 TN0078 Homo sapiens cDNA
10088	22583	35585	2.95	1.5E+00	AA017689.1	EST_HUMAN	602035771F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4183885 5'
10098	22593	35596	2.95	1.5E+00	AA017689.1	EST_HUMAN	z838g08.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361308 5'
11277	23730	36785	4.1	1.5E+00	AL134197.1	EST_HUMAN	z838g09.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361308 5'
11416	23887		8.57	1.5E+00	X07380.1	NT	DKFZp547P243_s1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P243 3'
12022	25010	30615	1.59	1.5E+00	D83480.1	NT	Maize mitochondrial rRNA-Ser gene and rRNA-Phe pseudogene
12255	24465		4.99	1.5E+00	AL445065.1	NT	Human mRNA for KIAA0149 gene, partial cds
32	12711	25169	1.8	1.4E+00	7681685	NT	Thermoplasma acidophilum complete genome; segment 3/5
32	12711	25170	1.8	1.4E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1774	14384	26809	1.32	1.4E+00	H1989.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2316	14898		0.88	1.4E+00	AF053357.1	NT	Yn57603.r1 Scores adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172540 5'
2372	14942		7.8	1.4E+00	U87822.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
							Ovis aries prion protein gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2693	15250	27820	1.45	1.4E+00	X7463.1	NT	Human papillomavirus type 7 genomic DNA
2802	16364	27922	2.79	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2802	16354	27823	2.79	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3376	15985		0.68	1.4E+00	5463733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4342	16928	28368	1.14	1.4E+00	AW900455.1	EST_HUMAN	GM0-NIN1005-140300-288-h08 NN1005 Homo sapiens cDNA
4342	16928	28370	1.14	1.4E+00	AW900455.1	EST_HUMAN	GM0-NIN1005-140300-288-h08 NN1005 Homo sapiens cDNA
4885	17287		1.78	1.4E+00	BF081547.1	EST_HUMAN	602166887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287558 5'
5875	18206	30687	1.78	1.4E+00	AW054978.1	EST_HUMAN	wt45g07.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2510460 3'
5719	18345		6.04	1.4E+00	AB032883.1	NT	Homo sapiens mRNA for KIAA1187 protein, partial cds
6425	19028	31811	2.73	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6437	26116		4.4	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds
6544	19143	31936	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6544	19143	31937	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6583	19181	31981	0.67	1.4E+00	11098333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6911	19570	32388	0.77	1.4E+00	AW83057.1	EST_HUMAN	GM3-NIN006-300300-132-b12 NN0006 Homo sapiens cDNA
7330	19867	32720	2.31	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7343	19870	32735	1.1	1.4E+00	AW497760.1	EST_HUMAN	hs23105.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2818873 3' similar to contains Alu repetitive element;
8277	20818		0.68	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8728	21268		4.01	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9023	21560	34487	2.13	1.4E+00	R20458.1	EST_HUMAN	yg33f12.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9126	21680	34803	3.72	1.4E+00	BE084867.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9158	21693	34637	0.58	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10109	22604	35594	0.77	1.4E+00	BF575543.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10160	22846	35637	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0188-281099-008-C04 HT0188 Homo sapiens cDNA
10150	22845	35638	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0188-281099-008-C04 HT0188 Homo sapiens cDNA
10418	22812	35912	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10418	22812	35913	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10948	23463	36485	2.18	1.4E+00	AA195528.1	EST_HUMAN	zr38e09.1 Scores NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11104	23814	38654	6.28	1.4E+00	AB006882.1	NT	Homo sapiens APECE1 mRNA for AIRE-1, complete cds
11283	23736	38781	3.92	1.4E+00	BE982107.2	EST_HUMAN	601855194R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11283	23736	38782	3.92	1.4E+00	BE982107.2	EST_HUMAN	601855194R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11304	23797	38855	3.19	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11304	23797	38856	3.19	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11865	24935		2.43	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12287	25108		2.38	1.4E+00	11548638	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA
508	13225		1.38	1.3E+00	Z73840.1	NT	Mus musculus gene encoding 4-Dihydroxyethyl-trisphosphate dehydrogenase
935	13548	28085	2.33	1.3E+00	AJ271192.1	NT	Carthartellus sp. partial 25S rRNA gene, isolate Tibet
1188	13770		22.19	1.3E+00	Y10213.1	NT	Homo sapiens putative psithrba pseudogene for hair keratin, exons 2 to 7
1340	13835	28458	13.67	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1340	13835	28457	13.67	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1400	13884		1.05	1.3E+00	U61730.2	NT	Cdx lacryme-jcb dihydrodipicolinate synthase (dapa) gene, complete cds
1653	14245		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 88 of 85 of the complete genome
2285	14859		1.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2586	15149		0.97	1.3E+00	BE968735.2	EST_HUMAN	601861233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2866	15581	28080	0.66	1.3E+00	8755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3657	16260	28732	0.81	1.3E+00	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c
4713	15581	28080	1.31	1.3E+00	8755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5705	18331	30835	1.08	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
6160	18781	31546	7.47	1.3E+00	AW382834.1	EST_HUMAN	PMO-CT0289-281189-004-708 CT0289 Homo sapiens cDNA
6169	18781	31547	7.47	1.3E+00	AW382834.1	EST_HUMAN	PMO-CT0289-281189-004-708 CT0289 Homo sapiens cDNA
6549	19147	31943	1.24	1.3E+00	M33486.1	NT	D melanogaster no-on-transient A gene product, complete cds
6847	19437		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 84 PROTEIN
8928	19585	32415	0.85	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA6) mRNA, partial cds
7033	19587	32394	1.01	1.3E+00	BE538819.1	EST_HUMAN	601081420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7157	19689	32593	0.79	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7481	20003	32888	3.97	1.3E+00	P24640	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATASE)
8239	20760	33701	2.08	1.3E+00	AJ009912.1	NT	Sus scrofa pig gene
8394	20924	33844	2.54	1.3E+00	BE663376.2	EST_HUMAN	601687145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
8498	21035	33956	0.89	1.3E+00	BE974280.1	EST_HUMAN	601680260R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950632 3'
8844	21183		1.57	1.3E+00	6910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8725	21264	34184	0.88	1.3E+00	AB27629.1	EST_HUMAN	w855a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
8073	21610	34540	0.48	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NBH8st Homo sapiens cDNA clone IMAGE:183078 3'
6073	21610	34541	0.48	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NBH8st Homo sapiens cDNA clone IMAGE:183078 3'
9434	21660		4.54	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9443	21668	34917	2.12	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9443	21669	34918	2.12	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9542	22042	35003	1.1	1.3E+00	AF050260.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
9598	22088	35052	1.62	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9685	22184	35137	1.21	1.3E+00	AB27629.1	EST_HUMAN	w855a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
9740	22238	35218	0.83	1.3E+00	AJ223882.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal Inversion Junction DNA
9740	22238	35219	0.83	1.3E+00	AJ223882.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal Inversion Junction DNA
6780	22278	35263	3.85	1.3E+00	BE663376.2	EST_HUMAN	601687145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
10114	22609	35600	1.26	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10130	22625	35615	2.41	1.3E+00	M29653.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10476	22970		0.65	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10504	22998		0.52	1.3E+00	8923637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
10507	23001	36008	0.48	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NBH8st Homo sapiens cDNA clone IMAGE:183078 3'
10507	23001	36009	0.48	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NBH8st Homo sapiens cDNA clone IMAGE:183078 3'
10573	23108		4.68	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
10785	23309	36316	2.3	1.3E+00	P25298	SWISSPROT	MIRNA 3'-END PROCESSING PROTEIN RNA15
10807	23330	36342	2.17	1.3E+00	Z18892.2	NT	Mus musculus deamin gene
11216	23718		1.87	1.3E+00	AW274791.1	EST_HUMAN	xp09603.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2738698 3'
11414	23865	36926	3.09	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11488	23937	37007	3.09	1.3E+00	Z88682.1	NT	Bacillus subtilis genomic DNA 23.6kb fragment
12011	24312		3.63	1.3E+00	AF187873.1	NT	CaMa porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds

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12192	24423	30948	3.47	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NC1 CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158462 5'
12204	24826		1.78	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12303	24500		2.08	1.3E+00	AF187035.1	NT	Stumra liliium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
12873	24904		1.26	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
678	13302	25784	0.76	1.2E+00	AA878248.1	EST_HUMAN	Z22d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
856	13472	25983	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
856	13472	25984	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
856	13472	25985	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
911	13524		1.9	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1203	13803	26316	4.87	1.2E+00	AF080248.2	NT	Eleis oleifera sesquiterpene synthase mRNA, complete cds
1247	13844	26361	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1247	13844	26362	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2054	14635	27206	63.59	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
2417	14885	27559	1.63	1.2E+00	AF156485.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3144	15768	28224	1.18	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3201	15813	28287	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3201	15813	28288	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3326	15936		3.43	1.2E+00	P64910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3399	16007	28489	0.97	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3774	16374	28839	8.68	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4058	16865	28121	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-050800-203-g08_1 FT0175 Homo sapiens cDNA
4386	18007	28489	1.12	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4570	17163		2.09	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4621	17204	29653	1.08	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4659	17241	29695	1.6	1.2E+00	AF158485.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4690	17272		9.41	1.2E+00	Y08200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4701	18008		0.77	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
5628	18258	30729	1.08	1.2E+00	U20780.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5743	18369	31077	2.27	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6034	18653	31395	0.72	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF181 (ZNF181) gene, complete cds
6300	18908	31678	2.17	1.2E+00	X74885.1	NT	D.hydral ey1 repeat cluster DNA, fragment D
6351	18665	31743	3.98	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-190-e03 BN0080 Homo sapiens cDNA
6433	19038	31822	1.43	1.2E+00	X89084.1	NT	C.glutamicum pls gene and ackA gene
6433	19038	31823	1.43	1.2E+00	X89084.1	NT	C.glutamicum pls gene and ackA gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6476	19076	31859	34.96	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares, testis_NHT Homo sapiens cDNA clone 1322374 3'
6829	19226	32030	2.26	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-005 ST0191 Homo sapiens cDNA
6895	19493	32314	1.18	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7007	19505	32324	2.8	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7300	19828		0.8	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7417	24782	32808	1.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cDNA Homo sapiens cDNA clone cdAAFH03 5'
7846	20156	33045	2.84	1.2E+00	X74207.1	NT	L. lactis pyrD and pyrF genes
8504	21043	33864	3.05	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
8597	21136	34051	0.89	1.2E+00	P38427	SWISSPROT	Homo sapiens CGI-30 protein (LOC51811), mRNA
8609	21348		0.53	1.2E+00	7708271	NT	MR2-GT0222-201098-001-007 GT0222 Homo sapiens cDNA
8955	21493	34416	2.03	1.2E+00	AW377210.1	EST_HUMAN	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9319	21833	34783	2.92	1.2E+00	Z32850.1	NT	HJM-MD1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
9523	22023	34681	1.86	1.2E+00	D11745.1	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
9844	22342	35324	3.47	1.2E+00	X56632.1	NT	Homo sapiens ENO3 gene for muscle specific enolase
10229	22724		0.67	1.2E+00	AB009686.1	NT	Homo sapiens klotho gene, exon 1
11224	23765	36813	2.19	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161199-001-001 ST0264 Homo sapiens cDNA
11262	23790		6.64	1.2E+00	BE180781.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11331	23026	36038	3.78	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11876	24607	30712	32.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11998	24304		2.11	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 8/14
489	13122	25608	1.19	1.1E+00	D86880.1	NT	Human mRNA for KIAA0227 gene, partial cds
1798	14389	26934	1.48	1.1E+00	AW995383.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
2617	15179	27746	1.09	1.1E+00	AF087124.1	NT	Wheat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds
3373	15981	28458	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28459	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3533	16138	28620	0.84	1.1E+00	8822841	NT	Homo sapiens chromosome 21 segment HS21C013
							W54h11.x1 Soares, NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12898 P53-BINDING PROTEIN 53BP1 ;
3639	16242	28718	1.08	1.1E+00	A1808380.1	EST_HUMAN	Xylella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28846	1.41	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28846	1.41	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3889	16488		0.61	1.1E+00	X65374.1	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4018	16814	29087	0.67	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4093	16688	28145	0.65	1.1E+00	8756209	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pemb7), mRNA
4295	16881		7.81	1.1E+00	5836331	NT	R.unicornis complete mitochondrial genome
6131	17703	30137	3.64	1.1E+00	U18468.1	NT	African swine fever virus, complete genome
6132	17704	30138	0.68	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5201	17766	30180	1	1.1E+00	U34740.1	NT	Emmericella nidulans sterigmatocystin biosynthetic gene cluster: (etcA), (etcB), (etcC), (etcE), (etcF), (etcI), (etcJ), (etcK), (etcL), (etcO), (etcQ), (etcS), (etcT), (etcU), (etcV) and (etcW) genes, complete cds
5230	17784	30213	0.66	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
6409	17968		1.04	1.1E+00	AE003869.1	NT	Xylella fastidiosa, section 15 of 229 of the complete genome
5510	18143	30555	1.62	1.1E+00	8078530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5798	18423	31139	19.98	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825635 3'
5815	18439	31161	3.23	1.1E+00	A1135682.1	EST_HUMAN	qdb5c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738260 3'
6242	18851	31621	1.25	1.1E+00	11419739	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter), member 14 (SLC8A14), mRNA
6420	19023	31807	0.71	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6539	19138	31831	0.71	1.1E+00	R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
6817	19408	32225	0.7	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7338	19865	32728	0.78	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7501	20023	32888	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7501	20023	32887	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7521	20041	32910	9.72	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7580	24787	32973	0.88	1.1E+00	11887980	NT	Mus musculus eilant mating type information regulation 2, (S.cerevisiae, homodop)-like (Sir2), mRNA
8074	20616	33530	2.8	1.1E+00	BF653988.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248828 5'
8163	20704	33920	0.76	1.1E+00	AJ478339.1	EST_HUMAN	tm39h11.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8672	21211	34130	0.75	1.1E+00	AB003068.1	NT	Acetabularia caliculus mitochondrial COXII-like gene
8749	21288	34208	0.78	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
8358	20287		0.68	1.1E+00	BE394878.1	EST_HUMAN	601278278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9546	22046	35007	0.68	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9590	22090		0.81	1.1E+00	Y12221.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9687	22186	35160	0.84	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds

Table 4

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9747	22245	35226	1.59	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
9860	22348	35330	4.82	1.1E+00	AL161615.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9909	22408	35381	19.39	1.1E+00	8764021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10395	22889	35883	1	1.1E+00	P73789	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10530	23087	36079	2.93	1.1E+00	11067364	NT	Homo sapiens KIAA0828 gene product (KIAA0828), mRNA
10688	23121		4.06	1.1E+00	AF068942.1	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
10978	18026		5.28	1.1E+00	8922873	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
10983	23497	36526	3.76	1.1E+00	AF012882.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
10983	23497	36527	3.76	1.1E+00	AF012882.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11234	23765	36922	8.02	1.1E+00	AI809696.1	EST_HUMAN	wf76e11.tl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381548 3'
11948	24275		1.82	1.1E+00	P07886	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12051	24335	30997	2.25	1.1E+00	AF216898.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12184	24903		1.84	1.1E+00	AF234169.1	NT	Dictyostellium discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
103	12778		3.22	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	12789	25271	3.48	1.0E+00	D88425.1	NT	Canis familiaris mRNA for serine/threonine kinase, complete cds
443	13078		2.14	1.0E+00	AB021884.1	NT	Marchantia polymorpha genes for 28S rRNA, 5S rRNA, 16S rRNA, 5.8S rRNA and 26S rRNA
602	13231	25704	1.53	1.0E+00	AI251860.1	NT	Girardinia tigrina mRNA for homeodomain transcription factor (so gene)
705	13328	25813	7.12	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
707	13328		0.89	1.0E+00	AF125684.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1429	15441		1.73	1.0E+00	X60416.1	NT	V. carterii Algal-CAM mRNA
1794	14384	26929	0.91	1.0E+00	AB006531.1	NT	Plasmodium falciparum virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2528	15090	27662	1.2	1.0E+00	P46355	SWISSPROT	DNA GYRASE SUBUNIT B
2528	15090	27663	1.2	1.0E+00	P46355	SWISSPROT	DNA GYRASE SUBUNIT B
2800	15517	27666	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2800	15517	27667	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2884	15610		0.83	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME 1
3232	15844	28324	0.91	1.0E+00	AA628453.1	EST_HUMAN	af28908.s1 Soares_tbal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA04208.3 CE04204.2 contains element MER22 MER22 repetitive element :

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3659	12779		0.78	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3744	16345	28813	1.55	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
4144	16736	29189	1.5	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4382	16949		0.64	1.0E+00	8022245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5165	17734		17.2	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5339	17800		0.6	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5432	18010	30394	1	1.0E+00	AB039022.1	NT	Oncorhynchus mykiss sst1 mRNA for rhamnose binding lectin STL1, complete cds
5488	18120	30527	2.56	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6013	18533	31368	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6013	18533	31369	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8111	18727	31480	1.22	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 8
8263	18871	31841	4.41	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
8269	18877	31845	1.99	1.0E+00	AW452782.1	EST_HUMAN	UHH-B13-abx-d-09-Q-U1.s1 NC1 CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068668 3'
8615	19212	32018	1.79	1.0E+00	U75602.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
8682	19258	32062	0.83	1.0E+00	AF104989.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
8742	19338		1.5	1.0E+00	P46508	SWISSPROT	SRB-11 PROTEIN
8874	19608	32442	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxapain
7192	19724	32573	1.22	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7483	20016		8.59	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7597	20206	33093	1.38	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7710	20219	33107	7.92	1.0E+00	AA775191.1	EST_HUMAN	ec79608.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:888781 3'
7902	20444	33349	1.49	1.0E+00	BE888267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7902	20444	33350	1.49	1.0E+00	BE888267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8084	17734		1.28	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8281	20832	33753	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8291	20832	33764	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8413	20953		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8447	20987	33902	0.48	1.0E+00	Q9Y5T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 18 (UBIQUITIN THIOLESTERASE 18) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 18) (DEUBIQUITINATING ENZYME 18) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8447	20987	33903	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 18 (UBIQUITIN THIOLESTERASE 18) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 18) (DEUBIQUITINATING ENZYME 18) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8475	24791		2.17	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0228-181088-011-906 HT0228 Homo sapiens cDNA
8513	21052	33974	1.06	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pcl protein (pcl) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8559	21198	34116	1.07	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
8195	21712	34655	2.05	1.0E+00	BE607592.1	EST_HUMAN	601407581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9402	21911	34860	1.34	1.0E+00	6763428	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9402	21911	34881	1.34	1.0E+00	6763429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9428	22028	34887	2.06	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
9534	22034	34963	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9634	22034	34984	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9767	22265	35248	0.5	1.0E+00	X16498.1	NT	Human Coronavirus gene for membrane protein
9767	22265	35249	0.5	1.0E+00	X16498.1	NT	Human Coronavirus gene for membrane protein
10021	22518	35510	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHC9FB) mRNA
10021	22518	35511	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHC9FB) mRNA
10106	22600	35592	0.78	1.0E+00	A1077920.1	EST_HUMAN	cy15d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10230	22725	35718	4.17	1.0E+00	AV758826.1	EST_HUMAN	AV758826 BM Homo sapiens cDNA clone BMFAW C04 5'
10372	22668	35959	19.78	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10372	22668	35960	19.78	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10404	22698	35993	0.83	1.0E+00	L11810.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10653	23374	36393	1.87	1.0E+00	S90825.1	NT	PBR1-proline-rich protein (intron 3) [human, Genomic, 898 nt]
11587	18120	30527	1.57	1.0E+00	Z97022.1	NT	Hardycore vulgare gene encoding cysteine protease
11837	24201		4.85	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12171	24410		3.08	1.0E+00	AW976184.1	EST_HUMAN	EST388293 IMAGE resequences, MAGN Homo sapiens cDNA
1816	14208	28742	0.97	9.8E-01	AF245456.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1818	14208	28743	0.97	9.8E-01	AF245456.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2664	16222	27794	1.17	9.8E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3695	16297		0.94	9.8E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5816	18440	31182	14.59	9.8E-01	P49867	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6028	18948	31389	0.83	9.8E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1280.5 IN CHROMOSOME II
9185	21702		1.39	9.8E-01	U05687.1	NT	Lycopodium esculentum putative M1 copy 1 nematode-resistance gene
9474	21873		2.61	9.8E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10593	23128	38142	1.88	9.8E-01	AJ005028.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtb8
549	13180	25658	1.77	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2336	14907		0.89	9.8E-01	AJ003108.1	NT	Caillitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2827	15379		2.05	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3969	16467	28930	0.95	9.8E-01	O87651	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEOTYLTRANSFERASE IV)
3872	16470	28933	0.61	9.8E-01	BE957439.2	EST_HUMAN	60163583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3872	16470	28934	0.61	9.8E-01	BE957439.2	EST_HUMAN	60163583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7250	19779	32834	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7250	19779	32835	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7841	20153	33038	1.13	9.8E-01	BF034016.1	EST_HUMAN	601496337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7841	20153	33039	1.13	9.8E-01	BF034016.1	EST_HUMAN	601496337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
8653	21182	34110	0.77	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10334	22828		0.58	9.8E-01	A4825565.1	EST_HUMAN	cd55d04.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10874	23386	36410	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350750 5'
10874	23386	36411	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350750 5'
11597	24040	37109	1.78	9.8E-01	A1690876.1	EST_HUMAN	bx42c10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12058	24341		1.39	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7212	19743	32597	2.51	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8440	20980	33895	1.7	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8448	20988	33901	1.28	9.7E-01	M60544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
11048	23962		5.23	9.7E-01	BF511208.1	EST_HUMAN	UI-H-B14-scd-e-07-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:3988140 3'
12658	24728		2.92	9.7E-01	AL114281.1	NT	Bombyx mori strain T4 cDNA library under conditions of nitrogen deprivation
4631	17116	20550	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4531	17115	20560	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4687	17140	20588	1.71	9.6E-01	AW769874.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5928	18580	31276	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2594
5928	18580	31277	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient G, genome position 2448-2594
8331	20872		1.23	9.6E-01	X95275.1	NT	P. falciparum complete gene map of plasmodium-like DNA (IR-A)
8785	21324	34248	0.47	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
8020	21557	34485	0.82	9.6E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
10988	23481	36507	1.81	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11395	23847	36912	5.18	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NPD Homo sapiens cDNA clone NPDBAG06 5'
11395	23847	36913	5.18	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NPD Homo sapiens cDNA clone NPDBAG06 5'
11733	24138		2.38	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12388	24983	30609	2.8	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2515	15079	27851	1.02	9.5E-01	7705501	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2691	15248	27817	1.2	9.5E-01	Q02834	SWISSPROT	ENDOGLUCANASE [PRECURSOR (EGI)] (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE I)
3850	16448	28909	1.89	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3850	16448	28910	1.89	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8931	21469	34397	0.63	9.5E-01	A1190162.1	EST_HUMAN	q667407.x1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9034	21571	34500	1.07	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0285-241189-011-402 CT0285 Homo sapiens cDNA
11123	23631	36874	1.71	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11328	23024	36033	1.69	9.5E-01	AW283769.1	EST_HUMAN	UI-H-B12-ahp-f-03-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3235	15847		1.8	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (pcsb) gene, partial cds
3254	15866		2.47	9.4E-01	AF080595.1	NT	Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8799	21338	34265	0.88	9.4E-01	M60724.1	NT	Human Fe-gamma-receptor (FCGR2A) gene, exon 4
1798	14358		0.95	9.3E-01	AF242382.1	NT	Homo sapiens phyenyl-CoA hydratase (PHYH) gene, exon 5
2892	16220	27792	1.09	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4107	16701	29154	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4107	16701	29155	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	18403	31119	1.41	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5856	18481	31204	3.69	9.3E-01	L38189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
8011	20553	33460	1.62	9.3E-01	AA847040.1	EST_HUMAN	060803.at NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1388367
8748	21267		1.13	9.3E-01	AF081981.1	NT	Xenopus laevis CCOH zinc finger protein CSH-2 (CSH-2) mRNA, complete cds
8887	21408	34330	1.01	9.3E-01	AL161634.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12508	24629	30863	1.87	9.3E-01	11440288	NT	Homo sapiens histidyl 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
12515	24634		2	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rPL34 mRNA, complete cds
3276	15987	28369	3.99	9.2E-01	BE822702.1	EST_HUMAN	801441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5004	17577		0.62	9.2E-01	BF129973.1	EST_HUMAN	801817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5894	18516		1.41	9.2E-01	7109410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (SLC30A4), mRNA
6140	18764	31512	4.4	9.2E-01	BF037586.1	EST_HUMAN	801461153F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3864661 5'
9578	22078	35042	1.31	9.2E-01	AL161666.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9663	22162	35135	1.16	9.2E-01	8671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10168	22681	35656	3.47	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10314	22808	35800	1.58	9.2E-01	BF593251.1	EST_HUMAN	768406.at NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10526	23063	36074	1.75	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
11568	24018	37086	2.27	9.2E-01	BF132402.1	EST_HUMAN	801334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
							801820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
							ye5201.a1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
1686	14259	26793	4.89	9.1E-01	T68676.1	EST_HUMAN	Alu repetitive element
2169	14748		2.38	9.1E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3239	15851	28331	0.83	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3239	15851	28332	0.83	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6315	18922	31699	1.42	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6630	19226	32031	2.82	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7677	20063	32670	15.95	9.1E-01	AA868023.1	EST_HUMAN	0671g08.at NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338862 3'
7719	20227	33115	3.12	9.1E-01	U72895.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12093	24976		33.14	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3241	15853	28335	0.81	9.0E-01	7681625	NT	Homo sapiens DKFZP584M2423 protein (DKFZP584M2423), mRNA
3401	18010		0.64	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4468	17054	29498	1.44	9.0E-01	AF068810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7424	19948	32814	0.78	8.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7460	19974		1.84	9.0E-01	D38821.1	NT	Xenopus laevis gene for aldolase, complete cds
9271	21787	34748	0.54	9.0E-01	AF080761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
9744	22242	35223	0.47	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
5875	18497	31222	2.49	8.9E-01	AF026188.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 h/ jolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6368	18088		1.27	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-OF DNA
8162	20693		0.47	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8365	20906	33824	1.04	8.9E-01	AF269887.1	NT	Oithona nana cytochrome-c oxidase subunit I (cod) gene, partial cds, mitochondrial gene for mitochondrial product
11616	24058	37122	2.59	8.9E-01	AE003844.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11927	24262		5.33	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 84 of the complete genome
4840	17222	28876	2.1	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5576	18207	30858	0.7	8.8E-01	AF310817.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10860	23476	36500	3.82	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11749	25087		2.27	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
490	13123	25609	1.48	8.7E-01	AF108953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2446	15013	27585	1.13	8.7E-01	6901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF-1), mRNA
2898	15515	27984	5.67	8.7E-01	AA595863.1	EST_HUMAN	m0511.1.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
4845	17423	29875	0.61	8.7E-01	AF158539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	29876	0.61	8.7E-01	AF158539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
5151	17721		3.08	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
7983	20525	33431	0.66	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
8860	21399	34322	0.75	8.7E-01	AI239456.1	EST_HUMAN	q336906.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
8860	21399	34323	0.75	8.7E-01	AI239456.1	EST_HUMAN	q336906.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9853	22152	35122	1.7	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10205	22700	35693	0.56	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308806 3'
10205	22700	35694	0.56	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308806 3'
10711	23239	36254	5.78	8.7E-01	BF363870.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11582	24028	37097	4.31	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11582	24028	37098	4.31	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12148	24881		4.44	8.7E-01	AV681898.1	EST_HUMAN	AV681898 GLC Homo sapiens cDNA clone GLOOYG07 3'
600	13132		1.68	8.0E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
861	13505	26024	8.72	8.6E-01	W69089.1	EST_HUMAN	z444603.r1 Sources_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2310	14882	27457	1.08	8.0E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3681	16282	28750	0.78	8.0E-01	AL161568.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
3870	16468	28931	1.38	8.0E-01	U49724.1	NT	Drosophila melanogaster merlin (Dimerlin) mRNA, complete cds
6067	18674	31416	9.08	8.0E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6057	18674	31416	9.08	8.0E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6810	19401	32216	1.88	8.0E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6810	19401	32217	1.88	8.0E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7868	20410		1.33	8.0E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7986	20528	33434	0.54	8.0E-01	AF077837.1	NT	Drosophila melanogaster collagen response mediator protein (CRMP) mRNA, complete cds
9803	22103		0.48	8.0E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12338	24812		1.73	8.0E-01	AL112182.1	NT	Bacillus cinereus strain T4 cDNA library under conditions of nitrogen deprivation
6826	19416	32232	1.32	8.0E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7533	20053	32628	2.38	8.0E-01	BE842812.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7932	20474	33383	0.51	8.0E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8357	20897	33817	0.84	8.0E-01	P08601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8357	20897	33818	0.84	8.0E-01	P08601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8441	20881	33808	0.51	8.0E-01	AJ243213.1	NT	Homo sapiens partial S-HT4 receptor gene, exons 2 to 5
10252	22747	35734	1.38	8.0E-01	AB008789.1	NT	Cyanidium caldarium gene for SigC, complete cds
10252	22747	35735	1.38	8.0E-01	AB008789.1	NT	Cyanidium caldarium gene for SigC, complete cds
12077	24978		3.12	8.0E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
12084	24355		7.92	8.0E-01	9607008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4882	17440	28890	0.62	8.0E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
5686	24747	30807	3.15	8.0E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
9685	24747	30808	3.15	8.0E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
9868	22365		2.68	8.0E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 8/6
771	13390	25889	2.48	8.0E-01	M83437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3129	18743	28212	3.28	8.0E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3883	18481	28943	0.66	8.0E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4084	18880	29140	3.24	8.0E-01	Y18177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5473	18107	30426	2.16	8.0E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9587	22087		3.14	8.3E-01	A1701952.1	EST_HUMAN	nm01112.y6 NCI_COAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
10019	22514	35507	1.11	8.3E-01	AF088070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10119	22514	35604	3.5	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10553	23089	36103	2.92	8.3E-01	AE000803.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10571	23108		2.52	8.3E-01	Z121472	NT	Phytophthora infestans mitochondrion, complete genome
11183	23688	36735	2.45	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2096	14875	27244	3.23	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2137	14715		1.45	8.2E-01	AF145589.1	NT	Mus musculus trophobin (Tnn) gene, complete cds
3989	15567	29036	1.12	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4209	19798	29245	0.61	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGLD82W
4209	19798	29247	0.61	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGLD82W
5270	17532	30258	1.08	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5420	17877	30385	2.11	8.2E-01	AB028957.1	NT	Homo sapiens mRNA for KIAA1034 protein, partial cds
6871	19505	32439	0.8	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SC1125 protein
6878	19554	32379	3.18	8.2E-01	AW378433.1	EST_HUMAN	CM4-HT0243-081189-037-601 HT0243 Homo sapiens cDNA
7313	24779	32700	4.21	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9938	22433	35409	0.63	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0650 protein, partial cds
9971	22466	35450	1.67	8.2E-01	AF052659.1	NT	Homo sapiens thiorodotin-related protein mRNA, complete cds
10123	22618	35609	0.59	8.2E-01	AF223988.1	NT	Oncofrynchus tsahwytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22618	35610	0.59	8.2E-01	AF223988.1	NT	Oncofrynchus tsahwytscha isolate T-20 somatolactin precursor gene, exon 1
10286	22781	35772	3.52	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10286	22781	35773	3.52	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11498	23947	37017	3.33	8.2E-01	L10127.1	NT	Mollusca contagiosum virus type 1 ORF1 and ORF2 DNA
11576	24022	37091	8.05	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11583	24029	37098	5.68	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Soares placenta_Biochweeks_2NHBP869W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12102	24364	39970	1.86	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2787	16340		1.79	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3504	16109	28585	2.99	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
3504	16109	28588	2.99	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5048	17619		0.68	8.1E-01	AF202634.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6487	19058	31843	0.88	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6735	19329	32134	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
6735	19329	32135	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7852	20394	33288	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nac) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gsra) gene, partial cds
7852	20394	33289	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nac) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gsra) gene, partial cds
8545	21084	34006	0.82	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8545	21084	34007	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8705	21244	34187	1.08	8.1E-01	AW242847.1	EST_HUMAN	nm01103.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2892459 3' similar to SW1LYAR_MOUSE
10032	22527	33522	0.54	8.1E-01	P08425	SWISSPROT	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTR5 repetitive element;
11358	23810	36869	2.97	8.1E-01	BE938558.1	EST_HUMAN	PROBABLE E4 PROTEIN
11358	23810	36870	2.97	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
11811	24183	31031	3.32	8.1E-01	AE001711.1	NT	RC0-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
188	12849		4.89	8.0E-01	AJ271510.1	NT	Thermotoga maritima section 23 of 138 of the complete genome
310	12985	25453	7.95	8.0E-01	AJ132772.1	NT	Staphylococcus aureus partial pla gene for phosphatase acyltransferase allele 15
2080	14861		1.47	8.0E-01	BF630862.1	EST_HUMAN	Bos taurus tub and rtf genes
3113	18728	28189	1.24	8.0E-01	AF127897.1	NT	602072473F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3354	15962	28439	1.13	8.0E-01	AB008193.1	NT	Salmir boliviensis olfactory receptor (SBO27) gene, partial cds
3765	16366		1.05	8.0E-01	AL162758.2	NT	Mus musculus gene for oviductal glycoprotein, complete cds
4830	17213	29684	5.65	8.0E-01	X83739.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
5117	17689	30127	1.09	8.0E-01	7857352	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7931	20473		2.32	8.0E-01	AW801489.1	EST_HUMAN	Mus musculus myosin IXb (Myos9b), mRNA
8462	21002	33919	1.17	8.0E-01	Y11095.1	NT	RC0-NN1012-270300-021-006 NN1012 Homo sapiens cDNA
479	13112	25602	1.37	7.9E-01	D11476.1	NT	Rice stripe virus RNA 3
744	13364		1.05	7.9E-01	AE002130.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
1648	14240		28.8	7.9E-01	AB040885.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1695	14288		1.11	7.9E-01	U32739.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
2303	14876	27452	6.78	7.9E-01	AB004816.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
						NT	Oryctolagus cuniculus mRNA for mitisugumin28, complete cds

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2304	14877	27453	5.48	7.9E-01	AF130469.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3697	19171	28863	2.33	7.9E-01	AF228884.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4389	18976	28863	0.78	7.9E-01	BE283612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4717	17298	29743	1.04	7.9E-01	8763745	NT	Mus musculus embigin (Emb), mRNA
4717	17298	29744	1.04	7.9E-01	8763745	NT	Mus musculus embigin (Emb), mRNA
5315	17877		5.8	7.9E-01	M29830.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6485	19086	31888	0.69	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8053	20585	33602	2.52	7.9E-01	X00098.1	NT	P. sativum GR gene
9466	21891	34948	4.37	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9882	22457	35440	4.27	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10003	22488	36487	0.76	7.9E-01	AV700880.1	EST_HUMAN	AV700880 GKC Homo sapiens cDNA clone GKCDRE12 3'
10405	22889	35894	0.71	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for elgma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10886	23407		2.28	7.9E-01	7882471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11089	23601	36839	2.72	7.9E-01	P18022	SWISSPROT	NEURAL-CADHERIN PREGURSOR (N-CADHERIN)
909	13522		1.4	7.9E-01	Z43765.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2314	14888	27461	1.4	7.9E-01	AW959587.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4811	17389	20840	0.81	7.9E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5189	17754		0.81	7.9E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6219	18829	31603	2.33	7.9E-01	AF115555.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6367	18971	31750	1.05	7.9E-01	P08231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6589	19183	31988	0.75	7.9E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome: segment 4/5
8428	20968	33881	1.04	7.9E-01	BF108927.1	EST_HUMAN	7154405.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9160	21695	34839	1.02	7.9E-01	Y10156.1	NT	D. discoideum rec-GAP gene
9255	21781	34733	0.53	7.9E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10031	22528		0.78	7.9E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12071	24657		2.33	7.9E-01	U29260.1	NT	Arabidopsis thaliana 1-aminio-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
150	12813	25300	4.65	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
755	13374		1.44	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (A2pha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-1b
2737	15282	27860	2.33	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3400	16009		0.62	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3660	16262	28734	4.78	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4488	17071	29521	3.17	7.7E-01	AF189488.1	NT	Coltutix cotutix japonica sub-species japonica beta-actin mRNA, partial cds
4488	17071	29522	3.17	7.7E-01	AF189488.1	NT	Coltutix cotutix japonica sub-species japonica beta-actin mRNA, partial cds
5749	18376	31084	1.33	7.7E-01	P18563	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5749	18375	31085	1.33	7.7E-01	P18563	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6110	18726	31479	0.8	7.7E-01	R08800.1	EST_HUMAN	Y24B02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9768	22266	35239	0.82	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
11957	24280		15.01	7.7E-01	11497623	NT	Archaeoglobus fulgidus, complete genome
4790	17370	29822	19.73	7.0E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
4790	17370	29823	19.73	7.0E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
6248	18857	31628	4.81	7.8E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6248	18857	31629	4.81	7.8E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6641	19237	32039	0.7	7.8E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6936	18043	30465	0.95	7.8E-01	A1253396.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6936	18043	30488	0.95	7.8E-01	A1253396.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7113	19453	32269	0.98	7.8E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8009	20551	33455	1.34	7.8E-01	AF148783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPILP (Tphilp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8088	20610	33522	1.76	7.8E-01	8857782	NT	Mus musculus adyllin (Adyllin), mRNA
8088	20610	33523	1.76	7.8E-01	8857782	NT	Mus musculus adyllin (Adyllin), mRNA
8287	20808	33727	0.55	7.8E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8287	20808	33728	0.55	7.8E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8897	21435	34359	0.91	7.8E-01	8753577	NT	Mus musculus cytochrome P450, 2b8, phenobarbital inducible, type a (Cyp2b8), mRNA
9203	21720	34684	3.33	7.8E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9203	21720	34685	3.33	7.8E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11236	23767	36824	2.74	7.8E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11238	23787	36825	2.74	7.8E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70

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11566	2404		6.74	7.6E-01	AL1692.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11711	24121		6.31	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIA0805 protein, partial cds
539	13170		1.32	7.6E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
610	13238	25712	1.13	7.6E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHL1) gene, exon 5
7530	20050	32623	0.74	7.6E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (gph) mRNA, complete cds
12027	24318		5.26	7.6E-01	AF163151.2	NT	Homo sapiens dentin alaphosphoprotein precursor (DSPP) gene, complete cds
12522	24638	30697	1.91	7.6E-01	D80807.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885
1169	13771	28276	1.36	7.4E-01	AI598148.1	EST_HUMAN	bt14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2187577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
3789	16389	28854	0.83	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4400	16886	29430	7.7	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7783	20328	33234	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7785	20328	33235	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8568	21107	34026	0.93	7.4E-01	BF346268.1	EST_HUMAN	602018456F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5'
8647	21186		0.64	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9026	21563	34492	7.17	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9083	21819	34554	1.19	7.4E-01	AA187988.1	EST_HUMAN	zp67h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE_P42632 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10301	22795	35786	0.59	7.4E-01	11424633	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11516	23984	37034	1.68	7.4E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11516	23984	37035	1.68	7.4E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11677	24096		4.11	7.4E-01	8763217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
11794	24176		1.28	7.4E-01	AI472841.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4723	17304	29748	0.72	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4810	17388	29839	2.93	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5260	17823	30248	0.69	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6720	19314	32116	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6720	19314	32117	5.88	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7151	24777	32525	0.82	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7549	20068	32642	7.77	7.3E-01	M28511.1	NT	V.algihydricus sucrose (scrB) gene, complete cds
7549	20068	32643	7.77	7.3E-01	M28511.1	NT	V.algihydricus sucrose (scrB) gene, complete cds
11307	23800	36859	3.86	7.3E-01	AA678019.1	EST_HUMAN	z129b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431768 3'

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11307	23800	36860	3.86	7.3E-01	AA078019.1	EST_HUMAN	z125508.s1 Soares fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
884	13479		1.98	7.2E-01	U29281.1	NT	Rattus norvegicus initiation factor-2 kinase (aif-2a) mRNA, complete cds
2000	14582	27141	3.04	7.2E-01	X79140.1	NT	N. tabacum Nif-JA13 mRNA
2601	15085	27639	1.36	7.2E-01	AB009806.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3103	15718	28188	1.29	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3500	16105	28580	2.97	7.2E-01	AF085006.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-5) gene, vsp417-5(A-1 allele, complete cds
3940	16538	29005	1.81	7.2E-01	BF338350.1	EST_HUMAN	602035939F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4186	16776	29222	0.6	7.2E-01	U02668.1	NT	Diclyocaulus viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
4884	17459	29911	2.54	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5348	17608	30323	0.9	7.2E-01	AF158600.2	NT	Streptococcus thermophilus bacteriophage Sf111, complete genome
5386	17846	30358	0.69	7.2E-01	AL161663.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7265	18763	32649	0.82	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8391	20931	33851	1.15	7.2E-01	AF238061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8893	21431		0.53	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10243	22738	35729	2.14	7.2E-01	BF670081.1	EST_HUMAN	602118381F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4275381 5'
10618	23150	36182	5.23	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12037	18776	29222	1.68	7.2E-01	U02668.1	NT	Diclyocaulus viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
12233	24449		4.42	7.2E-01	AP000093.1	NT	Aeropyrum pernix genomic DNA, section 8/7
12288	24995		1.67	7.2E-01	Y10188.1	NT	B. thuringiensis PK1 & cap genes, putative
721	13341	25831	10.56	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3098	16713	28185	18.71	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 16-18
4287	16873	29321	4.11	7.1E-01	7305380	NT	Mus musculus otogelin (Otog), mRNA
4287	16873	29322	4.11	7.1E-01	7305380	NT	Mus musculus otogelin (Otog), mRNA
6103	18719	31471	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6103	18719	31472	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
7029	18563	32390	6.04	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pt) gene, complete cds
8132	20673	33584	0.53	7.1E-01	H54244.1	EST_HUMAN	yq98d08.s1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:202961 3'
8871	21210	34128	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
8871	21210	34129	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
9769	22267	35252	1.46	7.1E-01	BE904405.1	EST_HUMAN	601466330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3698495 5'
10309	22803	35795	1.06	7.1E-01	M12861.1	NT	Human T-cell receptor gamma-chain J2 gene
12012	24878		2.58	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1272	13868	26387	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1272	13868	26388	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2492	15057	27630	1.22	7.0E-01	N82412.1	EST_HUMAN	yz73607 at Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2492	15057	27631	1.22	7.0E-01	N82412.1	EST_HUMAN	yz73607 at Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5213	17776		1.98	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5362	17822	30336	2.98	7.0E-01	AE003921.1	NT	Xylella fastidiosa, section 87 of 228 of the complete genome
6107	18723		1.03	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8319	20860		11.92	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1665 section 143 of 400 of the complete genome
9240	21768	34714	0.61	7.0E-01	U53888.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtd genes, complete cds
9240	21768	34715	0.61	7.0E-01	U53888.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtd genes, complete cds
10969	23513	36546	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
10969	23513	36547	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
12594	24918	30715	1.35	7.0E-01	8630464	NT	Bacteriophage N15 virus, complete genome
1005	13618	28130	10.2	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1005	13618	28131	10.2	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1353	13948	28472	2.8	6.9E-01	AA593530.1	EST_HUMAN	nm28a09 at NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1065176 3'
3256	15868	28348	1.7	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5954	18578	31310	0.8	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BbNA3 mRNA for nucleoside actin, complete cds
6508	19108	31893	1.31	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7921	20463	33369	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7921	20463	33370	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9098	21634		0.83	6.9E-01	AF118048.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9811	22111	35073	0.82	6.9E-01	AF206319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
9811	22111	35074	0.82	6.9E-01	AF206319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
10307	22801	35763	0.86	6.9E-01	BF242367.1	EST_HUMAN	601880580F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4109419 5'
11138	23646	36887	1.84	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
11138	23646	36888	1.84	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11661	24870		2.38	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK
12670	25003	30811	1.33	6.9E-01	AJ88312.1	EST_HUMAN	HEAD PROTEIN 1 (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)
992	13604	28118	1.28	6.8E-01	AF017784.1	NT	wn3162.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2447087.3'
2698	18266		1.25	6.8E-01	D90917.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2858	14249	28783	1.62	6.8E-01	AA854476.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 27/27, 3418832-3573470
4872	17264	28708	1.45	6.8E-01	J00782.1	NT	aj76a05.s1 Soares_parethyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402286.3' similar to gb:X56411.mt1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
9558	22056	35017	2.11	6.8E-01	AB037788.1	NT	Rat(hooded) prolactin gene: exon iii and flanks
10281	22766		0.48	6.8E-01	AA887938.1	EST_HUMAN	Homo sapiens mRNA for KIAA1345 protein, partial cds
10986	23480	38506	2.98	6.8E-01	AJ276876.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
10985	23480	38508	2.98	6.8E-01	AJ276875.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
10993	23507	38540	2.16	6.8E-01	AF038939.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
10993	23507	38541	2.16	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11178	23684	39730	2.2	6.8E-01	AF164151.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11475	23925	38985	1.77	6.8E-01	AF110520.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
11475	23925	38986	1.77	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
320	12074	25463	27.63	6.7E-01	AF213884.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
361	13010	25493	28.51	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1956	14539		0.97	6.7E-01	M12132.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2192	14768	27340	1.85	6.7E-01	AA451884.1	EST_HUMAN	Quali fast skeletal muscle troponin I gene, complete cds
2211	18480	27361	2.86	6.7E-01	AF186073.1	NT	zx12g12.s1 Soares_tbal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:786310.3' similar to contains element TART repetitive element;
3028	15642	28120	4.28	6.7E-01	6878580	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
4550	17133	28581	0.84	6.7E-01	X74421.1	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
							S. tuberosum mRNA for glucose-6-phosphate dehydrogenase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5100	17872	30111	0.98	6.7E-01	AW079110.1	EST_HUMAN	x895g12.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2574588 3'
5700	18326	30829	0.8	6.7E-01	J04838.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5700	18326	30830	0.8	6.7E-01	J04838.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6118	18732	31485	0.83	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6486	19086	31851	1.55	6.7E-01	9635036	NT	Galid herpesvirus 2, complete genome
6486	19086	31852	1.55	6.7E-01	9635036	NT	Galid herpesvirus 2, complete genome
7356	19882		4.12	6.7E-01	AE004608.1	NT	Pseudomonas aeruginosa PA01, section 107 of 528 of the complete genome
7376	19804	32768	0.9	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10049	22844		0.87	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
10832	23353	38388	2.52	6.7E-01	BF354649.1	EST_HUMAN	GM3-H10768-010600-197-c03 HT0768 Homo sapiens cDNA
11333	23031	38040	3.48	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2646	15110	27682	2.66	6.8E-01	AF076240.1	NT	Homo sapiens SLT1 protein (SLT1) mRNA, partial cds
2724	16279	27848	1.01	6.8E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3536	16141	28623	1.35	6.8E-01	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3719	16320	28786	3.42	6.8E-01	Y07688.1	NT	C.albicans random DNA marker, 282bp
4187	16777		0.67	6.8E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5227	17791	30210	0.97	6.8E-01	AI218230.1	EST_HUMAN	qh23a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845498 3' similar to contains PTRS.b2 MER28 repetitive element ;
6474	19075	31858	4.22	6.8E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7873	20188	33074	3.61	6.8E-01	AV660508.1	EST_HUMAN	AV660508 GLC Homo sapiens cDNA clone GLCGID04 3'
8501	21040	33961	0.64	6.8E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9582	22082		1.73	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9915	22411		0.68	6.8E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
12118	24377	30973	1.27	6.8E-01	AF110001.1	NT	Homo sapiens guanylate cyclase activating protein 3 (GCAP3) gene, exon 4 and complete cds
651	13274	25751	1.12	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
651	13274	25752	1.12	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3480	16088	28560	5.04	6.5E-01	AB041225.1	NT	Homo sapiens gene for Tob2, complete cds
4110	16704	28157	1.1	6.5E-01	4504832	NT	Homo sapiens gene for Tob2, complete cds
4369	16956	28398	3.28	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-3
4699	17281	29728	1.28	6.5E-01	D00584.1	NT	Oryza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	17784	30202	2.39	6.9E-01	U29921.1	NT	Phascolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5336	17897	30312	1.02	6.9E-01	Z70828.1	NT	H.sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
6826	19415	32231	1.28	6.9E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7663	20176	33082	0.68	6.9E-01	A1769882.1	EST_HUMAN	wc4602x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2321642 3'
9761	22249		1.25	6.9E-01	T76804.1	EST_HUMAN	yd21504.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:108847 3'
10238	22733	35726	2.49	6.9E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10512	23050	36061	3.36	6.9E-01	H87593.1	EST_HUMAN	yu17706.r1 Soares placenta 86sweeks_2NbpP869W Homo sapiens cDNA clone IMAGE:252516 5'
10566	23102	36118	4.35	6.9E-01	AA601287.1	EST_HUMAN	nc015c07.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10669	23201		4.26	6.9E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone IMAGE:1007810 5'
11470	23920	36889	2.7	6.9E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b gene, mitochondrial genes encoding mitochondrial proteins, complete cds
12087	24348		8.24	6.9E-01	BE485050.1	EST_HUMAN	h74810.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12321	24817		3.04	6.9E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YD097c
273	12830	25417	9.34	6.4E-01	U48948.1	NT	Drosophila melanogaster 8ld dyenin light chain mRNA, complete cds
3502	16107	28583	3.78	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16526	28993	1.33	6.4E-01	AB046927.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4591	17174	29819	0.68	6.4E-01	Y12488.1	NT	M.musculus whn gene
4591	17174	29820	0.68	6.4E-01	Y12488.1	NT	M.musculus whn gene
5402	17960	30371	0.97	6.4E-01	AE002551.2	NT	Neisseria meningitidis serogroup B strain MC58 section 183 of the complete genome
8549	21088	34010	1.78	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10001	22406	35486	8.26	6.4E-01	U82828.1	NT	Homo sapiens atada telangiectasia (ATM) gene, complete cds
10015	22510	35501	1.16	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12188	24420		29.87	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGC09 5'
469	13083	25587	3.75	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
660	13191	25669	56.3	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2207	14783	27358	3.24	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2614	15178	27744	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2614	15178	27745	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3050	15668		0.76	6.3E-01	Y17275.1	NT	Lycopodium obscurum p89a gene, complete cds
6214	18824	31595	0.78	6.3E-01	BE083908.1	EST_HUMAN	PMO-BT0757-010500-002-405 BT0757 Homo sapiens cDNA
6712	19003	32110	1	6.3E-01	L27768.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds
6712	19008	32111	1	6.3E-01	L27768.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8458	20998		3.32	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3856351 5'
8819	21358	34284	0.91	6.3E-01	S82827.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9147	21682	34627	1.15	6.3E-01	BF216884.1	EST_HUMAN	601884050F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4102598 5'
9341	21856	34804	2.9	6.3E-01	9827621	NT	Varidola virus, complete genome
9341	21856	34805	2.9	6.3E-01	9827621	NT	Varidola virus, complete genome
9851	22349		0.67	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10324	22818	35814	1.52	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10421	22915	35915	0.87	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10939	23456	36479	2.45	6.3E-01	AA877715.1	EST_HUMAN	nr09108.61 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1181371 3' similar to TR:002918 002918 HLARK.
11216	23719	36773	15.21	6.3E-01	AI804180.1	EST_HUMAN	CM-BT043-090299-049 BT043 Homo sapiens cDNA
11302	23795	36853	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11458	23808	36875	2.02	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 16.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11789	25042	30505	30.83	6.3E-01	9810293	NT	Mus musculus keratin complex 2, gene 8g (Krl2-8g), mRNA
11884	24219		1.85	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12082	24853		3.2	6.3E-01	X63528.1	NT	C. limicola pscD gene
8175	17742	30171	0.71	6.2E-01	AF167898.1	NT	Spermophilus aulicus isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
6030	18648	31380	2.03	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7506	20028		3.14	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (CaSR-rs4) mRNA, partial cds
7548	24786	32841	1.08	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8243	20784	33703	5.85	6.2E-01	H72255.1	EST_HUMAN	ys01608.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213542 3'
8780	21329	34254	0.54	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydrilase/ehikimata/NADP oxidoreductase gene, complete cds
9370	20309	33212	1.75	6.2E-01	BE592887.1	EST_HUMAN	601338149F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9429	21938		2.35	6.2E-01	M24481.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9890	22485	35472	5.85	6.2E-01	AL161811.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10429	22923	35927	3.78	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10429	22923	35928	3.78	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2438	15005		4.95	6.1E-01	6878078	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
4632	17215	28868	1.05	6.1E-01	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5141	17712	30142	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds
5141	17712	30143	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds
5727	18353	31057	1.54	6.1E-01	M50940.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
6981	19528	32351	3.55	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
6981	19528	32352	3.55	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
8175	20716	33632	3.57	6.1E-01	AF039353.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8730	21269	34187	1.23	6.1E-01	11431066	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8730	21269	34188	1.23	6.1E-01	11431066	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9336	21850	34788	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9336	21850	34789	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9766	22254	35238	1.15	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 528 of the complete genome
9859	22454	35436	1.8	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10837	23356		8.53	6.1E-01	X74507.1	NT	P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
11581	24027	37095	2.19	6.1E-01	S63182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11681	24027	37098	2.19	6.1E-01	S63182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12530	24643		1.91	6.1E-01	X06287.1	NT	M.mazei orfA, orfB, and orfC of archaeal ABC-transporter system
620	13162	25635	1.46	6.0E-01	D87678.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
587	13217		3.41	6.0E-01	5802898	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1406	13968	26528	1.83	6.0E-01	AF085253.1	NT	Human respiratory syncytial virus strain CH83-63b attachment protein (G) gene, complete cds
3887	19485	28948	0.96	6.0E-01	AJ233398.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4287	18853		1.16	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5485	18119	30528	1.93	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5631	18280	30732	2.28	6.0E-01	AW139713.1	EST_HUMAN	U1H-B11-ssb-e-10-Q-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE.2718618.3
6660	19256	32059	3.73	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6767	19360	32169	0.79	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7391	19918	32780	6.29	6.0E-01	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8066	20603	33520	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8066	20603	33521	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8737	22235	35214	2.22	6.0E-01	AB008183.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10174	22869		1.61	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10636	23463	38478	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10636	23463	38477	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11426	23877	36542	2.84	6.0E-01	AI420823.1	EST_HUMAN	100807.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2086821 3'
12168	24308	30978	1.82	6.0E-01	11421683	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12265	24476		1.88	6.0E-01	AA706087.1	EST_HUMAN	208605.a1 Soares fetal liver spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:462778 3'
12428	24879		1.28	6.0E-01	8803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12469	24885	30709	2.40	6.0E-01	8056303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12489	24810		6.92	6.0E-01	BE167817.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1038	13648	26160	1.08	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1447	14039	28568	1.08	5.9E-01	8880232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3308	13919	28398	5.12	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
3308	13919	28398	5.12	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4304	16890		4.32	5.9E-01	AF162756.1	NT	Rattus norvegicus cenech 2 mRNA, partial cds
6591	19188	31991	1.48	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7310	18938	32698	5.88	5.9E-01	AB023488.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7841	20483	33395	0.57	5.9E-01	D80911.1	NT	Synechococcus sp. PCC6803 complete genome, 13/27, 1576593-1718843
9482	21987	34943	0.93	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW/31/Cx major outer membrane protein (omp1) gene, complete cds
9827	22325		0.68	5.9E-01	P08463	SWISSPROT	E6 PROTEIN
10091	22569	35579	1.15	5.9E-01	P56284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10551	23087	36102	3.24	5.9E-01	Q8X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10557	23093	36105	1.75	5.9E-01	AF167944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10840	23361	36378	3	5.9E-01	AW937176.1	EST_HUMAN	PM1-DT0041-190100-002-h03 D T0041 Homo sapiens cDNA
11073	23585	36928	2.25	5.9E-01	AF064626.1	NT	Mus musculus strain SPRET/EL CD48 antigen (C48) gene, partial cds
11810	24182	31030	1.92	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12053	24338		2.88	5.9E-01	AB017706.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12280	24483		7.56	5.9E-01	P34826	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1952	14538	27092	1.8	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
4058	16953	28118	1.22	5.9E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078131 5'
4612	17185	28941	3.73	5.9E-01	AB008077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4914	17489		1.18	5.9E-01	AF110848.1	NT	Megascella scalaris sex-lethal homolog (Mscsl) gene, partial cds, alternatively spliced products
5577	18208		0.76	5.9E-01	AE002162.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5722	18348	31051	2.52	5.8E-01	Q10899	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6331	18937	31713	2.37	6.8E-01	D78869.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (Tfujihara) Homo sapiens cDNA clone GEN:500E06 5'
6454	19055	31840	0.71	6.8E-01	D60601.1	NT	Shigella sonnei DNA for 26 ORF6, complete cds
6903	19637		2.47	6.8E-01	S85091.1	NT	Cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7828	20370		2.57	5.8E-01	H41571.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8031	20573	33477	0.68	6.8E-01	A1280051.1	EST_HUMAN	q85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8031	20573	33478	0.68	6.8E-01	A1280051.1	EST_HUMAN	q85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8131	20672	33582	2.34	6.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8131	20672	33583	2.34	6.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8823	21382	34287	9.48	6.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 8-11
8802	21440	34383	0.88	6.8E-01	Q27388	SWISSPROT	TRANSCRIPTION FACTOR E2F
8803	21441	34384	0.56	6.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F48F2.2 IN CHROMOSOME X
9514	22014		0.89	6.8E-01	BF031808.1	EST_HUMAN	60155777F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
10689	23390	36405	9.44	6.8E-01	AJ243213.1	NT	Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5
10915	23434		3.68	6.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11021	23535		2.04	6.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3079	18694		0.68	5.7E-01	8756263	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3260	15872	28352	1.58	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOT1) (MOVOT1)
3552	16158		2.63	5.7E-01	AB033503.1	NT	Populus euphratica pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3973	18571	28041	3.08	5.7E-01	AF011591.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
6498	19097	31881	3.87	5.7E-01	BF035413.1	EST_HUMAN	601454982F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6812	19403	32219	0.72	5.7E-01	AA194201.1	EST_HUMAN	z738c08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:985874 5'
6845	18053	30478	1.28	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7741	20249	33142	1.97	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
7911	20493		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Lrpe5, Mash2, Tapa-1, Tesc4 and Tesc8 genes, alternative transcripts
9715	22213	35186	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9715	22213	35187	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10468	22982	35973	0.88	5.7E-01	BF540862.1	EST_HUMAN	602087712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
3410	18019	28498	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3410	18019	28499	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4324	16910	29351	0.69	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8738	21277	34200	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8738	21277	34201	4.42	5.0E-01	AV884703.1	EST_HUMAN	AV884703 GKO Homo sapiens cDNA clone GKCF5F05 5'
9297	21897	34844	1.11	8.0E-01	AB039782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11688	24085		2.5	5.0E-01	BE888280.1	EST_HUMAN	501514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11779	24168	36775	1.28	5.0E-01	AA483535.1	EST_HUMAN	ng75g10.at NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element;
12156	18028	30480	3.31	5.0E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12188	24419		2.98	5.0E-01	P60506	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12819	24688		3.11	5.0E-01	BF673829.1	EST_HUMAN	802132028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1253	13850	26307	1.13	5.0E-01	8393912	NT	Rattus norvegicus Prophenyl Coenzyme A carboxylase, beta polypeptide (Pcbb), mRNA
2726	16280	27847	13.6	5.0E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2725	15280	27848	13.6	5.0E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2943	19559	28033	0.69	5.0E-01	5802085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3102	15717		1.51	5.0E-01	H48219.1	EST_HUMAN	y018a10.st Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178268 3'
3271	15883	28365	2.68	5.0E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3755	16356	28825	0.97	5.0E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
8386	20926	33846	0.66	5.0E-01	A1791788.1	EST_HUMAN	cr82c01.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9682	22181		0.74	5.0E-01	U88415.1	NT	Chimera-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10279	22774	35763	0.84	5.0E-01	T05047.1	EST_HUMAN	EST02835 Fetal brain, Striatum (cat8838206) Homo sapiens cDNA clone HFBCQ35
151	12814	25301	12.97	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
151	12814	25302	12.97	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
611	13239	25713	1.6	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
611	13239	25714	1.6	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1314	13908	28428	2.58	5.4E-01	AW898087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2154	14731		3.8	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2288	14870	27448	2.18	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 16,15' beta carotene dioxygenase (beta-diox gene)
3584	16582	28053	0.82	5.4E-01	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5269	17822		1.04	5.4E-01	AW747872.1	EST_HUMAN	QV0-BT0041-061089-033-602 BT0041 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5388	13239	25713	0.59	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
5388	13239	25714	0.59	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
5388	18482	31185	0.81	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-010 CN0030 Homo sapiens cDNA
6338	18944	31723	1.49	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
7094	18665	32504	1.1	5.4E-01	BE88592.2	EST_HUMAN	601660278R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908090.3
7374	18600	32762	0.75	5.4E-01	Z21618.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7374	18900	32763	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7376	19902	32766	1.47	5.4E-01	Q84428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
9601	22398		1.98	5.4E-01	BF672836.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:42438890.5
10957	23472	36497	3.25	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11485	23934	37004	5.78	5.4E-01	Q80675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11485	23934	37005	5.78	5.4E-01	Q80676	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11586	18944	31723	2.42	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
11725	24132		2.52	5.4E-01	A1858398.1	EST_HUMAN	w137g04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126.3 similar to gb:M13452 LAMIN A (HUMAN);
542	13173	25663	2.29	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes.2
2811	15363	27631	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2811	15363	27632	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3280	15891	28370	3.13	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4280	18678		1.39	5.3E-01	U36887.1	NT	<i>Mycoplasma genitalium</i> section 9 of 51 of the complete genome
5648	18277	30753	1.91	5.3E-01	A1820821.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711.5
5649	18277	30754	1.91	5.3E-01	A1820821.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711.5
5742	18388	31075	0.87	5.3E-01	AA163672.1	EST_HUMAN	zu42g09.r1 Soares NIH-MPUs_S1 Homo sapiens cDNA clone IMAGE:668112.5
5742	18388	31076	0.87	5.3E-01	AA163672.1	EST_HUMAN	zu42g09.r1 Soares NIH-MPUs_S1 Homo sapiens cDNA clone IMAGE:668112.5
5827	18451	31174	1.84	5.3E-01	BE845820.1	EST_HUMAN	7673c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118.3 similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5827	18451	31175	1.84	5.3E-01	BE845820.1	EST_HUMAN	7673c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118.3 similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8836	21374		1.83	5.3E-01	L01980.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8886	21423	34348	0.63	5.3E-01	BF433986.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element ;
8885	21423	34348	0.63	5.3E-01	BF433986.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element ;
10112	22807	35597	0.48	5.3E-01	A1954210.1	EST_HUMAN	w84b02.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11435	23885	36952	6.92	5.3E-01	BE668291.1	EST_HUMAN	601339887F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
11850	24881		4.22	5.3E-01	AA918053.1	EST_HUMAN	cg30a05.s1 NCL_CGAP_B7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
849	13485	25973	19.16	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1208	13808	28319	10.07	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1233	13832	26348	2.91	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1830	14514		4.11	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2191	14787	27339	2.97	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3163	15787	28233	1.67	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3274	15886		0.71	5.2E-01	D73443.1	NT	Chlamydomonas abortus strain S203 POM81A and POM80A precursor, genes, complete cds
3452	18059		1.74	5.2E-01	AL110780.1	NT	Azotobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3482	18097	28572	2.49	5.2E-01	AA984165.1	EST_HUMAN	Beltyla cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3694	18265		0.92	5.2E-01	AF020269.1	NT	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1618504 3'
5161	17730		0.87	5.2E-01	7108444	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5314	17876		0.99	5.2E-01	AL163281.2	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
5834	19456	31179	0.97	5.2E-01	AA284261.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
9848	24795	35115	1.19	5.2E-01	X02218.1	NT	zc44d09.T7 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325169 3'
9848	24785	35116	1.19	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9845	22343	35325	0.94	5.2E-01	AA184518.1	EST_HUMAN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9940	22435	35411	1.65	5.2E-01	AF143952.2	NT	zc05b08.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
12590	24682		4.94	5.2E-01	P18516	SWISSPROT	Homo sapiens PELOTA (PELOTA) gene, complete cds
845	13288	25746	2.13	5.1E-01	M58509.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
678	13300	25781	3.98	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
						NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
676	13300	25782	3.98	5.1E-01	AJ233644.1	NT	Polyomavirus (strain PI wt) 16S rRNA gene
1692	14294		0.88	5.1E-01	X87886.1	NT	R.norvegicus mRNA for mammalian fusca protein
2069	14648		11.33	5.1E-01	BF083086.1	EST_HUMAN	602139319F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4268117 5'
4151	16743	26197	4.61	5.1E-01	A1858485.1	EST_HUMAN	w38b12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427283 3'
4266	16852	26300	3.03	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5226	17763		0.71	5.1E-01	BE091766.1	EST_HUMAN	IL2-BT0731-260400-077-G08 BT0731 Homo sapiens cDNA
6422	19025		0.76	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAU07 5'
6997	19495	32316	1.42	5.1E-01	R80873.1	EST_HUMAN	y64609.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8507	21046	33966	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8507	21046	33967	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9602	22102	35066	4.8	5.1E-01	J06412.1	NT	Human regenerating protein (reg) gene, complete cds
9605	22105	35068	3.4	5.1E-01	W22302.1	EST_HUMAN	6581 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10085	22690	35555	0.95	5.1E-01	M84579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11874	24805		2.04	5.1E-01	BF030207.1	EST_HUMAN	601550863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3926767 5'
12129	24385		2.01	5.1E-01	BF439882.1	EST_HUMAN	nec51110.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element
2180	14757	27326	1.4	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2180	14757	27327	1.4	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2189	14785	27335	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2189	14785	27336	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3740	16341	28609	5.58	5.0E-01	AE001785.1	NT	Thermotoga maritima section 97 of 138 of the complete genome
3811	16410	28675	0.85	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain Igm mRNA, antibody 363p.138, partial cds
3942	16540	29008	3.11	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
8467	21007		1.78	5.0E-01	M82304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8604	21143	34057	0.64	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9379	20318	33219	3.1	5.0E-01	BF317212.1	EST_HUMAN	601803871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4198832 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,8-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9543	22043	35004	1.34	5.0E-01	P36573	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9543	22043	35005	1.34	6.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) (INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)
10201	22788		1.04	6.0E-01	BE889218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849438 6'
11816	24187		3.46	6.0E-01	AF029215.1	NT	Mus musculus MIR3 OX-2 antigen homolog gene, exons 2-5, and complete cds
12564	24636		2.38	6.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12669	24668		4.27	6.0E-01	O13981	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
822	13439	25948	2.31	4.9E-01	BF571462.1	EST_HUMAN	602076948F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1699	14292	26827	1.6	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1949	14533	27089	1.35	4.9E-01	U40880.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
5902	18231	30681	1.32	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6187	18797	31565	2.35	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6187	18797	31568	2.36	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7475	19697	32862	1.9	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8920	21456		1.49	4.9E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9115	21651	34592	0.98	4.9E-01	AW339905.1	EST_HUMAN	hc90c02.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807268 3' similar to TR:095714
9220	25126		2.2	4.9E-01	10948863	NT	O95714 HERC2.;
10220	22715	35708	0.74	4.9E-01	AF053880.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
11704	24117		2.48	4.9E-01	AF176912.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12548	25081		6.73	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12556	24657	30872	1.74	4.9E-01	AL163301.2	NT	nc22611.st NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144652 3'
12830	24703		1.36	4.9E-01	11431438	NT	Homo sapiens chromosome 21 segment HS21C101
3591	16185		1.05	4.8E-01	AA912842.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4782	17011		0.62	4.8E-01	4504850	NT	alpha2a09.st Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
5698	18324	30827	8.6	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
6760	19381		4.22	4.8E-01	AA658878.1	EST_HUMAN	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
7357	19883		1.85	4.8E-01	5031650	NT	nu86f09.st NCI_CGAP_A1M1 Homo sapiens cDNA clone IMAGE:1217513
7582	20174	33061	0.87	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (DS2280E) mRNA
7738	20246	33138	3.72	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
7738	20246	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7738	20246	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7848	20388	33291	1.38	4.8E-01	AI820744.1	EST_HUMAN	MT7710.y6 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:184795 5' similar to contains element
9169	21748		1.13	4.8E-01	BE155148.1	EST_HUMAN	MER8 repetitive element;
9921	22417		0.58	4.8E-01	BF688833.1	EST_HUMAN	PM1-HT0350-201269-004-504 HT0350 Homo sapiens cDNA
10607	23141		2.02	4.8E-01	X93502.1	NT	602194287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
11786	24170		1.29	4.8E-01	AL163227.2	NT	Soares/visas ORFs from chromosome X
12648	24842		3.04	4.8E-01	AF227566.1	NT	Homo sapiens chromosome 21 segment HS21C027
12648	24895		3.38	4.8E-01	AJ132984.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6638	19234	32038	8.72	4.7E-01	BF217173.1	EST_HUMAN	Chlamydomonas reinhardtii cap gene, exons 1-3
7107	19447	32263	0.78	4.7E-01	AI204374.1	EST_HUMAN	601883880F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4086387 5'
7808	20349	33257	0.52	4.7E-01	T11414.1	EST_HUMAN	q72409.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1765644 3'
7808	20349	33258	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9005	21542	34473	0.8	4.7E-01	8981501	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
10467	22961	35972	0.78	4.7E-01	AW087791.1	EST_HUMAN	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10727	23253		4.94	4.7E-01	AF102873.1	NT	xc6891.1 x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2681580 3'
10883	23478	36503	2.19	4.7E-01	U41069.1	NT	Influenza A virus isolate hk51687 hemagglutinin (HA) gene, partial cds
11163	23870	38715	11.61	4.7E-01	BF628638.1	EST_HUMAN	Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds
11264	23784	38940	2.89	4.7E-01	AW889448.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181303 5'
11904	24243		1.92	4.7E-01	BE887763.1	EST_HUMAN	RC8-NT0026-240400-011-E08 NT0026 Homo sapiens cDNA
12038	24325		1.33	4.7E-01	AW341581.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12666	24738		1.38	4.7E-01	AP000007.1	NT	hd11c08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2609168 3'
3797	16397	28862	2.23	4.6E-01	AW819838.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt, position (777)
3808	16406	28870	1.68	4.6E-01	BF683300.1	EST_HUMAN	RC1-ST0278-040400-018-508 ST0278 Homo sapiens cDNA
3808	16406	28871	1.68	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5323	17885		1.03	4.6E-01	M11267.1	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5429	17886	30390	22.08	4.6E-01	AL163248.2	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C048
							AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA SUBUNIT) (GAMMA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 GAMMA SUBUNIT) (SCN7G) (GAMMA NAHC)
5440	17895	30400	1.37	4.6E-01	P51170	SWISSPROT	
5612	18241	30690	1.12	4.6E-01	BF131593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5612	18241	30691	1.12	4.6E-01	BF131593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5663	18290	30768	3.27	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18290	30768	3.27	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5735	18361	31067	2.39	4.6E-01	BE734781.1	EST_HUMAN	601568765F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3943637 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5748	18374	31082	4.22	4.9E-01	A1247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O16338 O16338 BUTYROPHILIN.;
5748	18374	31083	4.22	4.9E-01	A1247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O16338 O16338 BUTYROPHILIN.;
5766	18382	31094	1.4	4.9E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5828	18482		1.06	4.9E-01	AF212124.1	NT	Andis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5907	18529		0.88	4.9E-01	BE817247.1	EST_HUMAN	PMO-BNO260-120600-001-F07 BNO260 Homo sapiens cDNA
6069	18676	31417	0.76	4.9E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6404	19007	31788	1.05	4.9E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1168761 to 1176238 (section 100 of 148) of the complete genome
6865	19599	32428	1.36	4.9E-01	U82332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6865	19599	32430	1.38	4.9E-01	U82332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7712	20221	33108	0.88	4.9E-01	AA493577.1	EST_HUMAN	nt04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8282	20803	33721	13.23	4.9E-01	BF697388.1	EST_HUMAN	602130653F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287828 5'
9225	21741	34684	1.04	4.9E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9225	21741	34685	1.04	4.9E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9583	22083	35046	0.55	4.9E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9583	22083	35047	0.55	4.9E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9856	22383	35358	2.63	4.9E-01	A1815834.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
9896	22383	35359	2.63	4.9E-01	A1815834.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10870	23391		3.09	4.9E-01	P88183	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10879	23400	36416	4.13	4.9E-01	BE185448.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10879	23400	36417	4.13	4.9E-01	BE185448.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11346	23044	36054	5.52	4.9E-01	AF018369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11346	23044	36055	5.52	4.9E-01	AF018369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12854	24726		1.28	4.9E-01	M22360.1	NT	Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants 6J, 12J, 13J, and 17J mRNA, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1954	14538	27094	1.89	4.5E-01	AE001931.1	NT	Dainococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
1954	14538	27095	1.89	4.5E-01	AE001931.1	NT	Dainococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
2895	15512	27892	4.77	4.5E-01	AA977088.1	EST_HUMAN	255302.e1 Soares_Fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3348	16986	28431	0.84	4.5E-01	AW083761.1	EST_HUMAN	xc26c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2885200 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3348	16986	28432	0.84	4.5E-01	AW083761.1	EST_HUMAN	xc26c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2885200 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3359	15987	28444	6.18	4.5E-01	Q05703	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3424	16032	28512	1.15	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4100	16894	28195	1.35	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4149	16741	28195	0.73	4.5E-01	AI708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4255	18015	30092	4.04	4.5E-01	AW873496.1	EST_HUMAN	as96a09.x1 Barnstead acta HPLRB8 Homo sapiens cDNA clone IMAGE:2353460 3'
5078	17651	30092	1.16	4.5E-01	BE963445.2	EST_HUMAN	hc60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
6427	17864		26.74	4.5E-01	AF090196.1	NT	60187225R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868023 3'
5737	18363	31070	1.37	4.5E-01	AW608814.1	EST_HUMAN	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds
6719	19313	32834	1.38	4.5E-01	Q09856	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7443	19987	32834	1.89	4.5E-01	M37038.1	NT	COAT PROTEIN
7604	20117	32993	2.53	4.6E-01	AI858949.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
8248	20750		0.97	4.5E-01	M32861.1	NT	w82a02.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:2428618 3' similar to TR:Q92023 Q92923 SWISNF COMPLEX 170 KDA SUBUNIT.1
8342	20883	33804	4.02	4.5E-01	AI848598.1	EST_HUMAN	D melanogaster Shaw2 protein mRNA, complete cds
							ts56g11.x1 NCL_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2292844 3'
8494	21033	33954	0.89	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
8718	21255		1.74	4.5E-01	11444789	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
8929	21497	34385	0.89	4.5E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8853	22351		1.02	4.5E-01	9630316	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183). mRNA
10389	22883	35877	23.95	4.5E-01	M86006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10389	22883	35878	23.95	4.5E-01	M86006.1	EST_HUMAN	Bombix mori nuclear polyhedrosis virus, complete genome
							EST02531 Fetal brain, Stratagene (cat8938206) Homo sapiens cDNA clone HFBCY17
							EST02531 Fetal brain, Stratagene (cat8938206) Homo sapiens cDNA clone HFBCY17
10744	23268	36285	3.01	4.6E-01	AW591271.1	EST_HUMAN	xc14h01.x1 NCL_CGAP_U3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11131	23639		1.9	4.5E-01	AV719392.1	EST_HUMAN	Q94252 VIRAL INTEGRATION SITE PROTEIN INT-8 [1]; AV719392 GLC Homo sapiens cDNA clone GLCCED12 5'

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23828	36860	1.88	4.5E-01	BE086472.1	EST_HUMAN	RC3-BT0333-160300-016-a03 BT0333 Homo sapiens cDNA
11871	25070		3.3	4.5E-01	BE871481.1	EST_HUMAN	601449201F1 NIH_MGC_05 Homo sapiens cDNA clone IMAGE:3852881 5'
12370	24540		2.13	4.5E-01	BF337531.1	EST_HUMAN	602035279F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183280 5'
12442	24578		0.25	4.5E-01	11422009	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2081	14862		1.39	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
2432	14959	27572	3.26	4.4E-01	P49785	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3357	15968	28442	1.27	4.4E-01	AF056780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3357	15965	28443	1.27	4.4E-01	AF056780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3361	15969	28446	2.31	4.4E-01	BF056728.1	EST_HUMAN	791402.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4318	16804		1.26	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3008393 5'
5134	17706		2.07	4.4E-01	BE141398.1	EST_HUMAN	MR0-HT0078-131289-007-g05 HT0078 Homo sapiens cDNA
5277	17839	30265	0.94	4.4E-01	U61154.1	NT	Buzura suppressaria nucleopolydnavirus ecdytarddd UDP-glucosyltransferase (egt) gene, complete cds
5417	17974		0.9	4.4E-01	AW814885.1	EST_HUMAN	MR1-ST0208-120400-022-g07 ST0208 Homo sapiens cDNA
5613	18242	30892	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5613	18242	30893	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5867	18489	31215	1.72	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 360 nt]
5883	18505	31231	1.9	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
6108	18724	31476	1.53	4.4E-01	AI198413.1	EST_HUMAN	q162h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6108	18724	31477	1.53	4.4E-01	AI198413.1	EST_HUMAN	UNKNOWN PROTEIN ;
6387	18980	31771	1.89	4.4E-01	AW080783.1	EST_HUMAN	q162h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6470	19071		1.02	4.4E-01	AA776132.1	EST_HUMAN	xc27608.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O85154 O85154
7429	19953	32818	0.89	4.4E-01	AE000571.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
7782	20325		10.05	4.4E-01	Z11678.1	NT	ee85d11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
8698	21237	34160	1.01	4.4E-01	AA056427.1	EST_HUMAN	TYROSINE-PROTEIN KINASE LYN (HUMAN);
9078	21614	34549	0.76	4.4E-01	AF112540.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
9111	21847	34587	0.96	4.4E-01	AW612578.1	EST_HUMAN	S.tuberculosis mRNA for induced abdon lip protein (partial)
9214	21731	34674	1.13	4.4E-01	OB2836	SWISSPROT	z169a03.s1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:508836 3'
							HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
							hrc5c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2864222 3' similar to
							SW:MSH8_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
							ZINC FINGER X-CHROMOSOMAL PROTEIN

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9872	22369	35347	1.89	4.4E-01	AI268550.1	EST_HUMAN	q33909.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1810921 3'
9873	22370		2.12	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10009	22504	35495	4.51	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10278	22771	35789	1.43	4.4E-01	S78404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10278	22771	35789	1.43	4.4E-01	S78404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11939	24271	31016	4.88	4.4E-01	8877874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
11952	25000		14.88	4.4E-01	AL183282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12517	24635		1.5	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
438	13089	25564	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
438	13089	25565	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3088	15711	28182	0.91	4.3E-01	AW989477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4231	16818	28268	1.21	4.3E-01	J03308.1	NT	Human somatostatin 1 gene and flanks
4495	13089	25565	3.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4495	13089	25565	3.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5587	18198	30845	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5587	18198	30846	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6049	18968	31407	1.34	4.3E-01	BE181855.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6085	18982	31424	2.08	4.3E-01	AF178825.1	NT	Salmonella enterica serovar typhimurium (SSC186) gene, partial cds
6809	19400	32215	4.28	4.3E-01	AJ001878.1	NT	Coturnix coturnix japonica fnG gene
6949	19526		0.78	4.3E-01	Q33397	SWISSPROT	DNA GYRASE SUBUNIT B
7458	19980		1.78	4.3E-01	BF348001.1	EST_HUMAN	802023134F1 NCL_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4158286 5'
8366	20906		2.66	4.3E-01	U97040.1	NT	Methanococcus voltae flagellar-related protein C-1 (flaC-fla1) genes, complete cds
9179	21768	34702	0.7	4.3E-01	Y14604.1	NT	Erwinia amylovora rcaV gene
9842	22142	35109	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
9842	22142	35110	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
10128	22823	35614	0.57	4.3E-01	AW170559.1	EST_HUMAN	hm63e05.x1 Soares_NH06C_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10811	19816	32451	2.52	4.3E-01	AF075828.1	NT	TR:000189 000188 MU-ADAPTIN-RELATED PROTEIN 2 ;
11888	24031	37101	1.54	4.3E-01	A1874332.1	EST_HUMAN	Equs caballus microsatellite LEX027
11832	18198	30845	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
11832	18198	30846	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
12616	24898		2.81	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1402	15440	28524	1.39	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1891	14573		1.04	4.2E-01	AA761653.1	EST_HUMAN	nz24a09.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288686 3'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2688	14848		1.37	4.2E-01	AF286325.1	NT	Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds
3659	16270	28738	4.91	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 83 of 229 of the complete genome
3659	16300	28768	1	4.2E-01	AI280338.1	EST_HUMAN	ql94b01.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1878045 3'
3773	18014		0.6	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40488
3948	18548	28014	0.73	4.2E-01	AW83527.1	EST_HUMAN	QV0-LT0015-180200-127-015 Homo sapiens cDNA
4054	18851	29118	0.98	4.2E-01	Q04888	SWISSPROT	SOX-8 PROTEIN
4807	17385	28638	4.3	4.2E-01	AA534083.1	EST_HUMAN	IIH89H01.s1 NCL CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33800 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4895	17470	29928	4.04	4.2E-01	R13467.1	EST_HUMAN	Y77601.11 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:28278 5'
5232	17768		3.77	4.2E-01	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5891	18514	31241	1.82	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4108493 5'
5953	18575	31308	2.16	4.2E-01	AW854182.1	EST_HUMAN	RC3-C10254-000400-028-g04 C10254 Homo sapiens cDNA
6362	18957	31738	1.08	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7031	18565	32392	10.26	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7031	19565	32393	10.26	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7082	24776	32492	1.97	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7150	18683	32524	5.81	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7834	20478	33385	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST339413 MAGI resequences, MAGI Homo sapiens cDNA
7834	20478	33386	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST339413 MAGI resequences, MAGI Homo sapiens cDNA
8148	20889	33602	0.55	4.2E-01	4768039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
8235	21761	34708	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9236	21761	34707	0.52	4.2E-01	U67431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9380	22377		0.81	4.2E-01	AA705007.1	EST_HUMAN	395801.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10083	22578	35571	0.5	4.2E-01	AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10390	22884	35879	1.35	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
10921	23440	38461	3.88	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11273	23728	36780	2.65	4.2E-01	BE866485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908085 3'
12561	24661		1.46	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTF8HH05 5'
1133	13736	26245	1.59	4.1E-01	AI805481.1	EST_HUMAN	RC-BT081-210188-142 BT081 Homo sapiens cDNA
1142	13745	26254	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1142	13745	26255	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2735	15280	27858	1.58	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2967	15582	28061	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2687	16882	28082	2.11	4.1E-01	AL161636.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3342	18952	28428	0.68	4.1E-01	AA000344.1	EST_HUMAN	cd4608.s1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	16438	28899	0.58	4.1E-01	AW061292.1	EST_HUMAN	EST373384 MAGG EST sequences, MAGG Homo sapiens cDNA
3839	16438	28900	0.58	4.1E-01	AW061292.1	EST_HUMAN	EST373384 MAGG EST sequences, MAGG Homo sapiens cDNA
4391	16948	28390	2.82	4.1E-01	AJ248207.1	NT	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoJ, IsoK, IsoL, IsoM, IsoN, IsoO, IsoP, IsoQ, IsoR, IsoS, IsoT, IsoU, IsoV, IsoW, IsoX, IsoY, IsoZ genes
4393	16978		0.76	4.1E-01	AA000257.1	EST_HUMAN	on33402.s1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone NPCBDF10 5'
4774	17355	26807	1.31	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6141	18765	31513	3.97	4.1E-01	BF681383.1	EST_HUMAN	802168890F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4287319 5'
7480	18983	32948	2.74	4.1E-01	U87335.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7979	20821	33427	1.31	4.1E-01	BF574804.1	EST_HUMAN	802133281F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288238 5'
8019	21556	34484	1.28	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
9484	21041		0.61	4.1E-01	AF160597.1	NT	Volvox gymnocaudus Vgym560 cytochrome b (cyb) gene, complete cds; mitochondrial gene for mitochondrial product
10184	22869		1.28	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTG1168 complete genome, segment 3/8
10310	22804	35798	0.79	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10401	22895	35890	0.51	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10401	22895	35891	0.51	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10471	22965		2.29	4.1E-01	BF346382.1	EST_HUMAN	GM2-HT0137-200889-010-e08 HT0137 Homo sapiens cDNA
10719	23247	36282	46.22	4.1E-01	X68700.1	NT	Zea mays ZMPS2 gene for 19 kDa zein protein
11270	23008	36015	3.57	4.1E-01	Q08470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12280	25049		2.6	4.1E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
147	15408		4.55	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-260868-012-d10 CT0201 Homo sapiens cDNA
1077	13681	28181	0.82	4.0E-01	8404658	NT	Laqueus rubellus mitochondrion, complete genome
1384	13978	26905	1.51	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1532	14124		4.1	4.0E-01	6879268	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2049	15456	27200	1.22	4.0E-01	Z66933.1	NT	Ascaris lumbricoides msc2 gene
2049	15456	27201	1.22	4.0E-01	Z66933.1	NT	Ascaris lumbricoides msc2 gene
2204	14780	27352	17.82	4.0E-01	AE001831.1	NT	Dainococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
2204	14780	27353	17.82	4.0E-01	AE001831.1	NT	Dainococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
2631	12811	25289	1.45	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase 63 component n-recognition (Ubr1), mRNA
2985	15811	28090	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2985	15811	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	16359	28829	2.17	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (MIC), Y1D (MID), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3899	16498	28980	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3899	16498	28981	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4942	17517		8.41	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6068	18886	31429	1.16	4.0E-01	AW970610.1	EST_HUMAN	EST332891 MAG2 resequences, MAG2 Homo sapiens cDNA
6967	19165	31901	0.87	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C, SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7777	20288	33183	0.72	4.0E-01	P27648	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7869	20411	33317	0.48	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7954	20498	33408	0.99	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8938	21474	34394	0.98	4.0E-01	AA323289.1	EST_HUMAN	EST28066 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
11443	23893		1.85	4.0E-01	BF030282.1	EST_HUMAN	601568283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3829092 5'
11568	24015		3.52	4.0E-01	L76080.1	NT	Synochocystis sp. PCC 8413 transposase gene, complete cds
11958	24901		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12518	24936		1.42	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1420	14013	28543	1.98	3.8E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2668	15226	27798	3.8	3.8E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1163 protein, partial cds
2730	15285	27851	3.79	3.8E-01	X82032.1	NT	H. sapiens B-myb gene
2730	15285	27852	3.79	3.8E-01	X82032.1	NT	H. sapiens B-myb gene
3131	15745	28214	3.95	3.8E-01	AJ225898.1	NT	Sinorhizobium meliloti egl, syb2, cys3 genes and orf3
4153	16745	29199	1.49	3.8E-01	BF562811.1	EST_HUMAN	7181401.X1 NCL_CGAP_B16 Homo sapiens cDNA clone IMAGE:3339169 3'
5130	17702	30136	1.86	3.8E-01	BE726687.1	EST_HUMAN	601563949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833686 5'
6090	18706	31454	6.44	3.8E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6426	19029	31812	0.88	3.9E-01	U82895.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7896	20438	33343	0.78	3.9E-01	U78415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8795	21334	34268	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170869-004-b08 CT0105 Homo sapiens cDNA
8804	21343		0.7	3.8E-01	BF348634.1	EST_HUMAN	602018944F1 NCL_CGAP_B167 Homo sapiens cDNA clone IMAGE:4155322 5'
9161	21896	34840	1.24	3.9E-01	AW195888.1	EST_HUMAN	3x86d04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821 O94821 KIAA0713 PROTEIN;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9464	21989	34945	1.42	3.8E-01	A187337.1	EST_HUMAN	wp76402.x1 NCI_QGAP_Bm25 Homo sapiens cDNA clone IMAGE:2487698 3' similar to
9792	22280	35274	3.88	3.8E-01	M19879.1	NT	SW:RFN5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
9858	22354		0.5	3.8E-01	11485820	NT	Human elabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10071	22968	35531	0.69	3.8E-01	D86722.1	NT	Porphyria purpurea mitochondrion, complete genome
10482	22988	35883	0.46	3.8E-01	M18440.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10700	23220		1.82	3.8E-01	AV686974.1	EST_HUMAN	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
11728	24977		3.42	3.8E-01	AF304394.1	NT	AV686974 GKC Homo sapiens cDNA clone GK08QCC11.5'
11854	24214		1.42	3.8E-01	Q61870	SWISSPROT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
11930	24265	31015	1.56	3.8E-01	AE001811.1	NT	HOMEOBOX PROTEIN HLX1
12369	24551		1.37	3.8E-01	11433335	NT	Thermotoga maritima section 123 of 136 of the complete genome
171	12834		19.28	3.8E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
531	13162		3.11	3.8E-01	A3029291.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1811	14498		0.88	3.8E-01	AE003870.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
2605	15167	27734	1.89	3.8E-01	AF214117.1	NT	Xyella fastidiosa, section 18 of 228 of the complete genome
2681	15473	27791	3.94	3.8E-01	6878002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3034	15650		0.89	3.8E-01	AJ251087.1	NT	Mus musculus soluble carrier family 1, member 8 (Slc1a8), mRNA
3084	15688	28173	2.2	3.8E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213)
3530	16135	28815	9.83	3.8E-01	AL161518.2	NT	Pleurococcus americanus aminopeptidase N (ampN) gene, partial cds
3592	16186		0.59	3.8E-01	A1807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3609	16188		0.75	3.8E-01	A1807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3820	16420	28882	0.94	3.8E-01	BE154080.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3989	16587	29058	0.8	3.8E-01	6784096	NT	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4138	16730	29183	0.69	3.8E-01	AJ271361.2	NT	Mus musculus general transcription factor III I (Gt2), mRNA
5271	17833	30259	0.99	3.8E-01	BE544653.1	EST_HUMAN	Tadifugu rubripes wr12 (partial), frank1, cfr and frank2 (partial) genes
							601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
							yr88a11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:210428 5' similar to
							gb M87933 HUMAAAL0364 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb M88958
5412	17989	30378	1.07	3.8E-01	H84927.1	EST_HUMAN	EPIDERMAL GROWTH FACTOR-LIKE CRYPTO PROTEIN (HUMAN); contains Alu repetitive
5794	18419	31135	1.11	3.8E-01	Q04898	SWISSPROT	element; contains MER4 repetitive element ;
6481	19082		0.68	3.8E-01	S46825.1	NT	TRANSCRIPTION FACTOR SOX-10
6737	19331	32137	5.29	3.8E-01	BE072399.1	EST_HUMAN	piron protein [mink, Genomic, 2448 nt]
							QV3-BT0537-271299-049-602 BT0537 Homo sapiens cDNA
							ta54f11.x1 Soares fetal, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to
6857	19591	32423	3.97	3.8E-01	A1874801.1	EST_HUMAN	contains Alu repetitive element;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7019	19517	32339	1.33	3.8E-01	AL181513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7626	20046		4.75	3.8E-01	X81597.1	NT	M.musculus gene for kallikrein-binding protein
8238	20779	33700	0.49	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8492	21031	33951	2.34	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8660	21096	34019	1.14	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8761	21260	34210	1.12	3.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
9450	21679		4.03	3.8E-01	T95413.1	EST_HUMAN	ye43h08.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
11408	23859		3.5	3.8E-01	BE18219.1	EST_HUMAN	Alu repetitive element/contains PTR6 repetitive element ;
11541	23989	37080	2.95	3.8E-01	R42550.1	EST_HUMAN	RC9-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11541	23989	37081	2.95	3.8E-01	R42550.1	EST_HUMAN	Y82h11.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11940	24272		2.81	3.8E-01	AE001124.1	NT	Y82h11.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12089	24988		1.75	3.8E-01	U94788.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12199	24421		1.45	3.8E-01	BE929256.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
12555	24684		2.22	3.8E-01	U78031.1	NT	QV3-ET0063-100700-271-s05 ET0063 Homo sapiens cDNA
12638	24713	30896	1.25	3.8E-01	AF184972.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
2521	16085	27657	15.01	3.7E-01	AB037831.1	NT	Mus musculus developmental control protein mRNA, partial cds
3507	16112	28589	10.94	3.7E-01	AF056336.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3938	16536	29003	0.68	3.7E-01	AA319482.1	EST_HUMAN	Danio rerio bone morphogenetic protein 4 precursor (BMP-4) gene, complete cds
4313	16899	29344	9.19	3.7E-01	A1218707.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 5' end
4412	16997	29440	1.18	3.7E-01	AW878037.1	EST_HUMAN	ck39c07.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4478	17094	29514	3.13	3.7E-01	AE002408.1	NT	MR3-O10007-080300-104-b02 OT0007 Homo sapiens cDNA
5938	18557	31285	1.27	3.7E-01	AF135187.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
6105	18721	31474	0.84	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6633	19228	32033	1	3.7E-01	MT0806.1	NT	Homo sapiens chromosome 21 segment HS21C078
6651	19247		0.81	3.7E-01	L10353.1	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
7197	19728	32579	4.44	3.7E-01	11525843	NT	Mus sacicola hemoglobin mRNA, complete cds
8271	20812	33733	1.88	3.7E-01	11436739	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8271	20812	33734	1.88	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (G12ORF4), mRNA
8306	20847	33770	0.76	3.7E-01	AA902812.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 4 (G12ORF4), mRNA
9129	21694		1.54	3.7E-01	AJ271366.1	NT	ck43b11.s1 NCI CGAP Lel2 Homo sapiens cDNA clone IMAGE:1516701 3'
10074	22568		0.48	3.7E-01	K00691.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10111	22808	35596	4.17	3.7E-01	A1336411.1	EST_HUMAN	mouse Ig germline alpha membrane exons region
10808	23428	35446	3.47	3.7E-01	AJ287357.1	NT	qt46b07.x1 Soares Fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1850997 3'
							Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10909	23428	36447	3.47	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11341	23039	36048	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11849	23997		1.8	3.7E-01	AA973540.1	EST_HUMAN	cc48d03.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1699221 3' similar to gb:M77698
11603	24046		2.78	3.7E-01	6877878	NT	TRANSSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN); Mus musculus retinoblastoma 1 (Rb1), mRNA
11640	24601		1.82	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11821	24191		4.15	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
11913	24251		4.72	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12302	24489		2.84	3.7E-01	AL121154.1	EST_HUMAN	DKFZp782K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782K075 5'
12377	24545	30604	7.01	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
282	12938	25424	1.07	3.6E-01	AJ008009.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1033	13643		8.45	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1357	13951	26477	4.32	3.6E-01	T80285.1	EST_HUMAN	Y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1367	13951	26478	4.32	3.6E-01	T80255.1	EST_HUMAN	Y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1959	14543	27099	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg3302.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419 3'
1959	14543	27100	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg3302.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419 3'
1994	14576	27136	7.23	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2098	14877		0.88	3.6E-01	AF059827.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2309	14881		1.13	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2433	15000		2.49	3.6E-01	X76725.1	NT	P. Irregularis (P3804) gene for actin
2528	15082	27665	3.34	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-q07 ST0171 Homo sapiens cDNA
2659	15216	27789	1.38	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN:BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2824	16012		10.38	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3516	16121	28600	2.18	3.6E-01	X76758.1	NT	H. sapiens saccharin transporter gene, exons 9 and 10
3516	16121	28601	2.18	3.6E-01	X76758.1	NT	H. sapiens saccharin transporter gene, exons 9 and 10
4497	17051	28550	1.97	3.6E-01	BE707893.1	EST_HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4850	17428	28880	0.84	3.6E-01	AJ009608.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4867	17443	28894	0.65	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5153	17723	30154	2.28	3.6E-01	AW338993.1	EST_HUMAN	h02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5261	17824	30249	0.58	3.6E-01	BE087698.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6236	18845	31616	1.18	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 6 PRECURSOR (PHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6604	19201	32008	1.68	3.6E-01	Y10198.1	NT	Homo sapiens PHEX gene
7202	19733		4.57	3.6E-01	R64090.1	EST_HUMAN	Y74608.1:1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
7327	19854	32717	1.73	3.6E-01	AW027174.1	EST_HUMAN	wf72c10.x1 Soares_thymus_NHFrH Homo sapiens cDNA clone IMAGE:2813010 3' similar to TR:O15117
8186	20707	33623	0.88	3.6E-01	P88167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1];
8221	20762	33678	13.59	3.6E-01	AL161583.2	NT	SCO-SPONDIN
8932	21470	34388	3.06	3.6E-01	4504988	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8932	21470	34388	3.06	3.6E-01	4504988	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8932	21470	34388	3.06	3.6E-01	4504988	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9120	21658	34507	1.32	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9320	21834	34784	0.92	3.6E-01	X17550.1	NT	D. melanogaster elinged gene, exons 3, 4, 5 & 6
9320	21834	34785	0.92	3.6E-01	X17550.1	NT	D. melanogaster elinged gene, exons 3, 4, 5 & 6
9390	21813		0.54	3.6E-01	X82826.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
9777	22275	35260	16.16	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9904	22401	35374	0.53	3.6E-01	AW752801.1	EST_HUMAN	MR2-CT0222-211098-002-b10 CT0222 Homo sapiens cDNA
9904	22401	35376	0.53	3.6E-01	AW752801.1	EST_HUMAN	MR2-CT0222-211098-002-b10 CT0222 Homo sapiens cDNA
10823	23344	36359	2.51	3.6E-01	BE902390.1	EST_HUMAN	601678418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958897 5'
10987	23501	36531	4.15	3.6E-01	AB004263.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11055	23577	36815	2.02	3.6E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
11318	23016	36025	4.07	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11680	25109		2.45	3.6E-01	Y19210.1	NT	Homo sapiens HHb5 gene for hair keratin, exons 1 to 9
11768	24159		5.79	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11923	24258		4.7	3.6E-01	U66898.1	NT	Mus musculus Emr1 mRNA, complete cds
12308	24502		2.16	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 10 (AF10), mRNA
120	12761	25273	1.35	3.5E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
223	12884	25369	2.67	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
706	13327	26814	4.48	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
754	13373	25868	1.39	3.5E-01	7708138	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
754	13373	25868	1.39	3.5E-01	7708138	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
812	13430	25835	3.83	3.5E-01	BF128766.1	EST_HUMAN	601811060RT NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1682	14274	26807	1.91	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2322	14893	27469	1.12	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2637	16472	27770	1.92	3.5E-01	AA223282.1	EST_HUMAN	z08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2726	15284		11.8	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
3030	15646	28124	0.57	3.5E-01	AA057691.1	EST_HUMAN	z0403.71 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:612285 6'
3878	16476		1.27	3.5E-01	AA642136.1	EST_HUMAN	nr60d03.s1 NCI_QGAP_Lyn3 Homo sapiens cDNA clone IMAGE:1172357 3'
4349	16936	26377	2.3	3.5E-01	AF071283.1	NT	Danio rerio homeobox protein (hoxbb) gene, complete cds
5014	17588	30031	0.57	3.5E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07679, Z40498
5066	17639	30082	4.33	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5537	18169	30583	0.74	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5537	18169	30584	0.74	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5736	18364	31071	1.42	3.5E-01	D42046.1	NT	Human mRNA for KIAA0086 gene, complete cds
6384	18888		0.9	3.5E-01	AW883018.1	EST_HUMAN	PM4-SN0012-030400-001-s11 SN0012 Homo sapiens cDNA
6540	19139	31932	0.75	3.5E-01	AA431833.1	EST_HUMAN	zw7903.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1086935
6578	19176	31978	0.72	3.5E-01	U37150.1	NT	G1086935 F10F2.1;
6770	19363	32172	0.93	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7116	19458		3.51	3.5E-01	X98605.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE; CHLOROPLAST PRECURSOR (G6PD)
8016	20558		2.02	3.5E-01	11448042	NT	S. cerevisiae mRNA for CD31 protein (PECAM-1)
8019	20561	33482	0.85	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8403	20943		0.81	3.5E-01	AF051681.1	NT	RC4-ET0024-280600-014-d07 E70024 Homo sapiens cDNA
8857	21386	34319	1.12	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9651	22150	35120	1.93	3.5E-01	Q02284	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9801	22288	35284	4.91	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9877	22374	35351	1.14	3.5E-01	BE174764.1	EST_HUMAN	Xlaevis gene for albumin including HP1 enhancer
10813	23146	36157	4	3.5E-01	X81084.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10902	23422	36440	2.09	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
10902	23422	36441	2.09	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for cartonnectin, promoter and exon 1
11482	23912	36879	1.83	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11532	23950	37050	1.71	3.5E-01	L05145.1	NT	y20h12.r1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:260376 6'
						NT	Human glucokinase (GOK) gene, repeat polymorphism

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	28112		1.51	3.5E-01	AF287488.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
11851	24211		7.58	3.5E-01	X04505.1	NT	B. taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12014	24313		2.03	3.5E-01	AE001774.1	NT	Thermoboga maritima section 88 of 138 of the complete genome
12209	24433		2.21	3.5E-01	AE001691.1	NT	Thermoboga maritima section 3 of 138 of the complete genome
12843	24850	30825	2.84	3.5E-01	H60814.1	EST_HUMAN	ye84f11.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
12843	24850	30828	2.84	3.5E-01	H60814.1	EST_HUMAN	ye84f11.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
738	13356		1.5	3.4E-01	AJ242855.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1011	13821	26136	7.82	3.4E-01	Y09768.2	NT	Pseudomonas fluorescens cdiR, cdiS genes, ori222 and partial inaA gene
1013	13823	26138	8.97	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241189-019-g10 HT0261 Homo sapiens cDNA
1371	13965	26491	1.86	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2445	15012	27584	2.8	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11727, 1311235-1430418
3032	15648	28126	0.73	3.4E-01	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3032	15648	28127	0.73	3.4E-01	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3183	15788	28268	0.86	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11727, 1311235-1430418
3197	15809	28282	6.78	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3387	15986	28473	0.84	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3584	16188	28871	4.84	3.4E-01	AF108835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3858	16456		1.32	3.4E-01	BF448010.1	EST_HUMAN	7n84801.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8LJ15
4108	16702		1.23	3.4E-01	AF184614.1	NT	Q8LJ15 DJ18C8.1
4128	16718		1.56	3.4E-01	AA594198.1	EST_HUMAN	Homo sapiens p47-phox (NCF1) gene, complete cds
4584	17177	28824	0.7	3.4E-01	AF168341.1	NT	no11b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4749	17330	29773	2	3.4E-01	BE069912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4765	17348	29795	1.01	3.4E-01	BF314886.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5087	17680		4.2	3.4E-01	AJ240973.1	EST_HUMAN	601801632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130835 5'
5884	18488	31210	2.9	3.4E-01	AL181584.2	NT	q95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1887208 3' similar to contains Alu repetitive element
5979	18599		5.88	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
6158	18771		2.44	3.4E-01	L02871.1	NT	zn12d11.s1 Striatogene iNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
							Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6181	18791	31560	0.69	3.4E-01	BE748012.1	EST_HUMAN	601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6266	18895	31635	2.45	3.4E-01	AW2004505.1	EST_HUMAN	U1-H-B11-est-e-12-0-U1.1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6382	18986	31768	1.62	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6841	19431		1.32	3.4E-01	N062255.1	EST_HUMAN	z53a12.s1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
							tm83g05.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
7027	19561	32388	1.09	3.4E-01	AI468082.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7847	20389		0.51	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
9179	20720	33635	0.51	3.4E-01	Y14930.1	NT	Homo sapiens TORAV28 gene, allele A4, partial
8424	20804		1.92	3.4E-01	AA337083.1	EST_HUMAN	EST141765 Endometrial tumor Homo sapiens cDNA 5' end
8498	21037	33958	0.88	3.4E-01	L04690.1	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8788	21326	34249	1.63	3.4E-01		NT	Bovine enterovirus strain K2577, complete genome
9139	21674	34616	3.89	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9139	21674	34617	3.89	3.4E-01	AB017510.1	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9342	21866		0.59	3.4E-01	U19492.1	NT	Ephydra fluviatilis mRNA for PLC-gamma5, complete cds
9367	20306	33208	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9387	20306	33209	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9812	22112	35075	0.86	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scdf-1) mRNA, complete cds
9804	22302	35286	1.99	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10373	22887		0.54	3.4E-01	AE004086.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
						NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
10895	23416		4.42	3.4E-01	AE000881.1	NT	PROBABLE E4 PROTEIN.
10832	23450	36471	2.61	3.4E-01	P06925	SWISSPROT	
10869	23494	36512	2.72	3.4E-01	AF045981.1	NT	Rubus arceoli cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11164	23671	36716	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11164	23671	36717	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11372	23824	36887	2.27	3.4E-01	AB036507.1	NT	Rattus norvegicus mRNA for s-glycerinMUG18, complete cds
11401	23852	36917	4.39	3.4E-01	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11614	24056	37121	1.75	3.4E-01	BF081948.1	EST_HUMAN	7468412.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480648 3'
11655	24092		2.12	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
11771	24160		1.44	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
11873	24636		1.8	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwifp (cwifb) gene, complete cds
11996	24303		14.59	3.4E-01	L26339.1	NT	Human autubantigen mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12023	24895		3.18	3.4E-01	BE218552.1	EST_HUMAN	h42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12079	24974		2.44	3.4E-01	9838381	NT	PTR5 repetitive element ;
12108	24924	30860	2.68	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12427	25098		1.25	3.4E-01	AJ288948.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
							Clostridium cellulidicum partial spoIVB gene and spoA gene, strain ATCC 35319
12523	24639		2.55	3.4E-01	AF018413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
12861	24723		2.71	3.4E-01	11460174	NT	Neisseria glabreri mitochondrion, complete genome
16	12695	25151	13.68	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
110	12695	25151	3.76	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
473	13108	25589	1.08	3.3E-01	AL181545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
881	13285	25786	1.87	3.3E-01	7682486	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1242	13840	26358	2.68	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1350	13945	26469	3.58	3.3E-01	BF568880.1	EST_HUMAN	602194016T1 NIH_MGC 42 Homo sapiens cDNA clone IMAGE:4300251 3'
1649	14241	26775	1.43	3.3E-01	8753655	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1773	14363		1.44	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2079	14655		1.22	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
							Homo sapiens uridine monophosphate synthetase (uridate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2450	15017		5.41	3.3E-01	4507834	NT	Bacteriophage phi-Y603-12 complete genome
2976	15592	28074	2.14	3.3E-01	AJ251805.1	NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3049	15685		0.68	3.3E-01	O02743	SWISSPROT	Streptomyces argillaceus mithramycin biosynthetic genes
3081	16708	28178	0.82	3.3E-01	AJ007632.2	NT	Homo sapiens MTA1-L1 gene, complete cds
3542	16147	28628	0.99	3.3E-01	AB012822.1	NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3882	16480	28942	2.14	3.3E-01	O84845	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT
3890	16489	28949	0.85	3.3E-01	P22802	SWISSPROT	PROTEINASE (HC-PRO); PROTEIN P3j
4037	16635	29104	1.49	3.3E-01	AL181488.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4073	16669	29130	1.95	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4457	17043		1.44	3.3E-01	D31882.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
							bp78b12.x1 NCI_CGAP_Lu13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORT 1 (HUMAN);
4768	17377		1.57	3.3E-01	A1539114.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2668786
4964	17538	29880	1.44	3.3E-01	D84003.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18159	30573	2.76	3.3E-01	X69819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5527	18159	30574	2.75	3.3E-01	X69819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
6101	18717	31468	1.72	3.3E-01	BE619850.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
6101	18717	31468	1.72	3.3E-01	BE619850.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
6198	18798	31587	12.71	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROITE PROTEIN (CS)
6959	19546	32369	4.8	3.3E-01	A1828131.1	EST_HUMAN	ly84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6959	19546	32370	4.8	3.3E-01	A1828131.1	EST_HUMAN	ly84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7758	20268	33182	1.81	3.3E-01	N85148.1	EST_HUMAN	J2488F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2488 5' similar to TEGT
8497	21036	33957	17.55	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
8663	21202	34120	0.48	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8698	21235	34187	0.49	3.3E-01	AU128115.1	EST_HUMAN	AU128115 NT2RFP1 Homo sapiens cDNA clone NT2RFP1000130 5'
8698	21235	34188	0.49	3.3E-01	AU128115.1	EST_HUMAN	AU128115 NT2RFP1 Homo sapiens cDNA clone NT2RFP1000130 5'
9042	21578	34508	0.83	3.3E-01	Q82826	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9300	21900	34848	0.99	3.3E-01	BE28461.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9300	21900	34849	0.98	3.3E-01	BE28461.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9430	21939	34887	3.24	3.3E-01	N99886.1	EST_HUMAN	z667h01.s1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:287649 3'
9471	21870	34819	2.93	3.3E-01	BF378745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9902	22398		2.16	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
10800	23134	35147	2.93	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10800	23134	35148	2.93	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10905	23424		1.8	3.3E-01	BF528499.1	EST_HUMAN	602070802F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213585 5'
11110	23820	36681	17.52	3.3E-01	BE219351.1	EST_HUMAN	h51g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176878 3'
11223	23754	36812	4.87	3.3E-01	P47853	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 36) (CBP 36) (LAMININ-BINDING PROTEIN) (LECTIN L-26) (CBP30)
11595	24012		4.88	3.3E-01	AA808621.1	EST_HUMAN	6571g02.x1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338850 3'
11594	12895	25157	2.48	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
11759	24153	36771	1.98	3.3E-01	6598318	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12510	24631		36.28	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-644000 nt. position (2/7)
482	13115		1.78	3.2E-01	AF018281.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13387		0.78	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1204	13904	26317	27.98	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1325	13919	26441	1.39	3.2E-01	Z50202.1	NT	P. vulgaris arcd-1 gene
1434	14027	26555	7.37	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1811	14401	26948	0.92	3.2E-01	Z38041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1819	14409	26954	6.36	3.2E-01	AW957104.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1819	14409	26955	6.36	3.2E-01	AW957104.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1883	14469	27028	1.22	3.2E-01	AL111855.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2203	14781	27354	2.89	3.2E-01	BF203817.1	EST_HUMAN	601869804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2578	15140		2.24	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxact1), mRNA
2734	16289	27857	1.09	3.2E-01	AF060588.1	NT	Homo sapiens promyelocytic leukemia zho finger protein (PLZF) gene, complete cds
3663	16289		0.78	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4023	16621		0.81	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4483	17088	28518	1.94	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4597	17181	28628	1.56	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C19G7.04C IN CHROMOSOME 1 PRECURSOR
4844	17422		6.52	3.2E-01	BF603817.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 6'
5009	17582	30025	0.63	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5174	17741	30170	0.58	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888799 5'
5392	17850	30363	0.93	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5478	18110	30519	2.5	3.2E-01	BE173984.1	EST_HUMAN	CMD-HT0569-060300-289-f10 HT0569 Homo sapiens cDNA
6112	18728	31481	1.18	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
8831	19421		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8113	20654	33563	1.33	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8210	20751	33685	0.51	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat map NOS-D12Wax1
8308	20849	33772	11.34	3.2E-01	X02508.1	NT	H.sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8311	20852	33777	18.78	3.2E-01	BF311835.1	EST_HUMAN	601697107F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4126833 5'
8398	20938		1.43	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8437	20977	33891	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8437	20977	33892	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8508	21047	33968	2.72	3.2E-01	AE002016.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8503	21144	34058	0.69	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8605	21144	34069	0.69	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8997	21535	34485	0.58	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9007	21544		2.08	3.2E-01	M86811.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9077	21613	34547	0.48	3.2E-01	AF041826.1	NT	Homo sapiens 9-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9077	21613	34548	0.48	3.2E-01	AF041826.1	NT	Homo sapiens 9-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9805	22402	35376	3.22	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid bp32-2, erpC and erpD genes, complete cds; and unknown genes
10100	22595	35588	0.51	3.2E-01	BE328230.1	EST_HUMAN	h46h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568 3'
10213	22708		3.03	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10548	23084	36068	3.28	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stragene (cat#036206) Homo sapiens cDNA clone HFBDDZ21
11796	24698		4.31	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12344	24528		4.65	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12441	24819		3.37	3.2E-01	AF157625.1	NT	Bos taurus insulinol 1,4,5-bisphosphate receptor type I mRNA, complete cds
12489	24618		1.94	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12550	25041	30504	1.98	3.2E-01	BE385776.1	EST_HUMAN	601276480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618746 5'
2685	15282	27823	2.39	3.1E-01	R18051.1	EST_HUMAN	y901h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2722	15403	27843	3.67	3.1E-01	768197.1	NT	gb:M84241 QM PROTEIN (HUMAN);
2722	15403	27844	3.67	3.1E-01	768197.1	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2883	15501		1.35	3.1E-01	AW628036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3208	15820		3.53	3.1E-01	AB029089.1	NT	Mus musculus gene for Ser/Thr Kinase KIAMRE, exon 6
3978	16576	29046	0.91	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5055	17628	30072	0.79	3.1E-01	S68245.1	NT	carbanic anhydrase IV [rat, Sprague-Dawley, lung, mRNA, 1205 nt]
5097	17870	30109	0.82	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 228 of the complete genome
5208	17771	30194	0.98	3.1E-01	AL181503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5889	18298	30776	10.8	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5786	18411	31127	0.76	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5798	18421		0.99	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5945	18585	31295	2.16	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6592	19189	31892	2.63	3.1E-01	AW983549.1	EST_HUMAN	RC3-HNC001-310300-011-304 HNC001 Homo sapiens cDNA
6854	19250	32052	0.87	3.1E-01	AJ264458.1	EST_HUMAN	q136d01.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1874689 3'
6784	19375	32191	0.81	3.1E-01	XT1897.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region AB and AB
6863	19597		0.9	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-26 1099-005-H05 CT0222 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	24741	30468	2.4	3.1E-01	BE737392.1	EST_HUMAN	601308121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:38420 5'
7671	20183	33071	1.18	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8582	21121	34041	1.22	3.1E-01	R45318.1	EST_HUMAN	Y94801.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
8816	22314	36286	0.46	3.1E-01	6876323	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
8979	22474	35459	0.81	3.1E-01	BF698638.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281811 5'
8979	22474	35467	0.81	3.1E-01	BF698639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281811 5'
10036	22530	36526	1.7	3.1E-01	A1244001.1	EST_HUMAN	q181e11.x1 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:1883980 3' similar to gb:S66700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10204	22899		0.54	3.1E-01	T55325.1	EST_HUMAN	y947n08.s1 Stragene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar to gb:M91036_m2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10717	23245	36261	1.95	3.1E-01	BF218117.1	EST_HUMAN	601883562F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11411	23862	36923	2.03	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11921	24257		2.13	3.1E-01	AF284308.1	NT	Ardis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11980	24282		1.96	3.1E-01	AF304182.1	NT	Sizobedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12108	24370		3.31	3.1E-01	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
12496	24924		3.89	3.1E-01	AF186779.1	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), mRNA
12535	25035		1.62	3.1E-01	10948623	NT	Mus musculus protein kinase C, epsilon (Pkoa), mRNA
76	15382	25234	1.37	3.0E-01	6755083	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
276	12932	26419	11.51	3.0E-01	AJ271735.1	NT	x83308.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2774343 3'
1286	13863	26380	2.05	3.0E-01	AW300400.1	EST_HUMAN	Baleenoptera physalus gene encoding atrial natriuretic peptide
1555	14147	26680	6.64	3.0E-01	AJ008755.1	NT	Corynebacterium sp. ALY-1 alypG gene for polyglutamate lyase, complete cds
3248	15960		1.4	3.0E-01	AB030481.1	NT	PM1-ST0262-261189-001-g01 ST0262 Homo sapiens cDNA
3932	16530	26997	2.1	3.0E-01	AW817785.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
4046	16843	29109	1.01	3.0E-01	AJ271736.1	NT	Baleenoptera physalus gene encoding atrial natriuretic peptide
4811	17184	28840	1.78	3.0E-01	AJ008755.1	NT	Baleenoptera physalus cDNA clone IMAGE:3846734 5'
5554	18188	30601	5.34	3.0E-01	AJ741628.1	EST_HUMAN	Canis lupus familiaris hemagglutinin gene, complete cds
5627	18256	30726	0.88	3.0E-01	AF229247.1	NT	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5685	18321	30820	4.03	3.0E-01	BE065575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5695	18321	30821	4.03	3.0E-01	BE065575.1	EST_HUMAN	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
5731	18357	31062	4.57	3.0E-01	U01247.1	NT	Mouse cyclodextrin 15 gene, complete cds
5919	19578	32407	3.14	3.0E-01	D18313.1	NT	

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944	18082	30476	0.7	3.0E-01	U02360.1	NT	Strongylocentrotus purpuratus 34/67 kDa lamelin-binding protein mRNA, partial cds
7005	19503	32322	0.86	3.0E-01	AF226247.1	NT	Canigalo orthopoxvirus hemagglutinin gene, complete cds
7175	19707	32656	0.78	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7387	19893	32768	6	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7512	20033	32899	1.88	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL6 PspA (pspA) gene, partial cds
7887	20409	33316	1.07	3.0E-01	AE001755.1	NT	Thermotoga maritima section 87 of 138 of the complete genome
8314	20856		3.82	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f9), mRNA
8411	20951	33870	1.27	3.0E-01	BE568083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8763	21302	34223	0.82	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbC) gene, partial cds
8805	21344		0.95	3.0E-01	7681685	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA
9145	21880	34824	0.98	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9483	21893	34949	0.55	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 69.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9878	22375	35352	0.84	3.0E-01	BF674812.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10294	22788	35778	0.58	3.0E-01	AW118111.1	EST_HUMAN	6003410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10298	22790	35780	1.65	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds
10315	22809	35801	0.73	3.0E-01	BF883841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301087 5'
10315	22809	35802	0.73	3.0E-01	BF883841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301087 5'
11804	24047	37112	2.87	3.0E-01	H51028.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:194107 5'
11604	24047	37113	2.87	3.0E-01	H51028.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:194107 5'
11875	24287		1.37	3.0E-01	P54690	SWISSPROT	PONTICULIN PRECURSOR
12227	24984		2.93	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12528	25053		2.51	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
1924	14509	27084	2.27	2.9E-01	6174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2070	14850	27221	1.38	2.9E-01	AE000738.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2524	15088		1.22	2.9E-01	M32360.1	NT	Mouse apolipoprotein A-II (ApoA2) gene, complete cds
3289	15900	28379	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171298-001-f12 CT0328 Homo sapiens cDNA
3289	15900	28380	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171298-001-f12 CT0328 Homo sapiens cDNA
3865	16563	29032	0.71	2.9E-01	AI610838.1	EST_HUMAN	6021411.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4159	16751		0.67	2.9E-01	AW002902.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element ;
							6021411.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
							6021411.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4583	17166	29609	1.21	2.9E-01	AA284468.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4793	17372		0.63	2.9E-01	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6148	17718		1.02	2.9E-01	U00756.1	NT	Lymnaea dispar vitellinogenin gene, complete cds
6164	17724	30166	1.43	2.9E-01	7682160	NT	Homo sapiens KIAA0537 gene product (KIAA0537), mRNA
6285	17847		1.7	2.9E-01	A1070898.1	EST_HUMAN	wc0003.x1 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1 repetitive element:
5463	18098		1.25	2.9E-01	R37485.1	EST_HUMAN	y77612.e1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5592	19522	32344	0.70	2.9E-01	AF32100.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5937	18558	31286	5.1	2.9E-01	X55098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P18,18,28,30 and levanase
5937	18558	31287	5.1	2.9E-01	X55098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P18,18,28,30 and levanase
5849	18570	31302	6.08	2.9E-01	6678682	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6208	18816	31587	1.28	2.9E-01	AA418145.1	EST_HUMAN	z697612.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6427	19030	31813	0.83	2.9E-01	A1797128.1	EST_HUMAN	wc27c05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element:
6487	19088	31854	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6586	19183	31983	0.72	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6585	19183	31984	0.72	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7082	18081	30437	1.35	2.9E-01	AF142328.1	NT	Mus musculus Filh protein (Filh) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7153	19685	32527	2.87	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR508C
7213	19744	32598	1.81	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region: Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
7860	20402	33308	1.82	2.9E-01	BE540422.1	EST_HUMAN	60106830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33309	1.82	2.9E-01	BE540422.1	EST_HUMAN	60106830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8103	20844		0.88	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8531	21070	33990	0.66	2.9E-01	AU160910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8856	21395	34318	1.07	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
8963	21501	34423	0.71	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9170	21747	34689	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9170	21747	34690	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10773	23287	36302	2.24	2.9E-01	AF129843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11041	23556	36589	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11041	23556	36590	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11453	23903	39970	2.07	2.9E-01	AA835373.1	EST_HUMAN	nv5502.s1 NCI_CGAP_P412 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
11456	23908	39973	5.52	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6 wz58705.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2665921 3' similar to contains element MER20 repetitive element;
12172	24411	39944	1.84	2.9E-01	AW005871.1	EST_HUMAN	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12262	24472	39932	1.47	2.9E-01	AF092453.1	NT	601482039F1 NIH_MGC_08 Homo sapiens cDNA clone IMAGE:3894559 5'
12313	24505		1.4	2.9E-01	BE788189.1	EST_HUMAN	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12586	24679	39877	1.57	2.9E-01	Y06937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12586	24679	39878	1.57	2.9E-01	Y06937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
594	13224		2.08	2.9E-01	U87138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
599	13228		0.75	2.9E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1122	13725	28238	3.14	2.9E-01	AF169050.1	NT	Gulra gulra oocyte maturation factor Mos (o-mos) gene, partial cds
1320	13914	28435	3.51	2.9E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3183888 5'
1320	13914	28436	3.61	2.9E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3183888 5'
1334	13928	28448	1.03	2.9E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1765	14355	28902	2.01	2.9E-01	AW880020.1	EST_HUMAN	QV1-GT0364-120200-065-005 CT0364 Homo sapiens cDNA
2057	14638	27210	2.12	2.9E-01	AD47620.1	EST_HUMAN	DKFZp588l2321.1 598 (synonym: huter1) Homo sapiens cDNA clone DKFZp588l2321
2175	14752	27322	3.53	2.9E-01	AW511195.1	EST_HUMAN	hd44503.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2812333 3'
2511	15075	27648	2.41	2.9E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2511	15075	27649	2.41	2.9E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2684	15147		2.75	2.9E-01	AL181585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2688	15249	27813	1.21	2.9E-01	AB020875.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2898	15814		1.7	2.9E-01	AF179480.1	NT	Toxoplasma gondii 60kDa heat-shock protein (HSP60) mRNA, partial cds
2898	15815	28094	2.38	2.9E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2898	15815	28095	2.38	2.9E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3426	16033	28513	1.28	2.9E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt position (4/7)
4088	16684	28125	2.08	2.9E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4202	16781		0.62	2.9E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4276	16862		2.75	2.9E-01	A100888.1	EST_HUMAN	ov44g10.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4553	17136	28584	1.32	2.9E-01	AD21127.2	NT	Mus musculus chromosome X contigA; putative Magee9 gene, Caltractin, NAD(P) ⁺ steroid dehydrogenase and Zinc finger protein 185
4559	17142	28590	2.47	2.9E-01	P13815	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4887	17472	28928	1.07	2.9E-01	D15050.1	NT	Human mRNA for transcription factor AREB9, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4897	17472	29929	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4837	17512	29858	1.02	2.8E-01	AW594539.1	EST_HUMAN	hg68405.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2950569 3'
4949	17524	29985	1.17	2.8E-01	AF079238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4955	17530	29972	3.5	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4986	17560	30003	1.67	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4180129 5'
5013	17587	30030	2.82	2.8E-01	AJ272699.1	EST_HUMAN	q158c11.x1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1876828 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5514	24744	30558	21.59	2.8E-01	AA349897.1	EST_HUMAN	EST67072 Infant brain Homo sapiens cDNA 5' end
5781	18416	31132	2.76	2.8E-01	AB018625.1	NT	Homo sapiens OCTN2 gene, complete cds
5983	18603		0.97	2.8E-01	AW992583.1	EST_HUMAN	CM1-BN0024-180200-118-g12 BN0024 Homo sapiens cDNA
6078	18695	31442	0.69	2.8E-01	AA785286.1	EST_HUMAN	ca01408.s1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1903691 3' similar to gb:M34539 FK508-BINDING PROTEIN (HUMAN);
6323	25114		0.76	2.8E-01	M36888.1	NT	Bovine 880 bp repeated unit of 1.723 satellite DNA
6366	18970	31748	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6366	18970	31749	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6829	19419	32235	8.4	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-act-144-Q-J.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7487	19989		1.19	2.8E-01	U05633.1	NT	Mareilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl.) gene, chloroplast gene encoding chloroplast protein, partial cds
7768	20276	33174	0.69	2.8E-01	BE637151.1	EST_HUMAN	801063105F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449569 5'
8038	20578	33482	1.12	2.8E-01	AJ346128.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1826289 3' similar to gb:X06323_cds1
8038	20578	33483	1.12	2.8E-01	AJ346128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8150	20691	33605	2.18	2.8E-01	U51688.1	NT	qp48h01.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1826289 3' similar to gb:X06323_cds1
8451	20991	33909	0.47	2.8E-01	AA911629.1	EST_HUMAN	Homo sapiens lnc014714-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8525	21084		6.69	2.8E-01	BF347847.1	EST_HUMAN	af02h05.s1 NCL_CGAP_C012 Homo sapiens cDNA clone IMAGE:1418983 3' similar to gb:M87789 IG
9387	21810	34761	1.22	2.8E-01	U17251.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9827	22127		1.03	2.8E-01	L13854.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
9803	22301	35286	1.04	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
9803	22301	35287	1.04	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9861	22358	35338	0.84	2.8E-01	AF294393.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9972	22487	35451	1.91	2.8E-01	7706163	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
							Homo sapiens hypothetical protein (LOC51319), mRNA

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10215	22710		0.81	2.8E-01	6026164	NT	Fujinami sarcoma virus, complete genome
10255	22750	35738	0.47	2.8E-01	BE59727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
10622	23154	36168	2.28	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106350 5'
10622	23154	36167	2.28	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106350 5'
10651	23183	36187	2.83	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4076026 5'
10760	23284	36207	3.31	2.8E-01	AF051682.1	NT	Drosophila heteronema fruticosa (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11159	23685		4.99	2.8E-01	BF974023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4279853 5'
12213	24438		15.74	2.8E-01	D83326.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12328	24514	30920	8.89	2.8E-01	BE178899.1	EST_HUMAN	PM4-HT06068-030400-001-407 HT06068 Homo sapiens cDNA
12356	24533	30927	1.25	2.8E-01	BE600116.1	EST_HUMAN	601873020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955998 5'
12519	24988		2.21	2.8E-01	11433628	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
502	13134	25622	3.21	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
641	13284	28740	2.53	2.7E-01	AA450081.1	EST_HUMAN	z39b10.1 Scarsa_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:765827 3' similar to contains Alu repetitive element
1304	13888	26418	1.89	2.7E-01	AB004808.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1862	14255		2.17	2.7E-01	X79815.1	NT	G.lamblia SR2 gene
1767	14357	26903	3.34	2.7E-01	W59067.1	EST_HUMAN	zid22h10.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1813	14403	26948	4.14	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10
2181	15458		2.77	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoclinin transporter type 2, promoter region and exon 1
2405	14973	27545	7.35	2.7E-01	Y13888.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M85), partial
2498	15060	27634	3.82	2.7E-01	A1310859.1	EST_HUMAN	ts43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3013	15628		0.73	2.7E-01	BF089284.1	EST_HUMAN	CM1-HT0875-060800-385-905 HT0875 Homo sapiens cDNA
4082	16678	29138	1.98	2.7E-01	A1928015.1	EST_HUMAN	w62d11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4086	16691	29147	0.78	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4096	16691	29148	0.78	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4101	16695	29151	2.31	2.7E-01	L75589.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
5020	17594	30037	0.98	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds
5193	17758		3.82	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0288-230200-018-e03 CT0288 Homo sapiens cDNA
5471	18105	30424	2.07	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4)
5681	18308		0.96	2.7E-01	AB033171.1	NT	Astrepore myriophthalma mitochondrial cyb gene for cytochrome b, partial cds
6724	18318	32122	1.07	2.7E-01	AE001084.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6724	19318	32123	1.07	2.7E-01	AE01084.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6875	19809	32443	2.03	2.7E-01	Q61684	SWISSPROT	FIBRILLIN 1 PRECURSOR
7085	19856	32495	0.76	2.7E-01	U16987.1	NT	Drosophila melanogaster r640 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
7393	19918	32782	0.87	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0663.3 IN CHROMOSOME X
7582	20079	32954	0.95	2.7E-01	Q01188	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7662	20079	32955	0.96	2.7E-01	Q01188	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7877	20188	33076	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7877	20188	33077	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7720	20228	33116	0.82	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
7720	20228	33117	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
7805	20348	33258	0.95	2.7E-01	AA013147.1	EST_HUMAN	ze65b11.61 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
7969	20511		0.51	2.7E-01	AF049820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8078	20621	33534	0.58	2.7E-01	AW888503.1	EST_HUMAN	MR1-SN0082-100500-002-009 SN0082 Homo sapiens cDNA
8127	20668	33577	0.48	2.7E-01	R39257.1	EST_HUMAN	yc81h06.61 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8232	20773	33694	0.94	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8694	21233	34154	0.83	2.7E-01	Q14784	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8957	21495	34418	0.53	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9256	21782	34734	9.93	2.7E-01	O83609	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9256	21782	34735	9.93	2.7E-01	O83609	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9259	21785		2.02	2.7E-01	P37828	SWISSPROT	FIMBRIAE W PROTEIN
9716	22214	35188	0.67	2.7E-01	D89650.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9993	22486	35478	0.91	2.7E-01	AF081848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10026	22521	35517	2.5	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10148	22843	35834	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10148	22843	35835	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10691	23221	36233	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10691	23221	36234	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10702	23231	38244	3.66	2.7E-01	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12288	24863		1.72	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12501	24827		3.98	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
495	18419	25615	2.06	2.6E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
508	13139		1.24	2.8E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1437	14030	28558	2.19	2.8E-01	BE885087.1	EST_HUMAN	801510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1486	14078	28618	1.36	2.8E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1941	14525	27080	6.59	2.8E-01	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1941	14525	27081	6.59	2.8E-01	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2140	14718		13.12	2.8E-01	AW793152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2938431 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfactant protein 3 protein gene (MOUSE);
2197	14773	27347	1.41	2.8E-01	M11844.1	NT	Human prealbumin gene, complete cds
2612	18076		2.09	2.8E-01	Y12896.1	NT	B. maritimus rbcL gene
2683	18148		10.77	2.8E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980043 5'
3640	18243	28719	0.86	2.8E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3705	18306	28775	2.13	2.8E-01	AF228118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
4175	18769	28214	0.7	2.8E-01	AW969510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4234	18822	28273	19.98	2.8E-01	BE080598.1	EST_HUMAN	GV1-BT0630-040400-132-603 BT0630 Homo sapiens cDNA
4448	17034	29477	1.57	2.8E-01	AF175293.1	NT	Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4593	17176	29822	0.78	2.8E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29823	0.78	2.8E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4648	17228	29684	1.35	2.8E-01	AA457817.1	EST_HUMAN	aa88407.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4752	17333	29776	1.63	2.8E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4825	17403	29856	1.47	2.8E-01	AF142703.1	NT	Ophiostoma matricaria-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5107	17679	30118	3.56	2.8E-01	H04859.1	EST_HUMAN	y151e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:162288 5'
5193	17760		0.58	2.8E-01	AA884825.1	EST_HUMAN	am33b11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488605 3'
5544	18176		1.28	2.8E-01	AB035972.1	NT	Paramesitum caudatum gene for PAP, complete cds
5840	18269	30742	0.68	2.8E-01	M86060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCase and CcpA genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6760	18386		0.81	2.6E-01	AI892388.1	EST_HUMAN	td18a03.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
6947	18568	31289	0.69	2.6E-01	AF207650.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGMM enhancer 3 genes, partial cds; and unknown g>
8221	26113		2.36	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
8348	18953	31732	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDFI_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
8348	18953	31733	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDFI_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
8554	19152	31948	1.05	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2481 complete genome, segment 67
7103	18873	32512	0.97	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7457	24783		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/8
7721	20220	33118	1.6	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7791	20334	33240	1.14	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7845	20387	33280	1.18	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0166-181199-003-d12 HT0166 Homo sapiens cDNA
8083	20625	33338	0.67	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8083	20625	33339	0.67	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8276	20817	33738	2.99	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150396 5'
8349	20890	33810	1.89	2.6E-01	Q10109	SWISSPROT	HYPOPHOSPHATASE 2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8827	21168	34080	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8827	21168	34081	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9388	21811	34762	0.96	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.28)
9654	22153		0.5	2.6E-01	AF057121.1	NT	Lontra cernadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9782	22280	35285	0.93	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
9782	22280	35268	0.93	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10093	22588		0.5	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10403	22897		0.91	2.6E-01	Y10189.1	NT	Homo sapiens PHOX gene
10500	22894		0.51	2.6E-01	AI978881.1	EST_HUMAN	wf58b09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491865 3'

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11300	23762	38809	2.18	2.8E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11400	23851		30.68	2.8E-01	X51785.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11777	24185		1.72	2.8E-01	10180855	EST	Mus musculus Jerky (JMK), mRNA
11973	24991		4.08	2.8E-01	BE883491.1	EST_HUMAN	601511032F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912812 5'
12042	24329	30898	4.8	2.8E-01	AF138896.1	NT	Homo sapiens NaK-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
12398	24556		1.34	2.8E-01	D88425.1	NT	Cavia obaya mRNA for serine/threonine kinase, complete cds
12478	24812		1.88	2.8E-01	AE001713.1	NT	Thermoboga maritima section 25 of 138 of the complete genome
12528	24841		1.37	2.8E-01	AF141326.2	NT	Homo sapiens Inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12587	24868		3.74	2.8E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
282	12921	25407	1.48	2.8E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
283	12921	25407	1.77	2.8E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
276	12933		4.28	2.8E-01	M28601.1	NT	Starfish (P. ochreus) cytoplasmic actin gene, complete cds
885	13480	25894	1.02	2.8E-01	U08984.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1098	13703		1.03	2.8E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1160	13763	26274	11.89	2.8E-01	T88837.1	EST_HUMAN	yet1g07.r1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:117468 5'
1568	14158	26689	0.87	2.8E-01	AL115624.1	NT	Batrachoseps atrovirens strain T4 cDNA library under conditions of nitrogen deprivation
1768	14356		8.08	2.8E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1927	15454	27087	1.28	2.8E-01	BE686804.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
1927	15454	27088	1.28	2.8E-01	BE686804.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
2452	15019		12.83	2.8E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2536	15100	27673	0.93	2.8E-01	6678216	NT	Mus musculus protein-L-isocysteine (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2540	15104		1.48	2.8E-01	AA251887.1	EST_HUMAN	zs11a12.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684882 5'
3459	16086		3.41	2.8E-01	AW873471.1	EST_HUMAN	EST385484 MAGE resequencing, MAGM Homo sapiens cDNA
3587	16191	28875	0.84	2.8E-01	AF233876.1	NT	Danio rerio peptide YY precursor gene, complete cds
3603	16207	28885	7.97	2.8E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4143	16735		1.36	2.8E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4409	16994		0.8	2.8E-01	Q05314	SWISSPROT	RHIB PROTEIN
4722	17303	28747	0.59	2.8E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naipe6) gene, complete cds; and Naipe3 gene, exons 2-9 and 11-16
4860	17438		1.47	2.8E-01	Q27225	SWISSPROT	MOL T-INHIBITING HORMONE PRECURSOR (MIH)

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4889	17445	28998	4.89	2.9E-01	AF007788.1	NT	Charltonaera lumiferana deapause associated protein 2 (DAP2) mRNA, complete cds
4896	17471	29927	2.82	2.9E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of the complete chromosome
4924	17489		3.21	2.8E-01	AJ230113.1	NT	Mus musculus erminin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4959	17534	29978	0.61	2.9E-01	BE989785.1	EST_HUMAN	601437488F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
5282	12933		0.65	2.9E-01	M26501.1	NT	Starfish (P. coelatus) cytoplasmic actin gene, complete cds
5529	18181	30578	12.86	2.9E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6114	18730		0.84	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C0307
6738	18332	32138	0.83	2.9E-01	AJ251973.1	NT	Homo sapiens partial sterlin-1 gene
7389	18914	32778	0.82	2.9E-01	U13992.1	NT	Feline calicivirus CFI/68 RNA helicase/cytidine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7413	18938		1.35	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7832	20144	33025	4.48	2.9E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C0382
7786	20328	33236	2.31	2.9E-01	BF108040.1	EST_HUMAN	7157403.x1 Soares NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7797	20340	33248	0.7	2.9E-01	BE980712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828198 3'
8168	20709	33623	2.2	2.9E-01	BF038595.1	EST_HUMAN	601458238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882809 5'
8338	20877	33798	0.72	2.9E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN(E1B 19K)
8571	21110	34029	3.03	2.9E-01	H53236.1	EST_HUMAN	yq8407.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
8808	21347	34271	0.88	2.9E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9435	21981	34809	15.98	2.9E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Ras-1 gene, promoter region
9435	21981	34910	15.98	2.9E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Ras-1 gene, promoter region
9492	21948	34897	2.09	2.9E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9492	21948	34898	2.09	2.9E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10010	22505	35406	1.68	2.9E-01	AW581987.1	EST_HUMAN	RC3-ST0188-130100-015-407 ST0188 Homo sapiens cDNA
10438	22930	35937	1.53	2.9E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCLCGAP_UH1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSRT1 repetitive element;
10439	22933	35941	1.31	2.9E-01	X59481.1	NT	Mouse L1Md LINE DNA
10459	22953	35982	2.03	2.9E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10459	22953	35983	2.03	2.9E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10955	23470	36495	4.3	2.9E-01	D50814.1	NT	Human mRNA for KIAA0124 gene, partial cds
11712	24122	37153	5.28	2.9E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
11740	25075		10.13	2.9E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
578	13209	25687	1.67	2.4E-01	AA836316.1	EST_HUMAN	on70404.at Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
881	13495	26014	2.4	2.4E-01	BF578124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1347	13942	28484	21.38	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1347	13942	28485	21.38	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1427	14020	28548	0.83	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1891	14476		27.27	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1944	14528	27084	1.17	2.4E-01	AF261708.1	NT	Zoocys dhumades fructose-1,6-bisphosphatase mRNA, complete cds
2079	14659	27230	1.49	2.4E-01	AJ742958.1	EST_HUMAN	wg76d05.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:060287 O60287 KIAA0512 PROTEIN. ;
2183	14759	27329	1.04	2.4E-01	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2213	14788		1.04	2.4E-01	P46384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT PROTEASE)
2302	14876	27451	1.78	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2426	14993	27566	1.26	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2576	16138	27708	3.05	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2760	16343	27613	1.79	2.4E-01	X71783.1	NT	D.discoideum (A33-K) porA gene
2812	16364	27633	3.88	2.4E-01	AF030154.1	NT	S.pombe swi8 gene
3168	16780		3.27	2.4E-01	U72728.1	NT	Bovine adenovirus 3 complete genome
3182	16785	28287	1.38	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pd) genes, complete cds
3724	16325	28782	1.26	2.4E-01	AF169793.1	NT	H.sapiens AGT gene, Pad fragment of intron 4
3824	16424	28888	0.83	2.4E-01	AE000312.1	NT	Podospira ensarva HET-C protein (Het-c) gene, complete cds
4103	16697		0.6	2.4E-01	D26960.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
5008	17591	30024	1.08	2.4E-01	AE000305.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5220	17785	30203	0.93	2.4E-01	BE737992.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 185 of 400 of the complete genome
5302	17884		1.55	2.4E-01	K02402.1	NT	60157282F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839775 5'
5653	18280	30758	0.83	2.4E-01	AJ825707.1	EST_HUMAN	Human coagulation factor IX gene, complete cds
5653	18280	30759	0.83	2.4E-01	AJ825707.1	EST_HUMAN	w033d05.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2467128 3'
5678	18303	30785	0.85	2.4E-01	D60871.1	NT	w033d05.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5838	18460	31182	7.92	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5838	18460	31183	7.92	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
8050	24764		1.02	2.4E-01	AJ133836.2	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
							Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
8054	18672	31411	2.36	2.4E-01	BF692338.1	EST_HUMAN	7154d04.x1 NCL CGAP_Brt18 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
8138	18752	31510	2.5	2.4E-01	AF035548.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
							Drosophila melanogaster p38a MAP kinase gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	18849	31619	2.28	2.4E-01	7861801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6280	18898	31669	0.8	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDAAD11 5'
6868	19262	32066	2.43	2.4E-01	AI698989.1	EST_HUMAN	wc92c11.x1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03484
7381	19907	32772	8.84	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7709	20218	33108	1.08	2.4E-01	AF228644.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8139	20680	33591	0.71	2.4E-01	AJ006397.1	NT	Mus musculus DXIm48a protein (DXIm48a) mRNA, complete cds
8139	20680	33592	0.71	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae rro8 and hko8 genes; two component system 08
8280	20831	33762	1.66	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8535	21074	33994	0.97	2.4E-01	BF242794.1	EST_HUMAN	601877879F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4108298 5'
8588	21127		0.58	2.4E-01	BF678275.1	EST_HUMAN	602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4260372 5'
9059	21596	34526	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9059	21598	34527	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9492	21881	34928	8.84	2.4E-01	AI6983515.1	EST_HUMAN	wd436d2.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains
9820	22120	35083	0.8	2.4E-01	AF220057.1	NT	Drosophila melanogaster SKPB gene, complete cds
9820	22120	35084	0.8	2.4E-01	AF220057.1	NT	Drosophila melanogaster SKPB gene, complete cds
10335	22829	35823	1.95	2.4E-01	Q03682	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10847	23179	36192	3.25	2.4E-01	AL161484.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
10715	23243	36260	2.8	2.4E-01	AF030169.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11081	23593		2.28	2.4E-01	Z21647.1	NT	P. asiatica mosaic virus genomic RNA
11665	24089	37145	1.91	2.4E-01	AF217491.1	NT	Homo sapiens fragile 18D cDNA reductase (FOR) gene, exon 6
11807	24853		2.65	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
11868	24220		2.02	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12086	24838		2.18	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12320	25081		1.5	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-508 CT0413 Homo sapiens cDNA
12582	24882		2.31	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
412	13047	25538	0.91	2.3E-01	S78898.1	NT	aromatase [Poephilia guttata=zabira finches, ovary, mRNA, 3188 nt]
685	13289		4.4	2.3E-01	U39713.1	NT	Myoplasma genitalium section 35 of 61 of the complete genome
695	13318	25803	17.02	2.3E-01	U87596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
989	13580	26092	3.44	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1647	14239	26774	1.19	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1674	14268	26800	2.75	2.3E-01	Y10897.2	NT	Mus musculus odh5 gene, exon 1, partial
2089	14689		1.29	2.3E-01	AJ235553.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	18064	27628	2.03	2.3E-01	BE287718.1	EST_HUMAN	601175582F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531016 5'
2878	18238	27803	1.18	2.3E-01	M11318.1	NT	Human erythropoietin gene, complete cds
2861	14024	28552	1.42	2.3E-01	AB016033.1	NT	Martiniella agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2990	18608	28088	0.93	2.3E-01	AA601378.1	EST_HUMAN	no16d08.st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3120	18734	28173.1	6.96	2.3E-01	R21732.1	EST_HUMAN	Y121607.st Soares, placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3417	18025	28607	0.78	2.3E-01	H08838.1	EST_HUMAN	Y07h10.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:213283 5'
3908	18607	28989	1.02	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4008	18607	29468	5.14	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4442	17028	29468	0.83	2.3E-01	R82252.1	EST_HUMAN	Y1701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148017 5'
4489	17074	29578	2.4	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4548	17131	29578	0.87	2.3E-01	D80699.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4588	17189	29813	2.18	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4652	17234	29890	6.13	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (nuclear protein 15) (NP15) mRNA
5180	17585	30028	0.92	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5202	17787	30181	0.82	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5403	17981	30372	0.9	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5507	18140	30552	2.39	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5821	18250	30718	2.05	2.3E-01	BF058381.1	EST_HUMAN	7k30b08.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];
5721	18347	31050	4.56	2.3E-01	X88597.1	NT	C familiaris rom1 gene
5831	18455	31274	1.19	2.3E-01	L39112.1	NT	Vitreoscilla corneum small subunit ribosomal RNA gene
5828	18548	31274	0.78	2.3E-01	S80371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
6098	18712	31461	2.34	2.3E-01	A1708840.1	EST_HUMAN	aa27a12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318448 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6098	18712	31462	2.34	2.3E-01	A1708840.1	EST_HUMAN	aa27a12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318448 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6782	18355	32164	0.76	2.3E-01	AF198089.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit Via (coxVia2) mRNA, complete cds; nuclear gene for mitochondrial product
6958	18336	32360	4.1	2.3E-01	A1718148.1	EST_HUMAN	aa27a12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element;
7165	19897	32544	0.7	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7331	19858	32721	0.89	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7445	19969	32837	2.42	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7603	20116		3.63	2.3E-01	8764776	NT	Mus musculus myosin XV (Myo15), mRNA
7608	20121	32868	1.63	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7732	20240		2.68	2.3E-01	N80963.1	EST_HUMAN	za12908.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282358 5'
7783	20338	33243	0.58	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
7836	20477	33387	1.93	2.3E-01	M69931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8430	20970	33882	0.6	2.3E-01	U67899.1	NT	Mus musculus prosaposin (psapiSGP-1) gene, complete cds
9087	21604	34834	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST194081 Rhadomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X683388)
9087	21604	34835	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST194081 Rhadomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X683388)
9501	22001	34958	0.65	2.3E-01	6678318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9644	22144	35112	0.51	2.3E-01	BE277880.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2886739 5'
9697	22168	35169	0.76	2.3E-01	AW084480.1	EST_HUMAN	EST376833 MAGE resequences, MAGE Homo sapiens cDNA
9748	22244	35225	1.22	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9781	22279	35284	0.65	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281298-001-f04 DT0036 Homo sapiens cDNA
9847	22345	35329	2.8	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0559-240-400-014-g11 HT0559 Homo sapiens cDNA
9903	22400	35373	1.93	2.3E-01	AJ283261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10339	22833	35828	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22845		5.68	2.3E-01	BF133577.1	EST_HUMAN	601846155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10893	23414	36432	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10893	23414	36433	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11068	23580	36619	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11068	23580	36620	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11230	23761	36817	2.49	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 64 of the complete genome
11624	24066		1.6	2.3E-01	AV706738.1	EST_HUMAN	AV706738 ADC Homo sapiens cDNA clone ADCAGH01 5'
11788	24172		2.82	2.3E-01	U49428.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
11878	24226		57.94	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
11899	24804		1.31	2.3E-01	AA069819.1	EST_HUMAN	chn1424.esq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11908	24246		1.61	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-508 SN0012 Homo sapiens cDNA
11969	25002	30610	3.1	2.3E-01	AW303823.1	EST_HUMAN	xy21407.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12007	25053	30511	10.96	2.3E-01	BE882484.1	EST_HUMAN	601607202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908889 5'
12057	24340		1.84	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12107	24389		3.11	2.3E-01	AJ008519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12205	24429		1.36	2.3E-01	U48645.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12211	24369		1.67	2.3E-01	AJ008519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12480	24614		2.57	2.3E-01	BF475811.1	EST_HUMAN	nc339h12.x1 Lupsid_sclatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
12668	24888	30710	1.26	2.3E-01	AA094108.1	EST_HUMAN	MER38 repetitive element;
93	12769	25262	0.91	2.2E-01	AI052190.1	EST_HUMAN	ci1884 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
1611	14204	28738	2.85	2.2E-01	AF187850.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2063	14843		3.88	2.2E-01	AF171801.1	NT	Homo sapiens PPAR delta gene, promoter region
2136	14714	27287	3.16	2.2E-01	M34840.1	NT	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2447	16014	27588	5.61	2.2E-01	BF077538.1	EST_HUMAN	Fresh-water sponge Emri1 alpha collagen (COLF1) gene
2623	16185	27751	1.27	2.2E-01	BE618258.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249868 5'
2623	16185	27752	1.27	2.2E-01	BE618258.1	EST_HUMAN	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868190 5'
2703	16280		1.17	2.2E-01	AL163218.2	NT	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868190 5'
2808	15523	27893	4.28	2.2E-01	BE155925.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS2(C018
2808	15523	27894	4.28	2.2E-01	BE155925.1	EST_HUMAN	PM2-HT0353-281288-003-at12 HT0353 Homo sapiens cDNA
2847	15563		1.64	2.2E-01	AF020503.1	NT	PM2-HT0353-281288-003-at12 HT0353 Homo sapiens cDNA
3439	16047		2.67	2.2E-01	AL161562.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3898	16494		1.18	2.2E-01	AF155728.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4291	16877		1.28	2.2E-01	AF119102.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4300	16888	29330	7.03	2.2E-01	AF155142.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4350	16937	29378	2.59	2.2E-01	AF117340.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
4350	16937	29379	2.59	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
4447	17033	29476	1.36	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
4447	17033	29476	1.36	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4852	17527		1.35	2.2E-01	D50804.1	NT	Human scRNA (BC200 beta) pseudogene
4957	17532	29874	2.86	2.2E-01	AA211216.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5166	17761		1.33	2.2E-01	L13298.1	NT	zq87c05.11 Stratiotes nT neuron (#837233) Homo sapiens cDNA clone IMAGE:848968 5'
5203	17768		1.78	2.2E-01	AE001137.1	NT	Mus musculus vinculin gene, exon 3
							Borrelia burgdorferi (section 23 of 70) of the complete genome

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5291	17853	30277	1.2	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0087-201088-002-c10 HT0087 Homo sapiens cDNA
5316	17878		0.9	2.2E-01	S67585.1	NT	histamine H2-receptor [rat, Genomic, 1928 nt]
5919	18541	31287	2.46	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5930	18552		3.63	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2302729-2308889
6160	18763	31525	0.73	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6160	18763	31526	0.73	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6807	19388	32212	0.85	2.2E-01	AB038480.1	NT	Homo sapiens gene for fukutin, complete cds
7093	19684	32503	9.14	2.2E-01	AV759238.1	EST_HUMAN	AV759238 BIM Homo sapiens cDNA clone BMFAHC08 5'
7183	19715	32582	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7183	19715	32583	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7333	19860	32723	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7333	19860	32724	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7688	20197	33085	0.68	2.2E-01	AF287987.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7963	20505		3.08	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8032	20574	33479	0.84	2.2E-01	Z49633.1	NT	E.coli sepA and sepB genes
8815	21354	34277	0.67	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8815	21354	34278	0.67	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8827	21366	34280	3.48	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
8847	21386	34310	1.02	2.2E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
8952	21490		3.12	2.2E-01	AW85039.1	EST_HUMAN	PM3-CT0263-241289-008-b07 CT0263 Homo sapiens cDNA
9043	21580	34508	1.82	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dera1), mRNA
9126	21661	34604	1.95	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110800-008-c02 TN0045 Homo sapiens cDNA
9213	21730	34673	1.24	2.2E-01	W02988.1	EST_HUMAN	za0408.11 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291591 5'
9231	21953	34803	14.03	2.2E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9274	21800	34750	0.74	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9285	21885	34830	0.71	2.2E-01	7657428	NT	Mus musculus cathepsin specific factor 2 (OSF-2), mRNA
9288	21898	34845	3.69	2.2E-01	M89843.1	NT	Brachydanio rerio epandym beta and gamma chains (Epd) gene, complete cds
9839	22039	35000	0.59	2.2E-01	Q80880	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9729	22227	35204	3.1	2.2E-01	AF187941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
9884	22361	35341	2.23	2.2E-01	BF208507.1	EST_HUMAN	nuclear gene for chloroplast product
10078	22574	35569	0.87	2.2E-01	9825671	NT	601868724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10340	22834		0.81	2.2E-01	AF071001.1	NT	Human herpesvirus 6, complete genome
10384	22878	35870	0.72	2.2E-01	AE001562.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10384	22878	35871	0.72	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11005	23519	36554	1.6	2.2E-01	AF267772.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11299	23751	36808	5.56	2.2E-01	X01918.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11335	23033	36042	3.18	2.2E-01	7708215	NT	Drosophila 68C plus gene cluster
11715	24125		1.8	2.2E-01	BE870589.1	EST_HUMAN	Homo sapiens H-2K binding factor-2 (LOC61580), mRNA
11827	25065		6.34	2.2E-01	U82671.2	NT	601446857F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850870 5'
11910	24248		5.37	2.2E-01	AF188843.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
12024	18029	30491	1.7	2.2E-01	AW361098.1	EST_HUMAN	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12026	24317		1.86	2.2E-01	AW681922.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12676	25058		4.05	2.2E-01	AV694801.1	EST_HUMAN	h117502.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872623 3'
12659	24730	30855	2.44	2.2E-01	BF243095.1	EST_HUMAN	AV694801 GKG Homo sapiens cDNA clone GKCAHB02 5'
1008	13617	28132	1.36	2.1E-01	AA668289.1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104988 5'
1008	13618	28134	1.27	2.1E-01	AL161504.2	NT	nm31e11.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804
1183	13765		2.41	2.1E-01	AE002314.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1240	13838	26354	0.85	2.1E-01	8754289	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1240	13838	26355	0.85	2.1E-01	8754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1557	14149	26881	3.45	2.1E-01	AJ249895.1	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1957	14541	27097	1.84	2.1E-01	AA908824.1	EST_HUMAN	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
2201	14777	27350	3.39	2.1E-01	BF695073.1	EST_HUMAN	ok73e02.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1618610 3' similar to gb:K02765
2385	14864	27528	2.01	2.1E-01	8753235	NT	COMPLEMENT C9 PRECURSOR (HUMAN);
2851	15557	28041	2.53	2.1E-01	6912445	NT	602083128F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3879	16477		6.58	2.1E-01	9839381	NT	Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Ca2a2d3), mRNA
4129	16721	29178	1.22	2.1E-01	P11675	SWISSPROT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
							Beta vulgaris mitochondrion, complete genome
							IMMEDIATE-EARLY PROTEIN IE180

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4129	18721	29177	1.22	2.1E-01	P11875	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4338	18623		1.38	2.1E-01	AF124528.1	NT	Orchestia cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4465	17051		1.31	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4678	17258	29709	1.83	2.1E-01	AB010273.1	NT	Homo sapiens pshp47 gene, complete cds
5083	17658	30097	1.63	2.1E-01	U78409.1	NT	Lycopodium esculentum homeobox 1 protein (THOX1) mRNA, partial cds
5434	17980	30398	0.88	2.1E-01	J05082.1	NT	Vampire bat (D. rotundus) plasminogen activator mRNA, complete cds
5504	18138	30548	6.55	2.1E-01	BF872906.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288001.6
5987	18644	32368	1.16	2.1E-01	AJ223392.1	NT	Drosophila mitochondrial 16S rRNA gene, partial
6879	19477	32289	2.04	2.1E-01	U04442.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7438	19860	32825	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7438	19860	32828	1.24	2.1E-01	Q01958	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7447	19871		2.17	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7692	20201	33088	2.02	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7731	20239	33130	1.14	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (MDH-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7731	20239	33131	1.14	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (MDH-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7785	20273		0.88	2.1E-01	T87354.1	EST_HUMAN	Yd83b01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:114783.5
8017	20559		1.19	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
8439	20979	33894	4.93	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemoglobin processing protein (hmcC), putative ABC transporter (hmcB), putative haemoglobin structural protein (hmcA), and haemoglobin immunity protein (hmcI) genes, complete cds
8732	21271	34190	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614.5
8732	21271	34191	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614.5
8888	21428		0.47	2.1E-01	AB022524.1	NT	Homo sapiens APOL gene, exon 9
8987	21503	34428	5.93	2.1E-01	Z35788.1	NT	Saccharomyces chromosome II reading frame ORF YBL025w
9423	21932	34880	0.6	2.1E-01	N42538.1	EST_HUMAN	Yy11e10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270854.5
9423	21932	34881	0.6	2.1E-01	N42538.1	EST_HUMAN	Yy11e10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270854.5
9432	21958	34908	2.95	2.1E-01	X97378.1	NT	A.thaliana mRNA for A.RanBP1b protein
9638	22038	34998	1.57	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10232	22727	35719	1.04	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10283	22758	35745	1.98	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10289	22764	35751	0.67	2.1E-01	BF674254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831.5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10503	22889	38007	0.6	2.1E-01	AF284286.1	NT	Anelle lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
11438	23888		2.24	2.1E-01	11038647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11451	23901	36980	2.34	2.1E-01	BE180422.1	EST_HUMAN	RC3-H10822-040500-013-b11 HT822 Homo sapiens cDNA
11841	24802		1.39	2.1E-01	X57824.1	NT	Drosophila melanogaster ALA-E8 DNA, repeat region
12183	24418		1.48	2.1E-01	AF217480.1	NT	Homo sapiens fragile 100 odds reductase (FOR) gene, exons 8, 9, and partial cds
12483	24593		1.72	2.1E-01	BE822149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915875 5'
12807	24891	30858	2.08	2.1E-01	BE872330.1	EST_HUMAN	7a58802.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3223034 3'
12812	24895	30861	1.28	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 278 Kb, chromosome 7
214	12875	25382	1.86	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
558	13180		2.2	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
728	13348	25840	1.24	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
843	13450	26988	1.78	2.0E-01	AF027885.1	NT	Mus musculus Major Histocompatibility Locus class II region
1049	13656	26167	0.72	2.0E-01	D80905.1	NT	Synschoecia sp. PCC8803 complete genome, 7/27, 781449-820915
1184	13769	28278	3.24	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1287	13891	28414	1.37	2.0E-01	AJ132895.5	NT	Homo sapiens rec1 gene
1351	13948	28470	1.22	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-297288-002-c08 HT0422 Homo sapiens cDNA
1507	14089		1.22	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1534	14126	26663	23.08	2.0E-01	4503408	NT	Homo sapiens dystrorbrin, alpha (DTNA), mRNA
1599	14191	28722	3.03	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1604	14188	28728	1.23	2.0E-01	AF280700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1735	14326	28868	1.17	2.0E-01	U22348.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14345		1.83	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1793	14385		1.99	2.0E-01	U87528.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1834	14518	27073	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1934	14518	27074	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1937	14521	27077	1	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2386	14955		1.64	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2015	15532		0.68	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3534	18139	28621	0.7	2.0E-01	P48607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3628	18229		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15802.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element;
3788	18389	28835	0.8	2.0E-01	P34841	SWISSPROT	GED-11 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	18628	28088	0.78	2.0E-01	Z48808.1	NT	<i>Sus scrofa</i>
4102	18686	28162	0.68	2.0E-01	X83997.1	NT	<i>C. parvifera</i> espO gene
4522	17108	28552	0.76	2.0E-01	AF242431.1	NT	<i>Mus musculus</i> neuronal apoptosis inhibitory protein 8 (Nalpe8) gene, complete cds; and Nalpe3 gene, exons 2-9 end 11-18
4555	17247		8.43	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-903 EN0032 Homo sapiens cDNA
5192	17757	30186	7.09	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5228	18139	28621	0.62	2.0E-01	P48607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5636	18263	30737	2.38	2.0E-01	X58600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5918	18538	31263	2	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domain 2 (DUOX2), mRNA
6008	18628	31361	0.69	2.0E-01	X91856.1	NT	<i>F. rubripes</i> DNA encoding for valyl-tRNA synthetase
8210	18820	31591	6.48	2.0E-01	U16300.1	NT	<i>Saccharomyces cerevisiae</i> Hal5p (HAL5) mRNA, complete cds
8321	18928		0.71	2.0E-01	M76987.1	NT	Human hepatocyte growth factor gene, exon 1
8560	19158	31955	3.94	2.0E-01	X61033.1	NT	<i>M. auratus</i> mu class glutathione transferase gene
8650	19246	32049	3.93	2.0E-01	AW360895.1	EST_HUMAN	PM1-CT0247-141089-001-908 CT0247 Homo sapiens cDNA
7251	19780	32638	0.68	2.0E-01	U38724.1	NT	<i>Mycoplasma genitalium</i> section 48 of 61 of the complete genome
7336	19863	32727	1.18	2.0E-01	AF260371.1	NT	<i>Mus musculus</i> phosphofructokinase-1 C isozyme (Pfkfb) gene, exons 3 through 7
7778	20284	33181	1.53	2.0E-01	AK024427.1	NT	Homo sapiens mRNA for FLJ00016 protein, partial cds
7895	20437		6.45	2.0E-01	AF028028.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
8142	20683	33596	2.91	2.0E-01	X91161.1	NT	<i>M. musculus</i> ecp2 gene exon 14
8658	21197		0.53	2.0E-01	BE862247.1	EST_HUMAN	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877784 5'
9273	21769	34749	1.03	2.0E-01	U82511.1	NT	<i>Dictyostellium discoideum</i> random slug cDNA19 protein (res19) mRNA, partial cds
9312	21828	34776	0.66	2.0E-01	U71122.1	NT	<i>Arabidopsis thaliana</i> pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9476	21874		4.35	2.0E-01	AE001278.1	NT	<i>Chlamydia trachomatis</i> section 5 of 87 of the complete genome
9661	22160	35132	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9681	22160	35133	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9808	22304		1.88	2.0E-01	AF146892.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9854	22449	35431	1.78	2.0E-01	AF086807.1	NT	<i>Arabidopsis thaliana</i> root gravitropism control protein (PIN2) gene, complete cds
9864	22449	35432	1.79	2.0E-01	AF086807.1	NT	<i>Arabidopsis thaliana</i> root gravitropism control protein (PIN2) gene, complete cds
10072	22587	35562	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10072	22587	35563	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10115	22810		0.72	2.0E-01	X78388.1	NT	<i>D. melanogaster</i> DNA mobile element (hoppe)
10304	22798	35789	0.98	2.0E-01	X87121.1	NT	<i>R. norvegicus</i> mRNA for NTR2 receptor
10720	23248	36263	2.77	2.0E-01	D89088.1	NT	<i>Salvelinus pluvius</i> mRNA for transferrin, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10720	23248	36264	2.77	2.0E-01	D86088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
12182	24402		1.34	2.0E-01	AF206837.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12374	24887		1.95	2.0E-01	AF302773.1	NT	Homo sapiens nitrin-Lm isoform (nitrin) mRNA, complete cds
12388	24807	30788	2.81	2.0E-01	AY975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12425	24810	30888	3.97	2.0E-01	AI023592.1	EST_HUMAN	ov80a10 at Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1843910 3'
12449	24584		17.08	2.0E-01	AF078184.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
118	12788		6.22	1.0E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
374	13023	25509	5.4	1.0E-01	AF004933.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
684	13308	25792	1.47	1.0E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
684	13308	25763	1.47	1.0E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
691	13315	25800	6.6	1.0E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
692	13315	25800	6.82	1.0E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
1023	13633		1.92	1.0E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1143	13748	26258	10.04	1.0E-01	AA358813.1	EST_HUMAN	EST87784 Fetal lung II Homo sapiens cDNA 5' end
1413	14008	26534	2.41	1.0E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1482	14076		4.02	1.0E-01	AF184823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rp-2) gene, complete cds
2185	14761	27331	1.28	1.0E-01	AA916482.1	EST_HUMAN	044H09.at Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1526369 3' similar to gb:AC03911
2422	14900	27563	3.27	1.0E-01	8822533	NT	GLIA DERIVED NEXIN PRECURSOR (HUMAN);
2948	15565	28039	4.1	1.0E-01	U66086.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2985	15580		6.58	1.0E-01	J00922.1	NT	Sigmoidon hispidus p63 gene, partial cds
3033	15649	28128	1.05	1.0E-01	U25148.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3442	16050	28528	4.19	1.0E-01	D13187.1	NT	Rattus norvegicus brush border myosin-I (BBM1) mRNA, partial cds
3528	18131	28811	5.24	1.0E-01	R18487.1	EST_HUMAN	Mouse gene for immunoglobulin diversity region D1
3877	18475	28939	0.76	1.0E-01	AF264017.1	NT	y4210.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129547 5'
4084	18681	28123	3.86	1.0E-01	AB008784.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4157	18749	29202	1.86	1.0E-01	AW764108.1	EST_HUMAN	Schistosoma haematobium DNA for cytoplasmic dynein heavy chain, complete cds
4315	18901	29345	1.17	1.0E-01	BE834943.1	EST_HUMAN	CN3-CT0315-271189-045-b11 CT0315 Homo sapiens cDNA
4668	17161	29697	0.69	1.0E-01	AL161493.2	NT	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
5158	17728		1.11	1.0E-01	AF223642.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5789	18414		5.48	1.0E-01	AW130149.1	EST_HUMAN	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5828	18450	31173	7.81	1.0E-01	AF127837.1	NT	x28807.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2818444 3' similar to gb:M73778 RETINOIC
6005	18625	31360	0.73	1.0E-01	AF091216.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
							Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
							Mus musculus Wrm protein (Wrm) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046	18083		2.52	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT28P4 Homo sapiens cDNA clone NT28P4001328 6'
6469	19070	31855	1.97	1.9E-01	AI762391.1	EST_HUMAN	wf54f02.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394089 3'
6823	19123	31915	1.23	1.9E-01	AW148482.1	EST_HUMAN	x14c08.x1 NCL_CGAP_K108 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7050	18089	30480	1.37	1.9E-01	R43212.1	EST_HUMAN	Yg08a12.a1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31863 3' similar to contains MER13 repetitive element;
7072	19644	32481	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7072	19644	32482	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7503	20025	32889	1.3	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7643	20083	32937	2.89	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7827	20469	33378	1.71	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8820	21159	34074	12.12	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8876	21414	34337	1.38	1.9E-01	M14568.1	NT	Marulap cat beta-globin gene mRNA, partial cds
8875	21414	34338	1.38	1.9E-01	M14568.1	NT	Marulap cat beta-globin gene mRNA, partial cds
9789	22287	35271	0.72	1.9E-01	AA912488.1	EST_HUMAN	cl8g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1937506 3' similar to contains Alu repetitive element
10140	22635	35626	0.71	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
10140	22635	35627	0.71	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
10523	23081	36071	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10523	23081	36072	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10635	23187	38178	2.08	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11377	23829	36891	1.68	1.9E-01	M2253.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
11571	24018	37088	2.68	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12207	24431		1.33	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12582	24874		3.89	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
34	12713	25172	2.56	1.9E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
281	15412	25423	1.97	1.9E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
393	13039	25530	1.76	1.8E-01	4502632	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
776	13395	25898	0.77	1.8E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1018	13628	26141	0.78	1.8E-01	AJ812212.1	EST_HUMAN	wd7102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1130	13732	26242	1.28	1.8E-01	AF000880.1	NT	Dichosetium discoidium plasmid Ddp5, complete genome
1332	13928	26447	6.97	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1551	14143	28876	1.31	1.8E-01	8753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1551	14143	28677	1.31	1.8E-01	8753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1887	14472		2.79	1.8E-01	4605036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1907	14492		2.22	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCL CGAP_K143 Homo sapiens cDNA clone IMAGE:17618113' similar to TR:076836 O75836 GAMMA BUTYROBETAINE HYDROXYLASE;
1858	14542	27088	1.52	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2718	15273		2.29	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2023	16540		2.38	1.8E-01	AF184589.1	NT	Jaropisidium acule LEAFY protein (LEAFY2) gene, partial cds
2928	16544	28020	1.18	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2859758 3'
3158	15772	28239	1.31	1.8E-01	AW895178.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA
3413	16021	28501	0.71	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3683	16284	28752	0.78	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3683	16284	28753	0.79	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4333	16920	29362	0.78	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4426	17012		4.07	1.8E-01	D37864.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4654	17236	29691	6.59	1.8E-01	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4886	17461	29914	2.51	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4928	17503	29950	1.03	1.8E-01	X92179.1	NT	S. tuberosum mRNA for alcohol dehydrogenase
5198	17763	30188	2.18	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151298-112-g08 ST0203 Homo sapiens cDNA
5216	17781	30200	1.59	1.8E-01	AJ792382.1	EST_HUMAN	an28g07.y5 Gaasler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5257	17820	30245	1.5	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5281	17843	30270	1.07	1.8E-01	AI439881.1	EST_HUMAN	u57a04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134580 3'
5288	17850	30276	0.59	1.8E-01	AF132115.1	NT	Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds
5338	17898	30314	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17899	30315	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5398	17956	30367	2.04	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041186-010-001 ST0121 Homo sapiens cDNA

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5978	18698	31331	1	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
6082	18698	31446	1.01	1.8E-01	N28829.1	EST_HUMAN	y343h08.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:284063 5'
6277	18685	31953	1.1	1.8E-01	6878428	NT	Mus musculus Trf receptor-associated factor 6 (Trf6), mRNA
6277	18685	31654	1.1	1.8E-01	6878428	NT	Mus musculus Trf receptor-associated factor 6 (Trf6), mRNA
6835	19231	32035	2.03	1.8E-01	Q6QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6878	19271		2.24	1.8E-01	N64853.1	EST_HUMAN	y62h02.r1 Soares_multiple_sclerosis_2NbrHMSP Homo sapiens cDNA clone IMAGE:278163 5'
7077	19649	32487	1.22	1.8E-01	AB018591.1	NT	Citullus lanatus mRNA for wasu, complete cds
7077	19649	32488	1.22	1.8E-01	AB018591.1	NT	Citullus lanatus mRNA for wasu, complete cds
7117	19457	32272	0.71	1.8E-01	BE081363.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
8547	21086	34008	0.47	1.8E-01	AW968118.1	EST_HUMAN	EST1378181 MAGE resequences, MAGI Homo sapiens cDNA
9288	21792	34741	1.13	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9288	21896	34943	1.39	1.8E-01	6828232	NT	Bacteriophage like, complete genome
9412	21821			1.8E-01	AA493751.1	EST_HUMAN	nt02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.10 L1 repetitive element:
9494	21894	34950	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9494	21894	34951	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9532	22032	34990	0.95	1.8E-01	M26019.1	NT	S. commune araldine-5-phosphate decarboxylase (URA1) gene, complete cds
9532	22032	34991	0.95	1.8E-01	M26019.1	NT	S. commune araldine-5-phosphate decarboxylase (URA1) gene, complete cds
9694	22183	35166	0.82	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9698	22187	35170	0.89	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10039	22534			1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10271	22766	35753	1.22	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10516	23054	36068	2.37	1.8E-01	X77338.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10558	23094	36106	7.47	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10615	19649	32487	3.07	1.8E-01	AB018581.1	NT	Citullus lanatus mRNA for wasu, complete cds
10616	19649	32488	3.07	1.8E-01	AB018581.1	NT	Citullus lanatus mRNA for wasu, complete cds
10616	23148	36160	4.49	1.8E-01	AF019107.1	NT	Dictyostellium discoideum unknown (DG1041) gene, complete cds
10897	23417	36434	1.84	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11337	23035	36045	4.3	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11598	24042	37111	2.74	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11928	24068	37132	1.8	1.8E-01	U40487.1	NT	Mycobacterium smegmatis proton antiporter efflux pump (Hra), complete cds
14748	24348		2.04	1.8E-01	10088561	NT	Bovine echinermal fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11814	24188	31032	1.41	1.8E-01	BF34823.1	EST_HUMAN	602019928F1 NC1_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4166318 5'
12218	13928	26447	1.3	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12291	24491		5.81	1.8E-01	Q98882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12418	24689		23.47	1.8E-01	R24484.1	EST_HUMAN	YH4810.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12459	24590		2.76	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hck1)
12502	28045	30507	1.58	1.8E-01	9508952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolec), mRNA
603	13232	28708	6.83	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616788 5'
838	13454	28984	2.89	1.7E-01	X63330.1	NT	P. dumetii histone gene cluster for core histones H2A, H2B, H3 and H4
888	13608		8.83	1.7E-01	P35618	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1088	13701	28210	0.87	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1088	13701	28211	0.87	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1853	14441	26988	0.95	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2025	14807		2.84	1.7E-01	AF285051.1	NT	Homo sapiens BNIIP3H (BNIIP3H) gene, complete cds; nuclear gene for mitochondrial product
2885	18503	27973	1.98	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2885	18503	27974	1.98	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2853	18589	28044	1.93	1.7E-01	AA338909.1	EST_HUMAN	EST41851 Endometrial tumor Homo sapiens cDNA 5' end
3027	16643	28121	1.9	1.7E-01	AJ238738.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3027	15643	28122	1.9	1.7E-01	AJ238738.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3139	16753	28220	1.91	1.7E-01	AF081614.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3412	18020	28500	1.11	1.7E-01	N55763.1	EST_HUMAN	J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2348 5'
3494	18099	28574	1.28	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4012	18810	28083	4.99	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4658	17240		1.63	1.7E-01	X52836.1	NT	Schistosoma graxia alpha repetitive DNA
4877	17452	28904	0.94	1.7E-01	AF217480.1	NT	Homo sapiens fragile 180 oxidoreductase (FOR) gene, exons 8, 9, and partial cds
4885	17539	28981	1.07	1.7E-01	AJ247635.1	EST_HUMAN	qh57609.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element:
5210	17775		0.88	1.7E-01	U28378.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5242	17808	30227	1.02	1.7E-01	BF689718.1	EST_HUMAN	602186630F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288848 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5287	17859		1.08	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (se) gene, complete cds
5342	17903	30319	0.8	1.7E-01	BF030010.1	EST_HUMAN	601567268F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5421	17978	30386	7.82	1.7E-01	J04478.1	NT	S.pneumoniae DNA polymerase I (pda) gene, complete cds
5604	18233	30683	1.92	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.at NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17886 60S
5604	18233	30684	1.92	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.at NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17886 60S
5779	18404	31120	0.7	1.7E-01	U43598.1	NT	Brugia pahangi microfilarial stress protein SHP3 (shp3) gene, complete cds
6471	19072	31858	20.9	1.7E-01	H72118.1	EST_HUMAN	ys02008.at Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:213658 3'
6522	19122	31913	1.33	1.7E-01	A1370978.1	EST_HUMAN	ta28c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6522	19122	31914	1.33	1.7E-01	A1370978.1	EST_HUMAN	ta28c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6937	18045	30467	0.71	1.7E-01	BE300288.1	EST_HUMAN	600844087T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'
6960	19537		2.28	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7074	19846		0.67	1.7E-01	Z82910.1	NT	Homo sapiens HFE gene
7272	19800	32657	2.83	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7339	19866	32730	8.92	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843904 5'
7494	20017	32882	1.16	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7508	24784	32893	0.73	1.7E-01	Q01655	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
7602	20345	33253	1.28	1.7E-01	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
7904	20446	33352	0.54	1.7E-01	AF150969.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8219	20760	33674	6.92	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8219	20760	33675	6.82	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8631	21170	34087	0.68	1.7E-01	AW692873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8682	21201	34119	3.28	1.7E-01	D00384.1	NT	Rat (SHR strain) SKI gene
8776	21317	34239	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8776	21317	34240	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9095	21631	34569	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9095	21631	34570	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9609	22009	34987	7.72	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9814	22114	35077	0.56	1.7E-01	AW677455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9814	22114	35078	0.56	1.7E-01	AW677455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9831	22131	35086	2.47	1.7E-01	U18288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9704	22203	35174	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9704	22203	35175	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9722	22220	35186	0.81	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10132	22627		2.24	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10283	22787	35777	0.99	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10295	22789	35779	1.72	1.7E-01	AA827972.1	EST_HUMAN	nc80607.81 NCI_CGAP_C69 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gblL25081
10560	23086	36109	9.23	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10685	23215	36227	2.93	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813258 6'
10891	23503	36536	8.7	1.7E-01	7108300	NT	643603.81 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426824 3'
10991	23505	36537	8.7	1.7E-01	7108300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11558	24008		2.18	1.7E-01	P1272	SWISSPROT	AMP NUCLEOSIDASE
11643	24604		1.46	1.7E-01	AJ272584.1	NT	Blisbella aurantiacea mitochondrial partial COII gene for cytochrome c oxidase subunit II
11647	24079	37143	4.09	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
11782	26004		1.94	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12333	24517		1.38	1.7E-01	N40825.1	EST_HUMAN	yw82c12.1 Soares_placenta_8tc9weeks_2NHHP8tc9W Homo sapiens cDNA clone IMAGE:258742 5'
12381	24546	30905	12.95	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
12609	24693		1.33	1.7E-01	AJ132510.1	NT	Sus scrofa o-fos gene, exons 1-4
131	12788	26285	1.57	1.8E-01	AF217632.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
708	15388	25818	1.56	1.8E-01	R31497.1	EST_HUMAN	yW75f12.1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1569	14161	26892	4.35	1.8E-01	AF288117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1868	14552	27108	2.8	1.8E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2028	14610		1.08	1.8E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2427	15466	27569	0.86	1.8E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2535	15089	27672	1.12	1.8E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2917	15534	28008	11.95	1.8E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2917	15534	28007	11.95	1.8E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3041	15657	28137	1.17	1.8E-01	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3695	16296	28765	1.35	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3695	16296	28768	1.36	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3940	16439	28901	0.71	1.8E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4072	16668		2.65	1.8E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4422	17007	29460	11.02	1.8E-01	AF179880.1	NT	Homo sapiens epallin gene, complete cds
4554	17137		3.42	1.8E-01	AW686801.1	EST_HUMAN	EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4583	17148		4.68	1.0E-01	8753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5057	17630	30074	0.84	1.0E-01	P40831	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIG LH) [CONTAINS: LINKER HISTONE
5080	17653	30093	1.46	1.0E-01	AA089343.1	EST_HUMAN	z84h08 s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5101	17673	30112	1.28	1.0E-01	AJ008356.1	NT	E221986 39,986 BP SEGMENT OF CHROMOSOME XIV.;
5101	17673	30113	1.28	1.0E-01	AJ008358.1	NT	Lycopodium obscurum Real fragment 2, satellite region
5358	17818	30333	1.81	1.0E-01	BF209302.1	EST_HUMAN	Lycopodium obscurum Real fragment 2, satellite region
5359	17818	30333	1.23	1.0E-01	AJ087407.1	EST_HUMAN	601872523F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4096885 5'
5587	18218	30688	0.78	1.0E-01	L40608.1	NT	wm48a08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2439182 3'
5713	18339	30844	2.78	1.0E-01	AW107498.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5713	18339	30845	2.78	1.0E-01	AW107498.1	EST_HUMAN	hm43101.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2886869 3' similar to TR:O75884 O75884
5726	18351	31054	2.12	1.0E-01	AF034718.1	NT	HYPOPHYSICAL 127.8 KD PROTEIN ;
6178	18789	31558	0.84	1.0E-01	BE925803.1	EST_HUMAN	hm43101.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2886869 3' similar to TR:O75884 O75884
6559	19157	31953	2	1.0E-01	AL161598.2	NT	HYPOPHYSICAL 127.8 KD PROTEIN ;
6569	19157	31954	2	1.0E-01	AL161598.2	NT	hm43101.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2886869 3' similar to TR:O75884 O75884
7043	18083	30453	3.49	1.0E-01	AW291215.1	EST_HUMAN	HYPOPHYSICAL 127.8 KD PROTEIN ;
7763	20281	33157	1.44	1.0E-01	AW248399.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cbpe) gene, complete cds
7770	20278		0.76	1.0E-01	AU136825.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
7810	20353	33262	1.43	1.0E-01	L48349.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7988	20510		0.55	1.0E-01	BE244087.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8082	20604	33515	0.78	1.0E-01	U38243.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8567	21106	34025	0.77	1.0E-01	Z99119.1	NT	UI-H-B12-epi-b-08-Q-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
8780	21289	34220	0.65	1.0E-01	R13873.1	EST_HUMAN	2822248.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8863	21402		0.64	1.0E-01	L36881.1	NT	AU136625 PLACE1 Homo sapiens cDNA clone IMAGE:1004468 5'
8901	21439	34382	1.91	1.0E-01	Z49501.1	NT	Gorilla gorilla androgen receptor gene, partial exon
9039	21576		0.8	1.0E-01	AF11167.2	NT	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
9589	22089		1.83	1.0E-01	BF375171.1	EST_HUMAN	Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
9572	22072	35033	1.86	1.0E-01	Z49501.1	NT	Bacillus subtilis complete genome (section 16 of 21); from Z997771 to 3213410
							Y60H08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28873 5'
							Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
							S. cerevisiae chromosome X reading frame ORF YJR001W
							Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
							RC3-ST0200-041188-011-h01 ST0200 Homo sapiens cDNA
							S. cerevisiae chromosome X reading frame ORF YJR001W

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9807	22107		1.08	1.8E-01	BE155984.1	EST_HUMAN	PM2-HT0383-270100-004-f11 HT0383 Homo sapiens cDNA
10538	23073	38087	2.7	1.8E-01	AW850853.1	EST_HUMAN	IL3-CT0220-11189-028-G01 CT0220 Homo sapiens cDNA
10880	23401	36416	1.55	1.8E-01	BE269849.1	EST_HUMAN	801145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3181183 5'
10894	23508		8.03	1.8E-01	AF108064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11280	23741	36708	10.88	1.8E-01	8871582	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11880	25019		1.72	1.8E-01	8879468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11784	24168	38776	5.34	1.8E-01	AV716885.1	EST_HUMAN	AV716885 GLC Homo sapiens cDNA clone GLOEMF07 5'
12095	24382	30968	1.55	1.8E-01	L14933.1	NT	Rat convertase PCS mRNA, 5' end
12126	24392		1.75	1.8E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12229	24821		11.74	1.8E-01	AB046310.1	NT	Gueumia sativus KS mRNA for ent-kaurene synthase, complete cds
12407	24584		5.11	1.8E-01	AK024468.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12497	24825		3.96	1.8E-01	AF287344.1	NT	Fuchala hybrid cultivar Qlu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12521	24837	30898	1.88	1.8E-01	8508522	NT	Rattus norvegicus chondroin sulfatase proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
268	12828	26412	1.78	1.8E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
269	12826	25413	1.78	1.8E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
613	15387		2.18	1.8E-01	AV711686.1	EST_HUMAN	AV711686 DCA Homo sapiens cDNA clone DCAADH06 5'
815	13433	25938	1.04	1.8E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1131	13734	26244	0.84	1.8E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1138	13739	26248	2.28	1.8E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1152	13766		1.81	1.8E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1258	13855	26371	0.79	1.8E-01	AW195518.1	EST_HUMAN	xc39d11.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2698085 3'
1318	13912	26432	3.12	1.8E-01	D28538.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1318	13912	26433	3.12	1.8E-01	D28538.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1529	14121	26680	1.84	1.8E-01	AF117340.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1851	14535	27081	1.62	1.8E-01	AW444431.1	EST_HUMAN	U1-H-B13-akb-b-09-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733641 3'
2738	15291	27869	1.17	1.8E-01	BF895381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2838	15554		1.01	1.8E-01	AW572516.1	EST_HUMAN	xc56a02.x2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:4247537 5'
3070	15685	28157	0.82	1.8E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3395	16003	28484	0.87	1.8E-01	AA935049.1	EST_HUMAN	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3415	16023	28504	0.85	1.8E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3415	16023	28505	0.85	1.8E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3415	16023	28505	0.85	1.8E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3474	18080	28563	0.99	1.5E-01	AW612237.1	EST_HUMAN	h2802.x1 NCLCGAP_Lu24 Homo sapiens cDNA clone IMAGE:2856538 3' similar to contains element MER18 repetitive element;
3819	18419	28881	2.13	1.5E-01	U08894.1	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3835	18434	28896	0.94	1.5E-01	7108358	NT	XYNA; Thermococcusbarophilus; xyna; 4182 base-pairs
3849	18447	28908	0.58	1.5E-01	M97882.1	NT	h10906.LT Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
3924	16532	28999	2.74	1.5E-01	AW685983.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
3951	16549	29017	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3951	18549	29018	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4124	16717	29173	0.82	1.5E-01	AW36659.1	EST_HUMAN	RC2-HT0149-191099-012-c99 HT0149 Homo sapiens cDNA
4282	16848	29296	0.82	1.5E-01	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4833	17411	29884	1.28	1.5E-01	BF687693.1	EST_HUMAN	602097192F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4086223 5'
4863	16291	27859	2.03	1.5E-01	BF686391.1	EST_HUMAN	602093299F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4908	17481	29938	0.92	1.5E-01	BE173786.1	EST_HUMAN	CMO-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4908	17481	29939	0.92	1.5E-01	BE173786.1	EST_HUMAN	CMO-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5139	17711	30141	1.59	1.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5481	18098	30414	1.96	1.5E-01	P07896	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5489	18123	30530	0.8	1.5E-01	AF256852.1	NT	Calman crocodilus MHC class II beta chain (helibeta) gene, complete cds
5531	18163		5.8	1.5E-01	P19198	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5729	18355	31059	4.68	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5787	18393	31108	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
5787	18393	31107	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
6158	18769	31532	1.4	1.5E-01	8753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6158	18769	31533	1.4	1.5E-01	8753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6194	18804	31573	1.98	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6342	18948	31725	3.23	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833931 5'
6394	18997		1.96	1.5E-01	4508398	NT	Homo sapiens RAD54 (S cerevisiae)-like (RAD54L) mRNA
6484	19085	31867	1.75	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6628	24765	32027	1.94	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6652	19248	32050	4.83	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA

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8863	19259	32063	1.5	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6702	19297	32101	2.18	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6786	19377	32192	0.98	1.5E-01	AA714780.1	EST_HUMAN	hw30d10.s1 NCL CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6813	19404	32220	1.59	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7056	19074	30484	6.39	1.5E-01	AW970268.1	EST_HUMAN	EST382376 MAGE resequenced, MAGK Homo sapiens cDNA
7268	19798		1.9	1.5E-01	AF210842.1	NT	Homo sapiens HARP(HARP) gene, exon 17 and complete cds
7423	18847	32813	1.8	1.5E-01	A1973197.1	EST_HUMAN	wf52c08.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
7589	20104	32979	1.02	1.5E-01	AF286073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7589	20104	32980	1.02	1.5E-01	AF286073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7586	20110	32984	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-Q.U.I.T NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'
7598	20110	32985	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-Q.U.I.T NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'
7722	20230	33119	0.71	1.5E-01	U46660.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
8002	20544	33446	1.1	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8161	20702	33617	0.95	1.5E-01	AA970317.1	EST_HUMAN	oa85q12.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M28082
8254	20795		1.11	1.5E-01	BE864789.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8339	20890		1.15	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8372	20912	33832	1.82	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8972) Homo sapiens cDNA clone GEN-528H08 5'
8528	21068	33987	2.04	1.5E-01	D84476.1	NT	Pangasinodon glucose growth hormone (GH) mRNA, complete cds
8550	21089		0.88	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8772	21311	34234	1.23	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9033	21570	34499	2.48	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9121	21657	34598	1.08	1.5E-01	BF585485.1	EST_HUMAN	zaf59c06.s1 Sciat7a fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:286868 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9128	21663		2.63	1.5E-01	AV764819.1	EST_HUMAN	GVO000404 Human Pectrolas Differential Display Homo sapiens cDNA
9326	21840		0.94	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9374	20313	33215	7.21	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9731	22229	35206	0.48	1.5E-01	M77144.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds
9835	22333	35314	8.91	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/5-delta - 4-delta isomerase gene, complete cds
9835	22333	35315	8.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10104	22689	35591	2.54	1.5E-01	X98862.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10188	22683		3.34	1.5E-01	AB027759.1	NT	P. lentusculus mRNA for integrin beta subunit
							Mesocricetus auratus mRNA for collagen type XVII, complete cds

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10210	22705	35698	2.82	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10210	22705	35698	2.82	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10288	22783	35776	1.75	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10433	22827	35833	1.97	1.5E-01	AJ011864.1	NT	Claviceps purpurea ps1 gene
10433	22827	35834	1.97	1.5E-01	AJ011864.1	NT	Claviceps purpurea ps1 gene
10704	23233	36245	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10704	23233	36246	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10854	23488	36494	1.71	1.5E-01	AW841916.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11045	18947	32813	2.44	1.5E-01	AI973197.1	EST_HUMAN	wf5208.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11739	24875		79.5	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12126	24381		1.43	1.5E-01	AF030359.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12180	24899		7.05	1.5E-01	R63077.1	EST_HUMAN	yp87404.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:184430 5'
12288	24920		3.12	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
12406	24824	30794	16.12	1.5E-01	AL136074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/8
12821	24899	30882	3	1.5E-01	Q820Y8	SWISSPROT	VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (CAVT.3)
12832	24709	30865	11.33	1.5E-01	AJ278242.1	NT	Sus scrofa mRNA for sodium iodide symporter
321	12875		1.48	1.4E-01	AF008683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85SP to TCRBV21S2A2 region
843	13556		2.71	1.4E-01	D76838.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1302	13896		1.59	1.4E-01	T91894.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1784	14374		1.35	1.4E-01	6878980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1787	14377	26921	1.39	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
2028	14811		10.08	1.4E-01	AA720615.1	EST_HUMAN	ny72407.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2514	15078	27650	1.4	1.4E-01	P30708	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2818	15370	27840	4.1	1.4E-01	AI833496.1	EST_HUMAN	wm74d01.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441885 3'
4253	18841	29290	10.32	1.4E-01	AI698094.1	EST_HUMAN	bs56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4263	18841	29291	10.32	1.4E-01	AI698094.1	EST_HUMAN	bs56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4321	16907	29349	3.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z50b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057.ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4501	17085		0.61	1.4E-01	AA776287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
4784	17384	29815	0.59	1.4E-01	8453861	NT	

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5328	17890		1.74	1.4E-01	BE910013.1	EST_HUMAN	60148056F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900167 5'
5509	18142	30584	4.49	1.4E-01	T00877.1	EST_HUMAN	ye15c11.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'
5532	18164	30577	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5532	18164	30578	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6440	19042	31850	2.7	1.4E-01	BE328891.1	EST_HUMAN	h97e02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6608	19206	32012	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6608	19206	32013	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6688	19282	32085	3.78	1.4E-01	AW082798.1	EST_HUMAN	x571612.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3537581 5'
6699	19295		1.53	1.4E-01	BE268638.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6718	19312	32115	2.07	1.4E-01	BF378533.1	EST_HUMAN	QV1-UJ0036-080300-103-409 UM0036 Homo sapiens cDNA
7180	19712		0.81	1.4E-01	AL118568.1	EST_HUMAN	DKFZp781A0910_1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781A0910 5'
7419	19943		1.83	1.4E-01	AW015373.1	EST_HUMAN	U1H-B10-sar-c-09-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7617	20130	33005	1.84	1.4E-01	U85845.1	NT	Oryctolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cds
7733	20241	33132	1.77	1.4E-01	A1305192.1	EST_HUMAN	q180b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8410	20950		1.28	1.4E-01	AV656047.1	EST_HUMAN	AV656047 GLC Homo sapiens cDNA clone GLCFSH06 3'
8719	21258		0.62	1.4E-01	A1436083.1	EST_HUMAN	h92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128111 3' similar to TR:002710 002710 GAG POLYPROTEIN.;
8844	21383	34308	4.58	1.4E-01	AA307073.1	EST_HUMAN	EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8924	21492	34379	0.62	1.4E-01	AW023638.1	EST_HUMAN	d558b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9050	21587	34518	1.21	1.4E-01	R82748.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9050	21587	34519	1.21	1.4E-01	R82748.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9114	21650	34591	8.48	1.4E-01	BF10859.1	EST_HUMAN	601805485F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9198	21716	34660	1.09	1.4E-01	W93411.1	EST_HUMAN	z994804.r1 Soares_fetal_heart NBHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to containe element1 KER repetitive element;
9280	21808	34757	1.47	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
9280	21808	34758	1.47	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
9371	20310	33213	1.66	1.4E-01	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lai (IAL), and zinc finger protein (DNZ1) genes, complete cds
9898	22395	35371	1.18	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10000	22496	35484	0.51	1.4E-01	AW021908.1	EST_HUMAN	d728h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485084 5'
10000	22496	35485	0.51	1.4E-01	AW021908.1	EST_HUMAN	d728h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485084 5'
10157	22852	35845	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211298-013-408 ST0218 Homo sapiens cDNA
10157	22852	35846	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211298-013-408 ST0218 Homo sapiens cDNA

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10380	22854		0.73	1.4E-01	T84283.1	EST_HUMAN	yc47603.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'
10489	22983	35991	0.7	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2399451 to 2812870
10587	23122		1.89	1.4E-01	AA811480.1	EST_HUMAN	cc99a03.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
10722	23250	36285	3.2	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2NBH8t Homo sapiens cDNA clone IMAGE:164088 5'
10974	23489	36519	1.58	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD48E)
11172	23679	36724	1.82	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
11210	19943		1.96	1.4E-01	AW016373.1	EST_HUMAN	UHH-B10-sat-c-99-0-UI.s1 NC1_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710288 3'
11344	23042	36052	2.4	1.4E-01	U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
12081	24344	30983	4.44	1.4E-01	X74773.1	NT	P.salina plastid gene secY
12074	24352		3.85	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
12123	25092		1.52	1.4E-01	BE513802.1	EST_HUMAN	601316938F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634328 5'
12223	24444		0.33	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12235	24451		1.98	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
12315	25088		1.77	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12340	24522		2.01	1.4E-01	AA452305.1	EST_HUMAN	z330e12.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788014 5' similar to contains Alu repetitive element
12545	24900		3.55	1.4E-01	D82883.1	NT	Mus musculus mRNA for prelidase, complete cds
12827	24705		1.33	1.4E-01	AW377988.1	EST_HUMAN	MRO-HT0208-221288-204-c08 HT0208 Homo sapiens cDNA
344	12898	25481	2.28	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
344	12896	25482	2.28	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
555	13185	25584	3.25	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
684	13288	25789	3.03	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
684	13288	25770	3.03	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
877	13491	26009	0.78	1.3E-01	X63330.1	NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
827	13540	26059	1.44	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1084	13689	26179	1.38	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1183	13788		2.03	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1257	13854	26370	1.36	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1493	14085		0.97	1.3E-01	AF148277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2002	14584	27143	2.32	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2215	14790		1.21	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA6, pucB8, pucA7, pucB8, pucA8 and pucC genes and ORF151
2320	14900		1.58	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-d12 ST0173 Homo sapiens cDNA
2421	14888		3.74	1.3E-01	AE001018.1	NT	Archaeoglobus fulgidus section 81 of 172 of the complete genome
2622	15184	27750	1.55	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3402	16011	28480	0.61	1.3E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$)
3498	16103	28578	0.86	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3785	16385	28850	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3785	16385	28851	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3781	16391	28856	0.8	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 (AKR1C4), exon 2
3848	16388	28850	0.82	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3848	16385	28851	0.82	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3875	16473	28937	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4060	16857		1.3	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4126	13288	25769	1.65	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
4126	13288	25770	1.65	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
4218	16808		0.95	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4238	16826		4.04	1.3E-01	AW394341.1	EST_HUMAN	QV3-DT0018-081289-038-403 DT0018 Homo sapiens cDNA
4246	16834	28285	2.25	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4285	16851	28289	21.7	1.3E-01	AW273741.1	EST_HUMAN	xx2310.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813895 3'
4404	16889		1.55	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4577	17160	28603	0.62	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4631	17214	28685	2.35	1.3E-01	BE272339.1	EST_HUMAN	601128098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2880063 5'
4898	18009		0.94	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5'
5058	17829	30073	1.05	1.3E-01	D78842.1	EST_HUMAN	HUM520C02B Homo placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-520C02 5'
5276	17841	30268	4.06	1.3E-01	AI432631.1	EST_HUMAN	th38c10.x1 NCJ_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2120562 3'
5395	17854	30385	0.95	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1168000 nt. position (517)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5444	17899	30402	13.66	1.3E-01	AA881841.1	EST_HUMAN	cd45e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5444	17899	30403	13.66	1.3E-01	AA881841.1	EST_HUMAN	cd45e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5528	18160	30575	0.69	1.3E-01	AW468988.1	EST_HUMAN	hso7b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5686	18168	30642	2.78	1.3E-01	AW804417.1	EST_HUMAN	QVQ-UM00083-100400-189-a08 UM00083 Homo sapiens cDNA
5692	18318		0.78	1.3E-01	AF107783.1	NT	Emertella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5772	18397		0.70	1.3E-01	AF068890.1	NT	Hepatitis C virus 88 CL10 genome polyprotein-gene, partial cds
5899	18521	31248	0.89	1.3E-01	BF210820.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6609	19208	32014	15.81	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6684	19280	32083	2.07	1.3E-01	X88891.1	NT	C. jacchus ltron 4 of visual pigment gene (red allele)
6883	19818		0.82	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7305	19833		1.94	1.3E-01	H48684.1	EST_HUMAN	Y33402.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:207075 5'
7800	20442		0.67	1.3E-01	BE272339.1	EST_HUMAN	601128098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2880063 5'
7914	20466	33382	1.62	1.3E-01	11423284	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
7845	20487	33397	0.98	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288074 3'
8180	20721		0.47	1.3E-01	BE582528.1	EST_HUMAN	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8289	20827		4.61	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDLO54c
8325	20866		3.78	1.3E-01	8823919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8465	21005	33923	1.05	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288074 3'
8878	21418	34339	0.52	1.3E-01	R11172.1	EST_HUMAN	Y33611.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P28318 60S RIBOSOMAL PROTEIN ;
8878	21418	34340	0.52	1.3E-01	R11172.1	EST_HUMAN	Y33611.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P28318 60S RIBOSOMAL PROTEIN ;
9146	21681	34625	1.64	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9146	21681	34626	1.64	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9393	21816	34768	5.08	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+-ATPase alpha 2a subunit mRNA, complete cds
9888	22185		0.8	1.3E-01	N88348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 28
9884	22459		0.8	1.3E-01	8383940	NT	Rattus norvegicus peptidyl arginyl aminase, type IV (Pd14), mRNA
10038	22531	35528	0.93	1.3E-01	AW851599.1	EST_HUMAN	MR2-CT0222-201099-001-601 CT0222 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10292	24797	35776	0.9	1.3E-01	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10417	22811	35911	0.82	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10511	23049		3.33	1.3E-01	BF330690.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
10975	23480	36520	1.58	1.3E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11130	23638		5.15	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11486	23918	36984	3.61	1.3E-01	BE279449.1	EST_HUMAN	601168052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11802	24241	31007	1.64	1.3E-01	BE918346.1	EST_HUMAN	601482741F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3888003 5'
12048	24332		3.27	1.3E-01	AJ242780.1	NT	Gallus gallus sox1 gene for lymphoblastin, exons 1-3
12486	24594		1.63	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:Q60287
12647	24721		1.84	1.3E-01	BE958003.1	EST_HUMAN	TR:Q60287 O60287 KIAA0639 PROTEIN. ;
408	13081	28573	10.81	1.2E-01	A1421744.1	EST_HUMAN	601844622R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3928980 3'
449	12878		1.43	1.2E-01	U68912.1	NT	if39602.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05780_rna1
573	13203		2.58	1.2E-01	AF039442.1	NT	ANNEXIN V (HUMAN);
1419	14012	26541	2.31	1.2E-01	AU149148.1	EST_HUMAN	Dicystostellum discoidium ORF DG1016 gene, partial cds
1419	14012	26542	2.31	1.2E-01	AU149148.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1426	14019		3.28	1.2E-01	AV735249.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001891 3'
1431	14023		6.69	1.2E-01	AL445088.1	NT	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1554	14148		1.19	1.2E-01	AA887474.1	EST_HUMAN	Thermoplasma acidophilum complete genome; segment 4/5
1673	14286	26789	1.48	1.2E-01	Q14934	SWISSPROT	al49609.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1691	14283	26819	2.77	1.2E-01	A1265402.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1803	14395		21.02	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
1984	14548		2.23	1.2E-01	AW449388.1	EST_HUMAN	NFAT3 (NF-ATC4) (NF-AT3)
2226	14801	27373	1.31	1.2E-01	BF248480.1	EST_HUMAN	qf69f09.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1960553 3'
2325	14896	27470	1.08	1.2E-01	AL163213.2	NT	H. sapiens DNA for endogenous retroviral like element
2416	14884		1.05	1.2E-01	Z21405.1	EST_HUMAN	U1H-B13-44-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2625	15187	27754	1.38	1.2E-01	AW896556.1	EST_HUMAN	601821567F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4048224 5'
2754	15309	27875	1.11	1.2E-01	A1823388.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2868	15486	27859	1.22	1.2E-01	U16018.1	NT	HSAAAEBZ7 TEST1, Human adult Testis tissue Homo sapiens cDNA
							QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
							ts18q07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
							COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1]: contains element PTR5 repetitive element ;
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

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2927	15643	28019	2.37	1.2E-01	AF20470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLR77 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
2961	15577	28056	3.29	1.2E-01	M16394.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3037	15653	28132	0.83	1.2E-01	X56982.1	NT	Human creatine kinase-B mRNA, complete cds
3267	15879	28362	2.08	1.2E-01	AW370868.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3268	15907		1.19	1.2E-01	U97600.1	NT	QV1-BT0259-261098-021-005 BT0259 Homo sapiens cDNA
3525	16130		0.62	1.2E-01	Z89118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3573	16177	28859	0.82	1.2E-01	X56982.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2706131 to 3013540
3573	16177	28690	0.82	1.2E-01	X56982.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3688	16130		1.09	1.2E-01	Z89118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	16432		0.84	1.2E-01	BF126551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2706131 to 3013540
4281	16947	29284	1.98	1.2E-01	Z64265.1	NT	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053968 3'
4261	16847	29295	1.98	1.2E-01	Z64255.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4402	16987	29431	0.6	1.2E-01	M15891.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4830	17408	28862	0.98	1.2E-01	Z48183.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
							L. acculentum mRNA for glycocalyx-1
4909	17484		2.93	1.2E-01	AF221683.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5163	17732	30159	1.08	1.2E-01	BF577357.1	EST_HUMAN	602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4280165 5'
5275	17836	30262	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5275	17836	30263	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5423	17980		1.99	1.2E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2481 complete genome, segment 8/7
5457	18092	30408	0.71	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1282950 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5503	18137	30547	1.13	1.2E-01	AF223391.1	NT	
5513	18149	30557	2.28	1.2E-01	W33036.1	EST_HUMAN	z080402.r1 Soares_parethyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321698 5'
5571	18202	30632	2.3	1.2E-01	Z68266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5696	18322	30822	0.89	1.2E-01	Z48234.1	NT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6347	18952	31731	1.81	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6395	18998	31777	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6441	19043	31831	2.38	1.2E-01	AW845273.1	EST_HUMAN	IL0-CT0031-221098-113-e04 CT0031 Homo sapiens cDNA
6502	19102	31887	1.59	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6755	18348	32157	0.98	1.2E-01	BF347686.1	EST_HUMAN	602023112F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158388 5'
7833	20375		1.31	1.2E-01	BE07072.1	EST_HUMAN	PM3-BN0137-290300-002-609 BN0137 Homo sapiens cDNA

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7903	20445	33351	3.58	1.2E-01	AI913753.1	EST_HUMAN	wc89g03.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
7950	20492	33401	0.72	1.2E-01	Q02369	SWISSPROT	Q98735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ;
8261	20762	33709	0.9	1.2E-01	AI832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8335	20876		9.03	1.2E-01	AW083652.1	EST_HUMAN	at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2537597 3' similar to gb:M13492 LAMIN A (HUMAN);
8355	20895		4.17	1.2E-01	AF063772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8392	20932	33852	0.92	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8392	20932	33853	0.92	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8937	21078		0.83	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8923	21162		2.14	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 20 of 163 of the complete genome
8957	21198		0.85	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9491	21647	34898	2.68	1.2E-01	X77981.1	NT	S.cerevisiae HXT5 gene
9918	22414	35399	2.65	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone QAAKE08 5'
10155	22850	35644	0.48	1.2E-01	AI718395.1	EST_HUMAN	as58g09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2333056 3'
10766	23290		3.58	1.2E-01	D28184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10944	23460		3.87	1.2E-01	BE982324.2	EST_HUMAN	601865578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11028	23540		1.82	1.2E-01	BF314481.1	EST_HUMAN	60180763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11194	23642	36892	2.67	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAIL1 (DNAIL1) gene, exon 17
11193	23698	36748	1.57	1.2E-01	R40249.1	EST_HUMAN	y80c02.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28890 3'
11382	23834		1.8	1.2E-01	M65108.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11687	24090		4.22	1.2E-01	AV858033.1	EST_HUMAN	AV858033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12029	24319		4.43	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12109	26038	30503	3.9	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
12228	24447		1.95	1.2E-01	AF188892.1	NT	(CDW138) (CD138 ANTIGEN)
12230	24503		17.94	1.2E-01	AF039442.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12345	24628		1.81	1.2E-01	X53881.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds .
12440	24977	30815	0.8	1.2E-01	AJ299803.1	EST_HUMAN	R.norvegicus NF68 gene for 68kDa neurofilament
12463	24591		2.18	1.2E-01	L10187.1	NT	q20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12488	24872		9.71	1.2E-01	O98433	SWISSPROT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
							CYCLIN T

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12649	16130		1.65	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
590	13220	25698	0.8	1.1E-01	AI881003.1	EST_HUMAN	U18408.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167883 3'
643	13266	25743	2.98	1.1E-01	AA593006.1	EST_HUMAN	nm00811.a1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1069820 3' similar to gb:X08985_ma1
1092	13697	28207	1.54	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1124	13727		1.48	1.1E-01	AL161590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1201	16435	26314	3.68	1.1E-01	AW972156.1	EST_HUMAN	EST1394142 IMAGE:289885, MAGL Homo sapiens cDNA
1292	13887	26411	1.89	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2688787-3002885
1668	14160	26691	2.94	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone IMAGE:2000403 5'
2353	14924		3.72	1.1E-01	6755215	NT	Mus musculus pro T-cell antigen receptor alpha (Ptra), mRNA
2676	16401		1.24	1.1E-01	6978876	NT	Rattus norvegicus Procollagen II alpha 1 (Ccl2a1), mRNA
2802	16164		1.06	1.1E-01	AW821908.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2880	15498	27988	1.17	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit (mice, Genomic, 700 nt, segment 4 of 5)
3068	16983	28166	0.76	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3368	15994		1.87	1.1E-01	6763231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca α 1g), mRNA
3468	16076	28548	2.27	1.1E-01	BE363186.1	EST_HUMAN	601306879F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3927068 5'
3489	16104	28579	1.59	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3538	16143	28626	0.69	1.1E-01	R68948.1	EST_HUMAN	yc82g08.a1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3642	16245	28720	0.8	1.1E-01	Y07695.1	NT	Alu repetitive element;
3763	16364		1.36	1.1E-01	P97384	SWISSPROT	A.immerus gene for transposase
3771	16372	28837	1.61	1.1E-01	X62708.1	NT	ANNEXIN XI (GALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4188	16778	29223	1.61	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HM-G-14b, exons 4 and 5
4188	16778	29224	1.61	1.1E-01	AW819412.1	EST_HUMAN	MIR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4339	16928		12.27	1.1E-01	AF157066.1	NT	MIR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4374	16981	29407	0.63	1.1E-01	AW802056.1	EST_HUMAN	Drosophila melanogaster kirscht protein (klar) mRNA, complete cds
4745	17328	29768	1.11	1.1E-01	S44957.1	NT	Tape-1=Integral membrane protein TAPA-1 (mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7)
4958	17533	29975	1.21	1.1E-01	Y07695.1	NT	A.immerus gene for transposase
5189	16784		0.78	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
5431	17988	30392	4.82	1.1E-01	AV730599.1	EST_HUMAN	AV730599 HTF Homo sapiens cDNA clone HTFAAC12 5'
5431	17988	30393	4.82	1.1E-01	AV730599.1	EST_HUMAN	AV730599 HTF Homo sapiens cDNA clone HTFAAC12 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5435	16245	28720	0.57	1.1E-01	Y07895.1	NT	A. Immeus gene for transposase nt76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5950	18474		4.49	1.1E-01	AA747216.1	EST_HUMAN	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5974	18538	31261	1.17	1.1E-01	AF020927.1	NT	602039176F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4188818 5'
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4188818 5'
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4188818 5'
6001	18621	31356	2	1.1E-01	X68851.1	NT	S. pombe sis8 gene encoding protein kinase
6031	18650	31391	5.02	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6177	18787	31555	1.76	1.1E-01	AJ007979.1	NT	Homo sapiens LGMD2B gene
6197	18807	31576	1.6	1.1E-01	BE768192.1	EST_HUMAN	PM3-FT0024-130800-004-f12 FT0024 Homo sapiens cDNA
6216	18828	31598	7.81	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280899-011-e01 CT0254 Homo sapiens cDNA
6562	19160	31958	1.38	1.1E-01	AF035748.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6599	19196	32001	0.84	1.1E-01	AI216907.1	EST_HUMAN	q978008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6721	19315	32118	3.92	1.1E-01	O86835	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6805	19398		3.07	1.1E-01	AF032922.1	NT	Homo sapiens synlavin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6898	19623	32456	2.38	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7238	25119		0.97	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050853 5'
7345	24780	32737	0.92	1.1E-01	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt position (877)
7542	20082	32835	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140676F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7542	20082	32836	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140676F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7651	20183	33051	1.86	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7682	20193		0.7	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polypeptide synthase
7683	20194	33082	3.53	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
7809	20451	33358	1.41	1.1E-01	U87492.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN); Methanococcus Jannaschii section 34 of 150 of the complete genome
8149	20890	33603	1.6	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8149	20890	33604	1.6	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8197	20738	33650	1.18	1.1E-01	X91233.1	NT	H. sapiens IL15 gene
8235	20776		1.15	1.1E-01	AW817918.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
8292	20833	33755	1.54	1.1E-01	AL134349.1	EST_HUMAN	DKFZp947P194_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp947P194 5'
8752	21291	34211	8.48	1.1E-01	U02482.1	NT	Pedococcus acidiacetic H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8843	21382	34307	0.87	1.1E-01	A1807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8938	21478	34397	0.48	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
8973	21611	34433	2.22	1.1E-01	AA192153.1	EST_HUMAN	z96b12.11 Stratiogene muscle B37208 Homo sapiens cDNA clone IMAGE:627743 5'
8973	21611	34434	2.22	1.1E-01	AA192153.1	EST_HUMAN	z96b12.11 Stratiogene muscle B37208 Homo sapiens cDNA clone IMAGE:627743 5'
9082	21698	34529	0.82	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and argF gene
9092	21628	34585	2.28	1.1E-01	T72976.1	EST_HUMAN	y419d03.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9119	21655		0.87	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922048 5'
9343	21957		1.13	1.1E-01	BE142305.1	EST_HUMAN	CM9-HT0142-271089-028-g11 HT0142 Homo sapiens cDNA
9417	21928		2.2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN027-040800-005-a08 GN027 Homo sapiens cDNA
9824	22322		0.6	1.1E-01	AL161643.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10107	22602		1.03	1.1E-01	R60580.1	EST_HUMAN	y98a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
10240	22735	35727	0.88	1.1E-01	U60528.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10564	23060	36104	1.6	1.1E-01	AF248277.1	NT	Dictyostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
10684	15683	28155	2.12	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1402 3'
10802	23325		3.23	1.1E-01	AF189032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
10923	23442	36463	3.76	1.1E-01	R23708.1	EST_HUMAN	y438f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131769 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
10931	23449	36470	1.85	1.1E-01	688135.1	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA
10947	18567	31298	1.56	1.1E-01	AL110685.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11060	23572	36609	1.74	1.1E-01	X70058.1	NT	M.musculus cytokine gene
11085	23597	36633	3.35	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding rRNA guanine transglycosylase and DNA ligase
11085	23597	36634	3.35	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding rRNA guanine transglycosylase and DNA ligase
11188	23691	36738	2.99	1.1E-01	P17497	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11884	24231		4.61	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12143	24835		3.29	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950804 3'
12597	24694	30880	1.99	1.1E-01	BF238763.1	EST_HUMAN	601680550F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134085 5'
1243	13841		2.35	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1315	13909	26429	1.92	1.0E-01	A086499.1	EST_HUMAN	ws08401.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MIER7.13
1436	14028	26537	2.23	1.0E-01	AL161504.2	NT	MER7 repetitive element;
2531	15095	27687	0.97	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3563	16167	26849	1.04	1.0E-01	BF033691.1	EST_HUMAN	UI-H-B13-alc-4-07-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3782	16382	26847	0.82	1.0E-01	BF23816.1	EST_HUMAN	601456301F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3859849 5'
3804	16503	26964	1.41	1.0E-01	AF297081.1	NT	601680489F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134071 5'
							Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3904	18503	28986	1.41	1.0E-01	AF297091.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds, and unknown genes
4027	18926	29097	2.82	1.0E-01	BF385703.1	EST_HUMAN	QV2-NT0048-180800-3 (6-405 NT0048 Homo sapiens cDNA
4488	17080	29529	1.82	1.0E-01	AE002285.2	NT	Chlamydia pneumoniae AR39, section 91 of the complete genome
4853	17235		0.97	1.0E-01	AI782349.1	EST_HUMAN	an3204.y6 Gesaler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4822	17400	29853	1.8	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (for) mRNA, complete cds
4920	17485	29946	0.98	1.0E-01	AA765434.1	EST_HUMAN	oe05h03.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304117 3'
5050	17623	30088	2.12	1.0E-01	AW952344.1	EST_HUMAN	EST364414 MAGe resequences, MAGB Homo sapiens cDNA
5408	17885	30375	1.06	1.0E-01	AV721471.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBBQE10 6'
5415	17972		0.88	1.0E-01	AV783960.1	EST_HUMAN	EST364414 MAGe resequences, MAGB Homo sapiens cDNA
5524	18158		8.57	1.0E-01	W89490.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
6040	18659		0.95	1.0E-01	AK024472.1	NT	zh62h04.s1 Soares fetal_liver_spleen_1NF5_S1 Homo sapiens cDNA clone IMAGE:418895 3'
6175	18788	31554	11.01	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6477	19078	31881	0.98	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6489	19090	31873	0.82	1.0E-01	AA409039.1	EST_HUMAN	z441g10.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:756258 3' similar to contains
7091	19882		1.71	1.0E-01	R23821.1	EST_HUMAN	L1.13 L1 repetitive element;
7717	20236		2.33	1.0E-01	Y12488.1	NT	z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'
7874	20416						yn34h08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu
8107	20848						repetitive element;
							M.musculus whn gene
							ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:M34182 CAMP-
							DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
							Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8429	20869		0.83	1.0E-01	AW189787.1	EST_HUMAN	x109b01.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S
9113	21849	34590	1.08	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element;
9418	21825	34873	0.49	1.0E-01	R44683.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9426	21835		2.05	1.0E-01	M78729.1	NT	yq33h04.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:34549 3'
9489	21868		2.67	1.0E-01	AE001501.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9483	21840	34888	0.71	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99 section 82 of 132 of the complete genome
9735	22233	35211	1.87	1.0E-01	BF240154.1	EST_HUMAN	z666c10.s1 Soares fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:327282 3'
9848	22348	35327	8.17	1.0E-01	AB048786.1	NT	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9848	22348	35328	8.17	1.0E-01	AB048786.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10048	22543		2.05	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
							EST350615 MAGe resequences, MAGB Homo sapiens cDNA
							y628a06.s1 Stralagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:72562 3' similar to
							contains Alu repetitive element
10053	22548	35542	0.61	1.0E-01	T61952.1	EST_HUMAN	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	22729	35720	1.08	1.0E-01	BE792750.1	EST_HUMAN	601584804F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939098 5'
10837	23074		2.11	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10910	23429	36448	3.33	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10910	23429	36449	3.33	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11278	23731	38788	5.03	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939734 5'
11870	24581		3.49	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12104	24368		1.74	1.0E-01	7682168	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12122	24360		1.36	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12336	24519		2.27	1.0E-01	AA737981.1	EST_HUMAN	nt11c08.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255780 3'
12413	25031		4.74	1.0E-01	U52891.1	NT	Gonyulax polyedra putative type-1 serine/threonine phosphatase (PPT1) mRNA, complete cds
12445	24581		2.17	1.0E-01	BE637719.1	EST_HUMAN	60106554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12495	24823		1.93	1.0E-01	BE158905.1	EST_HUMAN	QV4-H10401-211289-064-g03 H10401 Homo sapiens cDNA
12511	25001		41.15	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12578	24874		7.73	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
							Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pkc-Ril) mRNA, complete cde
2806	15358	27925	0.93	9.8E-02	AF274098.1	NT	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
2813	15365	27934	1.95	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
2813	15365	27935	1.95	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
3305	15916	28393	1.98	9.8E-02	AF066810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
4025	16823	28095	0.84	9.8E-02	AB21837.1	EST_HUMAN	zu45c03.x5 Scorses ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740832 3'
7049	18068	30459	9.12	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
							repetitive element contains element MIR MIR repetitive element ;
7856	20398	33304	0.65	9.8E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2566528 3' similar to contains Alu
							repetitive element contains element MIR MIR repetitive element ;
7856	20398	33305	0.65	9.8E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2566528 3' similar to contains Alu
9181	21758	34704	1.1	9.8E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
589	13219		1.48	9.8E-02	X66338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3179	15792	28263	4.23	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4308	16894	28337	8.69	9.8E-02	AF257328.1	NT	Leptophaeria maculans beta-tubulin mRNA, complete cds
4308	16894	28338	8.69	9.8E-02	AF257328.1	NT	Leptophaeria maculans beta-tubulin mRNA, complete cds
7495	20018		0.99	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9178	21755		1.05	9.8E-02	M61943.1	NT	Human lamrin B1 chain gene, exon 26
11334	23032	36041	2.27	9.8E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3984287 5'
11840	24203		1.46	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1394	13988	28516	1.24	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1829	14221		1.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2301	14874	27450	2.11	9.7E-02	BE188980.1	EST_HUMAN	QV1-HT0518-070300-095-a04 HT0518 Homo sapiens cDNA
4055	18852		4.76	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5548	18180	30594	1.01	9.7E-02	AF069189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5548	18180	30595	1.01	9.7E-02	AF069189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6165	18777	31541	1.29	9.7E-02	AW854478.1	EST_HUMAN	EST366648 MAGE resequences, MAGE Homo sapiens cDNA
7340	18897	32731	3.28	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 10 of 21): from 2897771 to 3213410
7924	20488	33374	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA IMAGE:254788 3'
7924	20488	33375	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA IMAGE:254788 3'
8783	21322	34248	1.47	9.7E-02	AB853984.1	EST_HUMAN	wx78b06.x1 NCL CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_maf1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11076	23598		2.34	9.7E-02	U86337.1	NT	Mus musculus ligatin (Lgtb) mRNA, partial cds
2080	14840	27213	1.33	9.6E-02	AB080721.1	EST_HUMAN	cz47d11.x1 Soares_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2080	14840	27214	1.33	9.6E-02	AB080721.1	EST_HUMAN	cz47d11.x1 Soares_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4437	17023	28483	7.84	9.6E-02	Z32888.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
5142	17713	30144	1.03	9.6E-02	AW988230.1	EST_HUMAN	EST378303 MAGE resequences, MAGE Homo sapiens cDNA
6254	18863		2.74	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3800165 5'
8317	20858		0.61	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9483	21888	34944	1.34	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9788	22284		1.35	9.6E-02	BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5'
8932	22447	35429	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
8982	22447	35430	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35544	1.28	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10055	22550	35545	1.28	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10159	22654	35949	3.43	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
10821	23153	38185	7.28	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/182
11568	24013	37082	1.81	9.6E-02	AA625755.1	EST_HUMAN	z991g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
12496	24617		1.55	9.6E-02	HI14596.1	EST_HUMAN	ym19n03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
4177	16788	29217	2.24	9.6E-02	AW862395.1	EST_HUMAN	GM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
6286	17848	30274	1.12	9.5E-02	U863374.1	NT	Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5848	18470	31198	0.82	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7344	19871	32738	4.47	9.5E-02	AB003473.1	NT	Trimerus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7569	20086	32983	6.95	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7855	18470	31198	0.9	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7821	20363	33271	2.04	9.5E-02	BF035881.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
7821	20363	33272	2.04	9.5E-02	BF035881.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36107	3.19	9.5E-02	BF035881.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36108	3.19	9.5E-02	BF035881.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12557	24958		2.4	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1873	14458	27015	3.67	9.4E-02	BF071063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
1904	14489	27050	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1904	14489	27081	1.38	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3948	16547	28015	5.59	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC0073
5383	17942		0.83	9.4E-02	X88108.1	NT	Lactobacillus bacteriophage phi10 complete genomic DNA
6459	19060	31846	0.73	9.4E-02	AF007383.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8538	21075		2.32	9.4E-02	Z46883.1	NT	Acinetobacter sp. eyeD, cobQ, sodM, lyeS, rubA, rubB, estB, oxyR, ppk, mlpA, ORF2 and ORF3 genes
10813	20107	32882	2.33	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and lpr35 gene, partial cds
11722	24934		6.48	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12845	24719	30889	3.54	9.4E-02	U27698.1	NT	Human pepkBGT-1 betaine-GABA transporter mRNA, complete cds
3018	16634		1.68	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3083	15679		7.31	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3295	15808	28387	2.05	9.3E-02	BF575511.1	EST_HUMAN	602133089F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4232	16820	28269	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4232	16820	28270	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4840	17418		1.28	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 6'
5943	18487		0.73	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8190	20731	33843	0.52	9.3E-02	AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9032	21598		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9826	22128	35090	2.1	9.3E-02	BE862631.2	EST_HUMAN	601659881F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10094	22589	35581	3.18	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10094	22589	35582	3.18	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10222	22717		3.82	9.3E-02	AW208117.1	EST_HUMAN	U1-H-B11-afk-h-05-Q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
11892	24894		2.27	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12379	24888		18.03	9.3E-02	AW458850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
12598	24833		3.18	9.3E-02	AF100958.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RelDGS-like factor (RUF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
249	12809	25390	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12809	25391	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12809	25392	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2269	14843		1.58	9.2E-02	R64168.1	EST_HUMAN	yg8807.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3213	15826	28302	3.92	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3345	15955	28430	0.86	9.2E-02	AA534354.1	EST_HUMAN	nt76601.at1 NC1_CGAP_C63 Homo sapiens cDNA clone IMAGE:926138 3'
3848	18249		1.18	9.2E-02	6755216	NT	Mus musculus pte T-cell antigen receptor alpha (Ptrae), mRNA
4322	18908		1.42	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4395	19981		0.86	9.2E-02	BE289722.1	EST_HUMAN	G00844365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
4744	17326	29767	1.44	9.2E-02	X98402.1	NT	G.gallus Mia-CK gene
7851	20483	33402	1.75	9.2E-02	T48920.1	EST_HUMAN	ya95c09.r1 Stratagene placenta (#837225) Homo sapiens cDNA clone IMAGE:68808 5' similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8117	20658	33567	2.11	9.2E-02	X95256.1	NT	H.vulgaris xylose isomerase gene
12658	24830		2.09	9.2E-02	Z22150.1	NT	S.dysgalactiae fnbA gene
448	12877	25134	2.83	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
3733	16334		0.95	9.1E-02	AW372589.1	EST_HUMAN	PM2-BT0349-161289-001-402 BT0349 Homo sapiens cDNA
4582	17185	28608	1.55	9.1E-02	AL161554.2	NT	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 54
5805	18527	31253	1.5	9.1E-02	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G8c, G5b, G6d, G8a, G6f, BAT6, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7420	19944	32809	11.98	9.1E-02	AW160859.1	EST_HUMAN	au74605.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
7688	20180	33067	0.88	9.1E-02	AF000081.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7695	20204	33091	0.88	9.1E-02	U39073.1	NT	Mus musculus thymoprotein zeta mRNA, complete cds
8856	21394	34317	1.05	9.1E-02	Y14370.1	NT	Homo sapiens gamma adducin gene, exon 9
10325	22819		1.38	9.1E-02	T02894.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
10354	22848	35342	1.52	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Tripeustus grallia=sea urchins, embryos, Genomic, 5275 nt]
10380	22874	35867	0.73	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11658	24083		2.35	9.1E-02	6833484	NT	Bacteriophage Mu, complete genome
11808	25036		1.82	9.1E-02	AA178901.1	EST_HUMAN	zp38h12.xs1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3 HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA :

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11978	24289		2.21	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12487	24877		17.53	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
12872	24740		1.5	9.1E-02	AF226898.1	NT	Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
774	13393	25893	3.92	9.0E-02	P15328	SWISSPROT	ANTIGEN MOV18 (KB CELLS FBP)
1676	14298	26801	6.34	9.0E-02	BE220482.1	EST_HUMAN	h38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176942 3' similar to contains Alu repetitive element
2826	15381	27851	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2826	15381	27852	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
3390	15999	28468	0.83	9.0E-02	AF279135.1	NT	Dichostellum discoidium spore coat structural protein SP65 (cdE) gene, complete cds
4387	16973	29422	0.59	9.0E-02	S68787.1	NT	corticosteroid-binding globulin [Salimiri sciureus=squirrel monkey, liver, mRNA, 1474 nt]
4387	16973	29423	0.59	9.0E-02	S68787.1	NT	corticosteroid-binding globulin [Salimiri sciureus=squirrel monkey, liver, mRNA, 1474 nt]
4775	17356	28808	1.88	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5401	17959	30370	1.12	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
6146	18760	31519	18.48	9.0E-02	W56037.1	EST_HUMAN	z88a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6820	19410		1.1	9.0E-02	BF062651.1	EST_HUMAN	7h63403.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
6864	19598	32428	0.77	9.0E-02	R82805.1	EST_HUMAN	y11b08.e1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
							Escherichia coli strain E2348/69 pathogenicity island, rOr1 (rOr1), rOr2 (rOr2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CasD (casD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrU (orU), >
12300	24497		2.42	9.0E-02	AF022236.1	NT	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1486	14078	26617	1.48	9.0E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1486	14078	26618	1.48	9.0E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2430	14897	27571	9.68	9.0E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-401 HT0339 Homo sapiens cDNA
4277	16863		1.79	9.0E-02	AF28055.1	NT	Atichium angustatum AtranFlc2 protein (AtranFlc2) gene, partial cds
4741	17322	29762	1.91	9.0E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
6014	18634	31370	3.35	9.0E-02	AW452122.1	EST_HUMAN	UI-H-B13-abc-f08-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6014	18634	31371	3.35	9.0E-02	AW452122.1	EST_HUMAN	UI-H-B13-abc-f08-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6026	18645	31387	3.24	9.0E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
							FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
7244	19773	32630	1.76	9.0E-02	P47259	SWISSPROT	
7559	20077		2.15	9.0E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA20F8

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7994	20536	33439	0.89	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8072	20814	33528	0.89	8.9E-02	BF701885.1	EST_HUMAN	802128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8072	20814	33528	0.89	8.9E-02	BF701885.1	EST_HUMAN	802128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8534	21073	33983	4.81	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9538	22038	34998	0.83	8.9E-02	AI285827.1	EST_HUMAN	qu55605.x1 NCL_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1988880 3' similar to contains MER10.b1 MER10 repetitive element:
9538	22038	34999	0.83	8.9E-02	AI285827.1	EST_HUMAN	qu55605.x1 NCL_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1988880 3' similar to contains MER10.b1 MER10 repetitive element:
9848	22147	35118	0.55	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11721	24884		2.81	8.9E-02	P18824	SWISSPROT	MYOSIN-2 ISOFORM
11872	24224		4.82	8.9E-02	BF69918.1	EST_HUMAN	602128882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4288180 5'
12044	24330		3.07	8.9E-02	6880220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12307	25104		1.57	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposase gene, complete cds
1416	14009	26538	1.36	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
3971	16569	28038	1.08	8.8E-02	AA269128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4108	16700		4.3	8.8E-02	O00288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
4390	16978		0.98	8.8E-02	4580423	NT	Homo sapiens paired box gene 8 (enitridia, keratins) (PAX8), isoform b, mRNA
8918	21458	34376	1.18	8.8E-02	AA151872.1	EST_HUMAN	zn98e05.e1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:569288 3'
10997	23511	36543	3.11	8.8E-02	BE284485.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535848 5'
10997	23511	36544	3.11	8.8E-02	BE284485.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535848 5'
11142	23650	36692	10.91	8.8E-02	AL040126.1	EST_HUMAN	DKFZp334D1313_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp334D1313 5'
11948	24277	31019	1.73	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
3756	16357	28826	3.9	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3756	16357	28827	3.9	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4816	17394	28847	1.42	8.7E-02	AF178838.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5264	17828		1.2	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1178181 to 1189406 (section 101 of 148) of the complete genome
5517	18148	30581	5.18	8.7E-02	AA288875.1	EST_HUMAN	zn55508.e1 NCL_CGAP_G051 Homo sapiens cDNA clone IMAGE:701438 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5517	18149	30562	6.18	8.7E-02	AA288376.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6631	18560	32421	0.76	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6631	18560	32422	0.76	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7803	20346		0.48	8.7E-02	AA284532.1	EST_HUMAN	z20e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'
8452	20962	33910	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8452	20962	33911	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10580	23125		2.71	8.7E-02	L04758.1	NT	Oryzias latipes cytochrome P-450 (CYP4A4) gene, 5' end
11191	23898	36745	1.77	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans rRNA-16S and rRNA-23S genes
11935	24269		2.35	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12142	24389		2.72	8.7E-02	6878057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1295	13889	28412	6.51	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudobacterial region, segment 2/2
2288	14860	27435	2.47	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3222	15834	28312	2.42	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3708	16307		4.02	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds
4584	17167	28810	0.59	8.6E-02	U08179.1	NT	Oryzias latipes galecin-3 gene, untranslated exon and 5' flanking region
6244	18853	31624	5.78	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6512	19112	31899	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6512	19112	31900	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7591	20086	32974	1.14	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7871	20413	33319	1.23	8.6E-02	5730088	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7871	20413	33320	1.23	8.6E-02	5730088	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8015	20557	33460	0.76	8.6E-02	11427428	NT	Homo sapiens hypodermal protein FLJ11006 (FLJ11006), mRNA
8073	20615		0.65	8.6E-02	U00168.1	NT	Dictyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9652	22151	35121	1.18	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9658	22187		1.27	8.6E-02	AF0682153.1	EST_HUMAN	h20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10057	22552	35547	0.74	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
10824	23345	36360	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10824	23346	36361	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11128	23636	36677	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11128	23636	36678	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11315	23013	36022	7.58	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2440	15007	27579	2.52	8.6E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	18507		1.91	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6162	18776	31637	6.64	8.6E-02	AF233985.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8542	21081	34002	1.76	8.5E-02	6754778	NT	Mus musculus myosin XV (Myo15), mRNA
9760	22248	35230	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-605 OT0037 Homo sapiens cDNA
9760	22248	35231	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-605 OT0037 Homo sapiens cDNA
10378	22873	35966	0.92	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11036	23548		12.56	8.5E-02	AF165510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11060	23583	38598	4.42	8.5E-02	AB001582.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12354	24814		6.89	8.5E-02	AJ006586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
12536	24847		2.27	8.5E-02	AA382604.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2690	15474	27816	3.71	8.4E-02	W69330.1	EST_HUMAN	z444e11.1 Source: fetal heart_NHH19W Homo sapiens cDNA clone IMAGE:343532 5'
6200	17765		1	8.4E-02	X01472.1	NT	Drosophila melanogaster copin-like element 17.6
5368	17928	30343	0.88	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5515	18147	30559	9.48	8.4E-02	BE287153.1	EST_HUMAN	601190438F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35534383 5'
6761	18382	32167	1.67	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7872	20514	33421	7.35	8.4E-02	BE095074.1	EST_HUMAN	CM3-B10760-260400-182-05 B10760 Homo sapiens cDNA
8776	21316	34237	1.13	8.4E-02	AF218860.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10285	22760	35747	1.61	8.4E-02	A1795184.1	EST_HUMAN	aa88g10.x1 Barstead cotton HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
11858	24217	31042	1.92	8.4E-02	R79408.1	EST_HUMAN	O88312 GOB-4.1
2056	14637	27208	2.08	8.3E-02	5835680	NT	y83h12.1 Source: placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2056	14637	27209	2.08	8.3E-02	5835680	NT	ixodes hexagonus mitochondrion, complete genome
3652	16255	28728	8.88	8.3E-02	P75334	SWISSPROT	ixodes hexagonus mitochondrion, complete genome
3680	16281	28748	0.68	8.3E-02	A1436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG308 HOMOLOG PRECURSOR
3680	16281	28749	0.68	8.3E-02	A1436797.1	EST_HUMAN	th82g08.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5416	17873		1.71	8.3E-02	AW602857.1	EST_HUMAN	th82g08.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6406	18006	31761	0.89	8.3E-02	A042338.1	EST_HUMAN	QV3-NN1025-Q30500-173-604 NN1026 Homo sapiens cDNA
6504	19104	31889	3.05	8.3E-02	AF062683.1	NT	wa78f11.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2461561 3'
7922	20464	33371	3.57	8.3E-02	AF185787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7955	20497		1.31	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dydrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
8241	20782		4.14	8.3E-02	AA867873.1	EST_HUMAN	cg88g08.x1 NCL_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1456422 3' similar to contains L1.11 L1 L1
8457	21883	34635	1.55	8.3E-02	AW583503.1	EST_HUMAN	repetitive element
							cg81f10.x1 NCL_CGAP_K1d6 Homo sapiens cDNA clone IMAGE:1592779 3'
							ia05h10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
							SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.1

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9470	21968		1.94	8.3E-02	AL181595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10244	22739		0.56	8.3E-02	AF020409.1	NT	Dicotyledon discoidium Doca (dca) mRNA, complete cds
11550	23988	37070	1.7	8.3E-02	AA700756.1	EST_HUMAN	282d04.01 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435387 3' similar to
11953	25040		1.36	8.3E-02	BE989458.1	EST_HUMAN	contains element MER22 repetitive element;
1421	14014		0.32	8.2E-02	Y08170.2	NT	601044770F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3928883 5'
1542	14134	28688	1.79	8.2E-02	AF167077.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
3109	15724		2.23	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3874	16872		1.66	8.2E-02	AL161488.2	NT	Homo sapiens chromosome 21 segment HS21C008
4078	16875	29136	1.26	8.2E-02	AL163206.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4371	16958	29400	7.76	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C008
4371	16958	29401	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN C097 PRECURSOR
4371	16958	29402	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN C087 PRECURSOR
5240	17804	30225	3.53	8.2E-02	U76008.1	NT	LEUCOCYTE ANTIGEN C097 PRECURSOR
5400	17858	30369	0.9	8.2E-02	AL119830.1	EST_HUMAN	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5538	18170	30595	1.62	8.2E-02	BE897030.1	EST_HUMAN	AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5'
7092	19683	32502	3.11	8.2E-02	AF308555.1	NT	601439576F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3924523 5'
8707	21246	34169	2.98	8.2E-02	AW875126.1	EST_HUMAN	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
9517	22017	34974	4.88	8.2E-02	X04197.1	NT	RC2-PT0004-031289-011-d03 PT0004 Homo sapiens cDNA
9878	22177	35152	2.2	8.2E-02	BE254318.1	EST_HUMAN	Beet necrotic yellow vein virus RNA-2
11959	24281	31023	5.69	8.2E-02	AE002248.2	NT	601115055F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3355598 5'
12383	24806		4.6	8.2E-02	AF275386.1	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
5926	18551	31278	1.08	8.1E-02	AE004008.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6516	19116	31906	0.97	8.1E-02	T11632.1	EST_HUMAN	Xylella fastidiosa, section 152 of 229 of the complete genome
7248	18777		0.72	8.1E-02	AL163279.2	NT	A1484F Heart Homo sapiens cDNA clone A1484
7592	20097		1.03	8.1E-02	AI62881.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
8281	20822	33741	0.82	8.1E-02	11426974	NT	wd86008.x1 NCI_COAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8281	20822	33742	0.82	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8828	22324		1.7	8.1E-02	AY003150.1	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
11371	23823	36896	1.87	8.1E-02	AL163202.2	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
8	15405	25143	9.1	8.0E-02	AW654853.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
971	13582	26095	1.13	8.0E-02	U60315.1	NT	EST1366723 MAGE resequences, MAGE Homo sapiens cDNA
1738	16446	26869	10.88	8.0E-02	D26636.1	NT	Molluscum contagiosum virus subtype 1, complete genome
							Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1738	15449	26870	10.86	8.0E-02	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1947	14831	27087	3.32	8.0E-02	BC087219.1	EST_HUMAN	P43-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2413	14981	27556	1.14	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259
2413	14981	27557	1.14	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259
2609	15073		4.88	8.0E-02	BF248744.1	EST_HUMAN	80185548F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4075918 5'
2847	13733	26243	0.87	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2925	15541	28018	0.84	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome; segment 5/6
3888	16487	28948	0.59	8.0E-02	AW068118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
4148	16738		0.95	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4890	17485	28920	2.28	8.0E-02	A1434202.1	EST_HUMAN	H31902.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4939	17514		5.81	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
6051	18899	31408	3.07	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7232	18666	31408	1.42	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8059	20811	33524	3.68	8.0E-02	AL114983.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8311	21825	34773	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
8311	21825	34774	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10083	22558		0.57	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10671	23203	38218	3.89	8.0E-02	AF217788.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M58, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
11893	24302	30988	3.5	8.0E-02	AJ008375.1	NT	Drosophila arena hunchback region
12695	18738		3.88	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2218	14793	27386	4.15	7.9E-02	BE260008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
3007	15623	28101	11.7	7.9E-02	A1592028.1	EST_HUMAN	ar38c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173846 3' similar to gb:228878
3865	16463	28827	0.92	7.9E-02	AF030894.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG8 (cg8), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3817	16515	28978	3	7.9E-02	6881044	NT	CG2 (cg2), and CG7 (cg7) genes, complete cds
3817	16515	28979	3	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4834	17509		1.36	7.9E-02	AB008018.1	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
5390	17848	30360	0.58	7.9E-02	AF035672.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
5390	17848	30361	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
6788	19389		1.08	7.9E-02	BF369016.1	EST_HUMAN	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
7076	20617	33424	3.32	7.9E-02	U27832.1	NT	RC3-GN0042-310800-024-11 GN0042 Homo sapiens cDNA
						NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9841	22436	35412	4.71	7.9E-02	A01844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632485 3' similar to WP:C37A2.2 CE08811;
9841	22436	35413	4.71	7.9E-02	A01844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632485 3' similar to WP:C37A2.2 CE08811;
12479	24613		1.42	7.9E-02	A1781839.1	EST_HUMAN	wg56h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
1252	13849	26385	1.36	7.8E-02	A1793275.1	EST_HUMAN	cc69d02.y6 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570497 5' similar to contains L1.13 L1 repetitive element;
1252	13849	26386	1.36	7.8E-02	A1793275.1	EST_HUMAN	cc69d02.y6 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570497 5' similar to contains L1.13 L1 repetitive element;
4912	17487	28943	0.67	7.8E-02	BE836331.1	EST_HUMAN	PIM3-FND058-140700-005-f09 FN0058 Homo sapiens cDNA
5247	18412		2.77	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856683 5'
7136	19475	32297	1.34	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7136	19475	32298	1.34	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8720	21259	34179	1.46	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8813	21362	34274	0.6	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
8983	21521	34447	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8983	21521	34448	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9283	21893	34828	1.08	7.8E-02	AA469354.1	EST_HUMAN	nc88508.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731
9717	22216	35189	0.5	7.8E-02	Z09124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3993281 to 4214814
10544	23081	36094	1.67	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12384	24590	30808	1.95	7.8E-02	U72847.1	NT	Homo sapiens enocephalin (EVPL) gene, exons 15 through 18
1444	15442	26568	0.91	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3647	16250		2.62	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5129	17701	30135	0.92	7.7E-02	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
7850	20392	33285	5.56	7.7E-02	AA402849.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
9749	22247	35229	5.97	7.7E-02	P36080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22832	35527	0.75	7.7E-02	A1318682.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10037	22832	35528	0.76	7.7E-02	A1318682.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10869	23410	36428	4.97	7.7E-02	11422767	NT	Homo sapiens KIAA0828 gene product (KIAA0828), mRNA
12194	24894		1.91	7.7E-02	11439869	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3434	16042	28523	3.08	7.6E-02	BE514432.1	EST_HUMAN	801316428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634603 5'
3455	16082	28537	0.87	7.6E-02	AA288447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf18 gene and C11orf17 gene
3815	16218	28897	0.87	7.6E-02	AJ400877.1	NT	
4893	17567		2.04	7.6E-02	AW898844.1	EST_HUMAN	RC3-CT0347-110300-014-405 CT0347 Homo sapiens cDNA
6247	18856	31627	0.7	7.6E-02	A081275.1	EST_HUMAN	an25q02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1698730 3'
6497	18098	31882	0.83	7.6E-02	BE376328.1	EST_HUMAN	801238402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808401 5'
9292	21892	34839	1.24	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9811	22309		1.7	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10120	22815	35605	0.52	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-408 HT0545 Homo sapiens cDNA
10251	22748		0.49	7.6E-02	BE959638.2	EST_HUMAN	601854815R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10480	22974	35981	0.72	7.6E-02	X92656.1	NT	L. esculentum mRNA for trice phosphate translocator
10480	22874	35982	0.72	7.6E-02	X92656.1	NT	L. esculentum mRNA for trice phosphate translocator
11528	23974	37044	2.58	7.6E-02	AW889645.1	EST_HUMAN	QV3-BN0046-150400-151-404 BN0046 Homo sapiens cDNA
817	13435	25940	1.18	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
817	13435	25941	1.18	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4606	17189	26636	0.57	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, Intron 1 and exon 2
8280	20821	33740	1.15	7.5E-02	A1864397.1	EST_HUMAN	w62b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8444	20884	33899	1.18	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone IMAGE:1000284 5'
9845	22440		0.5	7.5E-02	BF221730.1	EST_HUMAN	7661c05.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element;
10387	22881	35975	0.9	7.5E-02	BF206809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10481	22975	35983	0.71	7.5E-02	X79480.1	NT	G.fim DSM 20113 16S rDNA
503	13135	25623	1.23	7.4E-02	AW838547.1	EST_HUMAN	RC6-LT0064-260100-011-H09 LT0064 Homo sapiens cDNA
1509	14101		0.97	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2616	15178		1.04	7.4E-02	6755009	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pibx1), mRNA
3664	16267	28729	0.84	7.4E-02	A0807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2356365 3'
4814	17392	26844	1.33	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4911	17486	26942	2.82	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5052	17626		1.65	7.4E-02	AE000866.1	NT	Methanobacterium thermoautotrophicum from bases 1076134 to 1086763 (section 92 of 148) of the complete genome
5076	17849	30090	1.67	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
5393	17851	30364	0.93	7.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6621	19218		1.64	7.4E-02	R17477.1	EST_HUMAN	y014q06.t1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7465	20008	32874	0.68	7.4E-02	AA605132.1	EST_HUMAN	no71d02.t1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
7842	20394	33288	1.23	7.4E-02	BE680112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895284 5'
8438	20878	33863	1.2	7.4E-02	U66089.1	NT	Human periodic tyrophen protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9093	21626	34566	0.92	7.4E-02	AW626605.1	EST_HUMAN	h167d11.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2887861 5' similar to SW:SCA2_HUMAN
9093	21626	34567	0.92	7.4E-02	AW626605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2. ;
9360	20269	33197	0.72	7.4E-02	A1672639.1	EST_HUMAN	h167d11.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2887861 5' similar to SW:SCA2_HUMAN
9360	20269	33198	0.72	7.4E-02	A1672639.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2. ;
9726	22226	35203	0.85	7.4E-02	U62293.1	NT	w074d02.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346818 3'
11800	24043		1.57	7.4E-02	U88282.1	NT	w074d02.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346818 3'
11912	24250		1.29	7.4E-02	11528693	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12187	25015		4.44	7.4E-02	AW379431.1	EST_HUMAN	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12351	24531	30926	2.8	7.4E-02	BF035089.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12361	24535	30901	1.37	7.4E-02	AJ223456.2	NT	GM4-HT0243-081198-037-411 HT0243 Homo sapiens cDNA
484	13127	26613	1.42	7.3E-02	BE964981.2	EST_HUMAN	601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3887738 5'
494	13127	25614	1.42	7.3E-02	BE964981.2	EST_HUMAN	Aspergillus nidulans pmD, pmX, pmA genes
713	13334	26820	2.68	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1528	16444	26850	4.47	7.3E-02	AW600281.1	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1895	16453		16.16	7.3E-02	AL163302.2	NT	Thermotoga maritima section 101 of 136 of the complete genome
							CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3,
							TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3,
							TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2P, TCRBV7S2A1N4T,
							TCRBV13S8/13S>
3838	16437		0.59	7.3E-02	U66059.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5137	17709		1.11	7.3E-02	U12283.1	NT	

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19178	31978	1.68	7.3E-02	AA779977.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 28S PROTEASE SUBUNIT 4 (HUMAN);
7484	20007	32872	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7484	20007	32873	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8109	20660		1.08	7.3E-02	7682107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9137	21672		1.38	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11095	19178	31978	3.07	7.3E-02	AA779977.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 28S PROTEASE SUBUNIT 4 (HUMAN);
							Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
125	12764	25279	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
126	12764	25280	1.36	7.2E-02	AE000882.1	NT	Homo sapiens chromosome 21 segment HS21C101
1524	14116	26652	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1524	14116	26653	2.11	7.2E-02	AL163301.2	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
2585	15148		2.76	7.2E-02	U14794.1	NT	U14794.1
3654	16552	28021	0.59	7.2E-02	AW288322.1	EST_HUMAN	U14794.1
4438	17024	29464	3.65	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4261860 5'
5223	17798	30207	0.89	7.2E-02	AB001682.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5491	18125	30533	2.8	7.2E-02	U87531.1	NT	Methanococcus jannaschii section 73 of 160 of the complete genome
5492	18126	30534	8.6	7.2E-02	P11120	SWISSPROT	CALMODULIN
6265	18873		0.93	7.2E-02	BF217695.1	EST_HUMAN	601883805F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098224 5'
7220	19751	32607	1.27	7.2E-02	BF218086.1	EST_HUMAN	601883688F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7261	19769		1.54	7.2E-02	9634897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8128	20668	33578	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8128	20668	33579	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8994	21532		0.5	7.2E-02	Y17217.1	NT	Lactococcus lactis capE gene
9495	21965		0.57	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9529	22029	34988	2.28	7.2E-02	AV1712452.1	EST_HUMAN	AV1712452 DCA Homo sapiens cDNA clone DCAUG01 5'
							Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9674	22173	35149	4.69	7.2E-02	L14581.1	NT	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
9628	22326	35307	1.01	7.2E-02	BF125398.1	EST_HUMAN	hg24111.x1 NCI CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340
9914	22410	35386	2.73	7.2E-02	AW873187.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10284	22749	35737	2.11	7.2E-02	U92895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10370	22884	35857	5.88	7.2E-02	BE568003.1	EST_HUMAN	601343928F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3685951 5'
10392	22896		3.22	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3451559 5'
10792	23316	36324	6.18	7.2E-02	A049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11822	24192	31033	1.54	7.2E-02	AA773898.1	EST_HUMAN	af81a04.r1 Soares_NHMPu ST Homo sapiens cDNA clone IMAGE:1048398 5'
11867	24216		4.88	7.2E-02	AJ230786.1	EST_HUMAN	AJ230786 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
11914	24282		2.01	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
11978	24290		3.69	7.2E-02	U92828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
11995	24858		7.52	7.2E-02	AW600682.1	EST_HUMAN	GM44NN1008-200300-118-011 NN1009 Homo sapiens cDNA
12514	24863		1.85	7.2E-02	AA401778.1	EST_HUMAN	z57c12.r1 Soares_basils_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1948	14532	27088	1.42	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene, partial cds
2331	14802	27473	4.53	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:4092881 5'
7848	20390	33292	0.84	7.1E-02	A1125264.1	EST_HUMAN	q982a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
11700	24113		6.04	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC 15 Homo sapiens cDNA clone IMAGE:3051234 5'
554	13185	25663	0.97	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1547	14139		1.43	7.0E-02	X98877.1	NT	Martella Micut-1 gene
1798	14398	26933	0.94	7.0E-02	AA056343.1	EST_HUMAN	z6604.s1 Strategene colon (H937204) Homo sapiens cDNA clone IMAGE:509599 3'
3084	15680	28153	2.03	7.0E-02	AW138152.1	EST_HUMAN	U1H-B11-acy-c-07-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3868	16584	29033	1.71	7.0E-02	AA816438.1	EST_HUMAN	af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 80S
4118	16712	29166	1.11	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4219	16807		1.11	7.0E-02	AW792962.1	EST_HUMAN	QV4-B10407-280100-090-e10 BT0407 Homo sapiens cDNA
4294	16880	29327	1.28	7.0E-02	AF077821.1	NT	CMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
5083	17636	30079	9.56	7.0E-02	BF381887.1	EST_HUMAN	Genis familiaris inducible nitric oxide synthase mRNA, complete cds
5580	18211		0.84	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4050071 5'
7431	19655	32820	0.88	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
9027	21564	34493	1.41	7.0E-02	9828113	NT	AV689285 GKc Homo sapiens cDNA clone GKCCAE08 5'
9515	22015	34873	1.25	7.0E-02	K02801.1	NT	African swine fever virus, complete genome
9883	22360	35340	0.73	7.0E-02	U27268.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11251	23781	36837	2.68	7.0E-02	AA724295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
							ah98a05.s1 Soares_NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
							TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
540	13171	25649	11.84	6.9E-02	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
540	13171	25650	11.84	6.9E-02	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13971		1.34	6.9E-02	4507988	NT	Homo sapiens regulator of Gs-selective protein signaling (ZGAP1) mRNA, and translated products
3680	16458	28921	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3680	16458	28922	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
6381	17840	30354	3.56	6.9E-02	AF121254.1	NT	Enterococcus faecium cytolysin aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucosidase specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
7098	20538		1.13	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2, 3, 4, 5 and 6, and complete cds
8488	21027	33944	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33945	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9048	21585	34518	0.61	6.9E-02	U22867.1	NT	Barbante duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11853	24213		17.91	6.9E-02	X74315.1	NT	Xlaeis xfd2 mRNA for fork head protein
12031	24321		1.98	6.9E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFH HOMOLOG
12258	24468		3.68	6.9E-02	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1928	14511	27085	1.83	6.8E-02	AA498759.1	EST_HUMAN	ae30702.r1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:597339 5' similar to gb:M22382
1928	14511	27088	1.83	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1950	14534	27090	3.99	6.8E-02	AF156973.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
2023	14805	27170	1.88	6.8E-02	BE263781.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
4851	17233		0.86	6.8E-02	BE141076.1	EST_HUMAN	601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537708 5'
6980	18478		4.83	6.8E-02	BE091890.1	EST_HUMAN	MFG-HIT0069-071099-001-c05 HT0069 Homo sapiens cDNA
7324	19851	32713	6.08	6.8E-02	AL163288.2	NT	RC1-BT0254-060300-017-d09 BT0254 Homo sapiens cDNA
8230	20771	33690	5.36	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C088
8230	20771	33691	6.36	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
11048	25064		2.48	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 5/6
11783	24188		2.42	6.8E-02	AA758014.1	EST_HUMAN	FB448 Fetal brain, Stratiogene Homo sapiens cDNA clone FB448 3' end similar to LINE-1
12380	24547		1.37	6.8E-02	AW975839.1	EST_HUMAN	ah8705.at Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
12444	24560		2.87	6.8E-02	6810585	NT	EST367948 MAGE sequences, MAGN Homo sapiens cDNA
12650	25008		1.54	6.8E-02	6978885	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1676	14169		1.51	6.7E-02	AF115538.1	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1838	14522	27078	3.82	6.7E-02	AI220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3780	16380	28944	4.81	6.7E-02	P12728	SWISSPROT	HOMEOBOX PROTEIN HOXD-4 (HOXA)
4842	17420	28973	3.51	6.7E-02	AP001814.1	NT	Bacillus halodurans genomic DNA, section 8/14
7792	20335	33241	0.83	6.7E-02	X62693.1	NT	Hi sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7792	20335	33242	0.83	6.7E-02	X62693.1	NT	Hi sapiens DNA for cGMP phosphodiesterase (exons 4-22)
9918	22018	34976	0.76	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-ecr-g-01-Q.U.1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9918	22018	34978	0.76	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-ecr-g-01-Q.U.1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
2228	14800	27372	3	6.8E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3610	16115	28594	9.7	6.8E-02	R64306.1	EST_HUMAN	Y18b10.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3624	16129	28609	3.24	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3624	16129	28610	3.24	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4154	16748	29200	1.83	6.8E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5114	17686	30122	11.2	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5114	17688	30123	11.2	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5164	17733	30160	0.57	6.8E-02	AA393244.1	EST_HUMAN	Z174907.11 Soares testis NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5164	17733	30161	0.57	6.8E-02	AA393244.1	EST_HUMAN	Z174907.11 Soares testis NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6998	19294	32089	4.11	6.8E-02	X08411.1	NT	P. vulgaris mRNA for chalcone synthase
7888	20430	33339	1.58	6.8E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8408	20949	33869	0.72	6.8E-02	AF060055.1	NT	Dicotyledium discoidium darlin (darA) gene, complete cds
8714	21253	34312	0.48	6.8E-02	O60873	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8852	21391	34312	0.52	6.8E-02	9828188	NT	Human respiratory syncytial virus, complete genome
8852	21391	34313	0.52	6.8E-02	9828188	NT	Human respiratory syncytial virus, complete genome
9862	22359	35339	0.58	6.8E-02	AI458752.1	EST_HUMAN	ig97g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149488 3'
9868	22494	35483	1.54	6.8E-02	Y07648.1	NT	Homo sapiens EWS, gar22, mp22 and bam22 genes
10028	22624	36378	0.53	6.8E-02	11430569	NT	Homo sapiens vinculin (VCL), mRNA
10842	23363	36378	7.09	6.8E-02	BF374248.1	EST_HUMAN	MRI-SN0064-010600-008-a12 SN0064 Homo sapiens cDNA
12251	24462		2.87	6.8E-02	9837981	NT	Mus musculus DIPB gene (Dipb), mRNA
12585	24878		1.36	6.8E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
608	13236	25710	1.65	6.5E-02	BF027639.1	EST_HUMAN	601871048F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1024	13635	26161	2.61	6.5E-02	7706088	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1435	14028	26556	3.4	6.5E-02	U47824.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1770	14360	26905	1.42	6.5E-02	AE000784.1	NT	Aquifex acidicus section 98 of 109 of the complete genome
5348	17809	30324	0.88	6.5E-02	D45899.1	NT	Caenorhabditis elegans DNA for ryanodine receptor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	18373	31081	1.79	6.5E-02	AA443991.1	EST_HUMAN	z446h12.a1 Soares ovary tumor NBOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6684	19260	32064	0.89	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-3 BETA CHAIN (HUMAN);
7051	18070	30481	0.96	6.5E-02	U22661.1	NT	602119887F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4276028 5'
9854	22352	35332	0.85	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 8048 negative regulator MucB (mucB) gene, partial cds
9854	22352	35333	0.86	6.5E-02	BE963200.2	EST_HUMAN	601650817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	22857	35849	0.59	6.5E-02	BF106500.1	EST_HUMAN	601650817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10518	23058	36067	5.88	6.5E-02	AA195848.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11689	24091		6.28	6.5E-02	M21496.1	NT	z322505.a1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:865144 3'
12040	24327		3.84	6.5E-02	AF102683.1	NT	Rabbit microsomal epoxide hydrolase
801	13230	25703	1.74	6.4E-02	X84549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
6641	18270	30743	1.21	6.4E-02	AH91958.1	EST_HUMAN	A. cerea precursor of peridinin-chlorophyll-protein (PCP) gene
6261	18669	31839	6.4	6.4E-02	AF052733.1	NT	q607b01.x1 Soares NIH_MGC_83 Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
6261	18669	31640	5.4	6.4E-02	AF052733.1	NT	LTR8 repetitive element;
6534	19134	31927	0.88	6.4E-02	AI972896.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6907	19841	32477	4.7	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
8278	20819		2.86	6.4E-02	6753323	NT	we73g12.x1 Soares Dieckgrafe cdon_NHCD Homo sapiens cDNA clone IMAGE:2346780 3'
8999	21138	34062	3.58	6.4E-02	AA093305.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
9055	21592	34522	0.85	6.4E-02	AF150195.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (Zeta) (Cct6a), mRNA
9606	22008		0.81	6.4E-02	BE834083.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9833	22133	35088	1.79	6.4E-02	AB011128.1	NT	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
10162	22657	35852	0.88	6.4E-02	AF087150.1	NT	RC1-OT0083-150800-014-g06 OT0083 Homo sapiens cDNA
10162	22657	35853	0.68	6.4E-02	AF087150.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11554	24002	37074	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37075	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11931	24971		4.88	6.4E-02	AF107890.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11966	24296	30863	2.86	6.4E-02	AJ277174.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
							Drosophila melanogaster mRNA for mod(mdg4)51.4 protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1791	14381	26928	3.03	6.3E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t genes, partial cds; emRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3684	18268		2.41	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6285	18893	31662	1.1	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087489 5'
7281	18819		1.05	6.3E-02	X97889.1	NT	H. sapiens gene encoding La autoantigen
9215	21732	34876	0.86	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominica gene, exons 1-3
9827	22423	35397	2.86	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10172	22667		0.87	6.3E-02	AV688070.1	EST_HUMAN	AV688070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10584	18883	31662	3.6	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087489 5'
4337	18824	28365	3.3	6.2E-02	AL191572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4431	17017		1.04	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4882	17264		6.75	6.2E-02	G82191	SWISSPROT	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6889	16824	32459	0.75	6.2E-02	D49330.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7623	20136	33014	0.78	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8877	25123		0.81	6.2E-02	M81101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9287	21783	34742	0.5	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9401	21910	34859	1.05	6.2E-02	8877888	NT	Mus musculus stromal cell derived factor receptor 2 (Sdrf2), mRNA
11027	23541	36576	1.74	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11226	23757	36814	1.89	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (cht) gene
11770	25097		8.34	6.2E-02	AE000760.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12200	24428	30951	3.56	6.2E-02	BF112039.1	EST_HUMAN	783708.x1 Soares, NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3823816 3' similar to
277	12934	25420	4.8	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4063	16660		2.78	6.1E-02	U73325.1	NT	Arabidopsis thaliana K ⁺ inward rectifying channel protein (AKC1) gene, complete cds
4768	17340	29768	1.09	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4759	17340	29787	1.09	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6262	18870		1.42	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8207	20748	33661	3.31	6.1E-02	X99288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8595	21134	34048	0.95	6.1E-02	BE971853.1	EST_HUMAN	601851086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834804 3'
8595	21134	34049	0.95	6.1E-02	BE971853.1	EST_HUMAN	601851086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834804 3'
10608	23142	36153	6.34	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C08 HT0618 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11726	26009		23.38	8.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12317	24890		1.39	8.1E-02	AI898811.1	EST_HUMAN	ts5907.x1 NCL_CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2292901 3'
12484	24592		7.98	8.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1303	13899	28419	1.01	8.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 139 of the complete genome
2700	16257	27825	1.15	8.0E-02	AW068848.1	EST_HUMAN	EST380824 MAGE resequences, MAGJ Homo sapiens cDNA
2801	16353		1.58	8.0E-02	AB031289.1	NT	Mesocricetus cord mitochondria DNA, NADH dehydrogenase subunit 4, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2863	12777	25269	1.09	8.0E-02	AA188730.1	EST_HUMAN	zp78cd04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:826310 5'
2863	12777	25269	1.09	8.0E-02	AA188730.1	EST_HUMAN	zp78cd04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:826310 5'
3268	18878	28360	1.24	8.0E-02	AA372378.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3268	18878	28361	1.24	8.0E-02	AA372378.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3597	19298		1.01	8.0E-02	BE994443.2	EST_HUMAN	601658160R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
6104	17676	30118	0.95	8.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5595	18225		1.89	8.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-504 B70253 Homo sapiens cDNA
6384	18988	31746	1.43	8.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1 repetitive element;
7063	18082	30438	2.73	8.0E-02	5174898	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7063	18082	30439	2.73	8.0E-02	5174898	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7239	19768	32824	2.17	8.0E-02	BF382349.1	EST_HUMAN	601816274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4048226 5'
7672	20184	33072	1.94	8.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764169 3'
8361	20901		0.67	8.0E-02	11468495	NT	Recitomonas americana mitochondrion, complete genome
9198	21713	34856	1.12	8.0E-02	AI823187.1	EST_HUMAN	ts78cd03.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9198	21713	34857	1.12	8.0E-02	AI823187.1	EST_HUMAN	ts78cd03.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9327	21841	34762	2	8.0E-02	AJ245365.1	NT	Adipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9327	21841	34763	2	8.0E-02	AJ245365.1	NT	Adipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9819	22317	35269	0.51	8.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' and similar to similar to heat shock protein 1, 60 kDa-like
9819	22317	35300	0.51	8.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' and similar to similar to heat shock protein 1, 60 kDa-like
11214	23717		2.13	8.0E-02	AA128386.1	EST_HUMAN	zn87cd08.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:XB99181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
11895	24295	30982	1.43	8.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12394	24554		8.04	8.0E-02	AI809273.1	EST_HUMAN	wf68h03.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2360886 3' similar to TR-O60298

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
260	12810	26393	4.78	5.9E-02	AW634719.1	EST_HUMAN	RC1-D70001-280100-012-010 DT0001 Homo sapiens cDNA
3012	18628	28107	2.78	5.9E-02	AF180289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4768	17349	28789	0.97	5.9E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4768	17349	29800	0.97	5.9E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4852	17430		0.8	5.9E-02	AF168111.1	NT	Duck parvovirus strain 80-2193 capsid protein (VP3) gene, partial cds
4998	17570	30014	0.86	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5973	24774	32374	0.97	5.9E-02	AF145880.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8552	21091	34011	1.99	5.9E-02	9055249	NT	Mus musculus Inroquia related homeobox 6 (Drosophila) (Inr6), mRNA
9372	20311		0.82	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105894 5'
10884	23198		3.41	5.9E-02	6878870	NT	Mus musculus foliellin-like (Fetl), mRNA
10898	23419	36438	2.35	5.9E-02	11433358	NT	Homo sapiens nilein (LOC51198), mRNA
11429	23880		1.83	5.9E-02	AJ240793.1	NT	Gallus gallus HKC9 telomere junction
988	13578		5.2	5.9E-02	D80110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1700	14293	26828	1	5.9E-02	Q61788	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
2888	16504		0.88	5.9E-02	AJ223821.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3725	16326	28763	1.35	5.9E-02	AE001776.1	NT	Thermotoga maritima section 87 of 138 of the complete genome
4446	17032	28473	5.29	5.9E-02	AW051927.1	EST_HUMAN	wc24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4448	17032	28474	5.28	5.9E-02	AW051927.1	EST_HUMAN	wc24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
						EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to
4845	17227	29882	5.04	5.9E-02	AJ247505.1	EST_HUMAN	gbM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4845	17227	29883	5.04	5.9E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to
4874	17258		1.98	5.9E-02	AF098284.1	NT	gbM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
						NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5284	17856	30282	0.57	5.9E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5284	17856	30283	0.57	5.9E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6068	18685	31428	1.52	5.9E-02	AA190894.1	EST_HUMAN	zp88a11.s1 Stragene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:627088 3'
7670	20182	33069	2.73	5.9E-02	M89150.1	NT	Human polymorphic microsatellite DNA
7670	20182	33070	2.73	5.9E-02	M89150.1	NT	Human polymorphic microsatellite DNA
8801	21140	34054	0.76	5.9E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C089
11871	24223		2.86	5.9E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12177	25085		6.45	5.9E-02	AA604268.1	EST_HUMAN	nc75a11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:112884 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3093	13708	28179	1.13	6.7E-02	A01844.1	EST_HUMAN	cu03505.s1 NC1_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632485 3' similar to WP:C37A2.2
3107	13722	28183	1.6	5.7E-02	AF11917.1	NT	CE08811 ; Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3769	16370		0.98	6.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin B.1 (ctt-8.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3871	16489	28932	2.44	5.7E-02	AW989791.1	EST_HUMAN	EST378885 MAGE resequences, MAGI Homo sapiens cDNA
4795	17373		1.08	5.7E-02	M95089.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
5334	17895	30310	0.89	5.7E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6039	18658		0.8	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8098	20637	33548	1.48	5.7E-02	AJ290080.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv0.2 gene)
8784	22262	36245	0.85	5.7E-02	6881260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11087	23579	36617	4.17	6.7E-02	AJ752685.1	EST_HUMAN	cn18b08.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11087	23579	36618	4.17	6.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11227	23768		1.56	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12085	24891		12.98	5.7E-02	D50320.1	NT	Pig DNA for SPAI-2, complete cds
12257	24467		1.71	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12334	24985		3.31	5.7E-02	AF217490.1	NT	Homo sapiens fragile 180 odds reductase (FOR) gene, exons 8, 9, and partial cds
12483	25074		8.94	5.7E-02	AF261280.1	NT	Pen tropodocytes apolipoprotein-E gene, complete cds
12922	24700	30863	1.58	5.7E-02	R48513.1	EST_HUMAN	y934410.s1 Soares breast 2NBH8at Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element ;
1874	14167	26668	1.2	5.8E-02	AF094455.1	NT	Hydrocotyle radundifolia ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
4746	17327	29769	1.21	5.8E-02	AB013100.1	NT	Lycopodium obscurum LE-ACS5 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4808	17384	29834	1.2	5.8E-02	AA290588.1	EST_HUMAN	zs45c01.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6768	19358	32168	5.98	5.8E-02	AW172708.1	EST_HUMAN	x02c10.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2886050 3' similar to TR:084979 094979 KIAA0905 PROTEIN ;
6971	19548	32372	0.9	5.8E-02	AA886182.1	EST_HUMAN	cd47112.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7205	19736	32589	3.1	5.8E-02	BE008001.1	EST_HUMAN	QYG-BN0147-280400-214-q07 BN0147 Homo sapiens cDNA
8737	21278	34188	2.2	5.8E-02	BE542683.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8737	21278	34188	2.2	5.8E-02	BE542683.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9726	22224	35201	1.07	5.8E-02	AA482864.1	EST_HUMAN	m49d07.a1 NCLQGAP_A1M1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G768859 G768859
11439	23689		2.33	5.6E-02	AF260225.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C.;
2670	15237	27804	6.14	5.5E-02	X37869.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3251	15883	28345	3.83	5.5E-02	U75550.1	NT	H.sapiens gene encoding La autoantigen
4268	16882	26328	1.12	5.5E-02	L41581.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
5840	18464	31188	3.19	5.5E-02	Q01174	SWISSPROT	Gallid herpesvirus mRNA fragment
6178	18464	31188	3.86	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7412	18637	32802	1.77	5.5E-02	U75590.2	NT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8063	20805	33516	0.77	5.5E-02	AF170811.1	NT	Mus musculus tubulin 1 (Tubf1), mRNA
8063	20805	33517	0.77	5.5E-02	AF170811.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35034	0.81	5.5E-02	10947034	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35035	0.81	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9684	22163	35136	1.28	5.5E-02	U69492.1	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
							Mus musculus second IL11 receptor alpha chain (IL11RA2) gene, exons 1 and 2
10868	23418	36435	11.52	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), gene for putative Bowman Birk trypsin inhibitor
3054	15870		0.85	5.4E-02	AJ277488.1	NT	Oryza sativa rbb13-1 gene for putative Bowman Birk trypsin inhibitor
3469	18013		6.27	5.4E-02	BE073488.1	EST_HUMAN	RC6-BT0558-140200-012-C03 BT0558 Homo sapiens cDNA
3982	16580	29051	0.58	5.4E-02	U85808.1	NT	RC6-BT0558-140200-012-C03 BT0558 Homo sapiens cDNA
5119	17691	30129	2.48	5.4E-02	U53528.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8067	20808		1.11	5.4E-02	Z99118.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
9001	21538	34467	0.81	5.4E-02	AF260225.1	NT	Bacillus subtilis complete genome (section 13 of 21); from Z395261 to 2613730
							Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10578	23113	36126	1.88	5.4E-02	U20780.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11058	23570	36808	1.58	5.4E-02	BF371288.1	EST_HUMAN	RC6-FN0112-180700-021-D08 FN0112 Homo sapiens cDNA
11058	23570	36807	1.56	5.4E-02	BF371288.1	EST_HUMAN	RC6-FN0112-180700-021-D08 FN0112 Homo sapiens cDNA
11988	24882		2.9	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1091	13698	26205	1.58	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-e09 ST0213 Homo sapiens cDNA
1091	13698	26206	1.58	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-e09 ST0213 Homo sapiens cDNA
							ye37112.11 Stratiogene lung (8637210) Homo sapiens cDNA clone IMAGE:118651 5' similar to gb:K01506
1653	14145	26878	21.83	5.3E-02	T84759.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2541	15105	27677	2.71	5.3E-02	AJ276408.1	NT	Pseudomonas putida tfgS gene
2969	15585	28066	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2868	15385	28087	0.88	6.3E-02	M58417.1	NT	Drosophila melanogaster laritinin B2 gene, complete cds
3187	16798	28271	4.92	6.3E-02	AJ276408.1	NT	Pseudomonas putida ttpS gene
5248	17811	30234	0.75	6.3E-02	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya6-pa, Scya6 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Scya6 pseudogene, small inducible cytokine A6 precursor, complete cds
5260	17813	30236	8.25	6.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5522	18164	30568	1.97	6.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
5522	18164	30568	1.97	6.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6251	18880	31832	0.71	6.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
6984	19541	32363	4.23	6.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7149	19682	32523	1.56	6.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7398	19921		2.05	6.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
7818	20280	33180	0.52	6.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF9-SPO11 INTERGENIC REGION
8344	20885		0.54	6.3E-02	U10098.1	NT	Mus musculus 129/Sv evstatin C (cat3) gene, complete cds
9053	21590	34521	1.83	6.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10038	22533	35529	0.54	6.3E-02	AB022805.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7)methyltransferase, complete cds
10038	22533	35530	0.84	6.3E-02	AB022805.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7)methyltransferase, complete cds
10156	22651		0.82	6.3E-02	Y07607.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurule, 9-18 hpf and postmitotogenesis, 20-28 hpf)
10235	22730	35721	0.65	6.3E-02	X88432.1	NT	B. rerio pou(c) mRNA for transcription factor
2324	14883		116.92	6.2E-02	6031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEPTA) mRNA
3148	15762	28228	2.4	6.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3148	15762	28228	2.4	6.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4013	16611	29084	0.7	6.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4366	16952	28392	3.81	6.2E-02	U07132.1	NT	Human steroid hormone receptor Nkr-1 mRNA, complete cds
4848	17424	28877	1.29	6.2E-02	L33248.1	NT	Drosophila melanogaster filament protein homolog (sept) gene, complete cds
6076	18683	31438	0.89	6.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
8255	18884		1.42	6.2E-02	AB030965.1	EST_HUMAN	vi80604.XT NC_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
7318	19845	32706	1.19	6.2E-02	P36322	SWISSPROT	MER15 repetitive element: DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8136	20677		1.98	6.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8845	22145	35113	1.97	6.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
8845	22145	35114	1.97	6.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12224	24445		1.84	6.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
12327	24513		1.27	6.2E-02	D63362.1	NT	Mouse DNA (a regilgamma protein, complete cds
2402	14970		1.14	5.1E-02	AL134071.1	EST_HUMAN	DKFZp647D073_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp647D073 5'
4282	19868	29315	0.73	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4908	17483	29641	8.03	5.1E-02	AF085187.1	NT	Hordeum vulgare receptor-like kinase ARK1A5 gene, partial cds
5203	17770	30163	1.14	5.1E-02	BE957423.2	EST_HUMAN	60165366R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE3838361 3'
6777	19389	32182	0.76	6.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
6842	18050	30472	1.8	6.1E-02	BF378825.1	EST_HUMAN	QVO-JM0051-250800-350-808 UM0051 Homo sapiens cDNA
8195	20736	33645	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8195	20736	33647	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8268	20829	33750	1.48	6.1E-02	AJ131968.1	NT	Spodoptera littoralis mRNA for 3-dehydroacylase 3beta-reductase
8818	21357	34282	0.83	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8818	21357	34283	0.83	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9723	22221	35168	8.16	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10084	22379	35572	1.83	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10709	23237	36250	2.86	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10709	23237	36261	2.86	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12232	24448		1.51	5.1E-02	AF082467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
508	13141	25628	1.76	5.0E-02	AF088004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1248	13643	26360	6.63	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2034	14816	27182	3.63	5.0E-02	P02810	SWISSPROT	4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) (CONTAINS: PEPTIDE P-C)
2846	13634	28150	1.78	5.0E-02	U72742.1	NT	Opisthotegus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3381	16980		1.42	5.0E-02	7305810	NT	Mus musculus Utrc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3655	16258		1.06	5.0E-02	U32782.1	NT	Mus musculus Influenzae Rd section 97 of 163 of the complete genome
3747	16348	28816	5.6	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
5102	17674	30114	1.11	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitous tetrahydrobiopterin containing protein RoXan mRNA, partial cds
6278	18887	31656	0.74	5.0E-02	AF098264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6450	19051		1.23	5.0E-02	AJ242825.1	NT	Mus musculus Dimp-1 gene, exons 1-8
7544	20064	32938	10.74	5.0E-02	P35818	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10101	22596	35568	1.13	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fisd) mRNA, complete cds
11364	23816	36877	2.87	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
11758	24924		7.22	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
242	12901		23.23	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
392	13038	25529	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3328	15938	28414	1.58	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3628	18231		0.63	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.a1 Striatogene hNT neuron (4937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3651	18254	28728	0.91	4.9E-02	AA400914.1	EST_HUMAN	z178a03.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3651	18254	28727	0.91	4.9E-02	AA400914.1	EST_HUMAN	z178a03.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4966	17540	29882	1.59	4.9E-02	AW187821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2832388 3'
4966	17540	29883	1.59	4.9E-02	AW187821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2832388 3'
6372	17631	30345	0.61	4.9E-02	7882818	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
6408	17684		0.91	4.9E-02	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
6425	17682		0.98	4.9E-02	AE001774.1	NT	Thermoboga maritima section 86 of 138 of the complete genome
6437	17692	30398	1.03	4.9E-02	M94083.1	NT	Brucella ovis heat shock protein hsp70 (dnaK) gene, complete cds; heat shock protein hsp40 (dnaJ) gene, complete cds
5573	18204	30654	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5573	18204	30655	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7198	19727	32578	0.99	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8551	21090		0.88	4.9E-02	AE002308.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8689	21228	34140	0.7	4.9E-02	AL181559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10193	22688	35681	0.64	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11280	23733	36788	3.87	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12148	24391		1.44	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12431	24573		2.92	4.9E-02	M18964.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
352	13002	25487	1.15	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
353	13002	25487	1.87	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
514	13147	25631	9.43	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2312	14884	27459	1.98	4.8E-02	W51983.1	EST_HUMAN	z049b02.e1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3244	15856	28339	2.34	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4778	17359		1.32	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5308	17871	30293	0.87	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
5360	17939	30352	4.1	4.8E-02	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
5380	17939	30353	4.1	4.8E-02	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8060	20822	33535	1.42	4.8E-02	AW398497.1	EST_HUMAN	MR2-ST0128-221098-012-502 ST0128 Homo sapiens cDNA
9057	21594	34524	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9057	21594	34525	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12018	24315		1.83	4.8E-02	9832893	NT	Streptococcus thermophilus bacteriophage Sfi19, complete genome
6918	19577	32408	2.88	4.7E-02	W01153.1	EST_HUMAN	Y20709.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
6965	19542	32384	0.78	4.7E-02	BF686825.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
6965	19542	32385	0.78	4.7E-02	BF686825.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
6998	19486	32317	1.97	4.7E-02	M62752.1	NT	Rat etatin-related protein (e1) gene, complete CDS
8193	20734	33644	8.66	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
8883	21421	34348	1.12	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8908	21444		2.28	4.7E-02	AB026878.1	NT	Callus gallus Wpca-8 gene, complete cds
8184	21689	34633	6.91	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
8563	22065	35024	0.55	4.7E-02	BF305237.1	EST_HUMAN	601892892F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9650	22149		0.55	4.7E-02	A873042.1	EST_HUMAN	we78c10.x1 Soares_NFL_Y_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10834	23168	36177	1.55	4.7E-02	8754585	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11430	23881	36945	1.89	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11430	23881	36948	1.89	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11961	26087		6.94	4.7E-02	AV848521.1	EST_HUMAN	AV848521 GLC Homo sapiens cDNA clone GLC8K02 3'
12322	26089		1.47	4.7E-02	P52951	SWISSPROT	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
282	12648	25435	0.81	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
769	13388	25887	2.44	4.6E-02	AE000446.1	NT	Escherichia coli K-12 MG1685 section 335 of 400 of the complete genome
1335	13929		1.37	4.6E-02	A1014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P00633
1403	13996	26525	9	4.6E-02	AV727059.1	EST_HUMAN	Pe0533 LIMA ; contains element LTR1 repetitive element ;
2530	15094	27866	2.77	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTC8WC01 5'
2834	12848	25435	1.83	4.6E-02	BE153583.1	EST_HUMAN	xn24f03.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2894853 3' similar to SW:GRF1_HUMAN
3042	15658	28138	0.7	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3543	15658	28138	0.95	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4201	18790		0.87	4.6E-02	AF220365.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5909	18631	31266	1.44	4.6E-02	AF076982.1	NT	Mus musculus nuclear RNA helicase II/Gu (ddx21) gene, complete cds
6377	18981	31780	3.77	4.6E-02	X61824.1	NT	Haplochromis burtoni gonadotrophin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
							C.reinhardtii atp2 (atpB) mRNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	18981	31781	3.77	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6891	19625	32451	1.39	4.6E-02	A1149574.1	EST_HUMAN	qc80b06.x1 Scaree_plecanta_8to9weeks_2NbHP8a9w Homo sapiens cDNA clone IMAGE:1713971 3'
8590	21129	34048	2.82	4.6E-02	BE154006.1	EST_HUMAN	similar to contains L1 t3 L1 repetitive element ;
11281	23734	38789	4.28	4.6E-02	AA913328.1	EST_HUMAN	PNU-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
12541	24651		2.54	4.6E-02	X57808.1	NT	cl27n02.g1 Scaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
472	13105	25598	2.71	4.6E-02	P22448	SWISSPROT	Human germline immunoglobulin lambda light chain gene
1260	13857	26373	0.78	4.6E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1280	13857	26374	0.78	4.6E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1840	14428	26980	3.54	4.6E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
2156	14733	27308	3.85	4.6E-02	AE003064.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3768	16386	23852	3.84	4.6E-02	AL163278.2	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
8378	18982	31762	1.88	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
8631	19227	32032	0.89	4.5E-02	AL1163280.2	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8332	20873	33795	1.8	4.5E-02	AF036864.1	NT	Homo sapiens chromosome 21 segment HS21C080
9860	22637	35337	5.91	4.5E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10117	22612	35902	0.77	4.5E-02	AB000470.1	NT	EST28187 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
11947	24276	31018	2.92	4.5E-02	11418013	NT	Gallus gallus mRNA for alpha1 Integrin, complete cds
12667	24973	30636	6.27	4.5E-02	AA191097.1	EST_HUMAN	Homo sapiens ret finger protein-like 3 (RFLP3), mRNA
237	12897		3.08	4.4E-02	BE972733.1	EST_HUMAN	zq491f1.1 Stratigene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632463 5'
2144	14722		6.8	4.4E-02	P31568	SWISSPROT	601852154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2532	15098	27668	2.82	4.4E-02	AW675475.1	EST_HUMAN	HYPOTHETICAL PROTEIN (ORF 2280)
3702	16303	28771	1.5	4.4E-02	AF159160.1	NT	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
4733	17314	28756	1.23	4.4E-02	AF109807.1	NT	Mycococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4733	17314	28757	1.23	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32551	1.56	4.4E-02	AF095824.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32552	1.56	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8687	21228	34146	2.04	4.4E-02	AA738698.1	EST_HUMAN	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
10951	23488	36489	4.58	4.4E-02	AF080659.1	NT	nm13h03.at NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239221 3'
11080	23592	36628	2.63	4.4E-02	AA498739.1	EST_HUMAN	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
							ae33104.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11864	24098		3.26	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
813	13431	25936	8.91	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2803	15185	27732	1.18	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3477	15083	28557	8.12	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3720	18321		1.12	4.3E-02	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6822	19219	32023	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6822	19219	32024	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6830	19420	32236	0.68	4.3E-02	AA852268.1	EST_HUMAN	ns60c12.st NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188988
8450	20990	33908	0.74	4.3E-02	AF283359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8736	21276	34198	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8736	21275	34197	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
855	13471	25982	1.97	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
899	13513		2.24	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
929	13542	26060	0.69	4.2E-02	AW003845.1	EST_HUMAN	wk34g01.x1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:2543584 3' similar to TR:Q63291 Q63291
1753	14348		1.32	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 L1 repetitive element;
							Thermoplasma acidophilum complete genome; segment 4/5
3190	15802	28274	0.98	4.2E-02	A469472.1	EST_HUMAN	q96f10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M55718
3728	16327	28794	1.36	4.2E-02	P23091	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN);
4410	16985	29437	1.03	4.2E-02	U26674.1	NT	TRANSFORMING PROTEIN MAF
4410	16985	29438	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4854	17432	28983	0.98	4.2E-02	BF342965.1	EST_HUMAN	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
							502017105F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4162872 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5802	18427	31145	1.49	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
							4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5802	18427	31146	1.49	4.2E-02	AF280107.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7534	20054	32927	5.28	4.2E-02	AF276752.1	NT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
8746	21284	34208	3.5	4.2E-02	P05095	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-58)
10069	22564	35558	1.17	4.2E-02	Q16950	SWISSPROT	on33b11.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M55280
10919	23438	36459	3.12	4.2E-02	AA978118.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11167	23692	36739	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-008-d10 BN0174 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11187	23692	36740	2.3	4.2E-02	BE919822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11379	23631	36894	2.08	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12226	28023		3.4	4.2E-02	A1863484.1	EST_HUMAN	w48g10.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2810850 3'
636	13167	25648	0.7	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2701	15256	27826	2.87	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4571	17154		8.95	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-184-08 NN0012 Homo sapiens cDNA
5295	17857		0.69	4.1E-02	X86860.1	NT	Limonocycogenes type 3 partial lap gene (strain 443)
5824	18448	31170	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535FT NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343856 5'
5824	18448	31171	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535FT NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343856 5'
6082	19539		0.97	4.1E-02	X75881.1	NT	A.thellens mRNA for plasma membrane intrinsic protein 1a
7166	19688	32632	1.92	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7622	20042	32611	1.78	4.1E-02	7682347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
7742	20250	33143	3.14	4.1E-02	AF026188.1	NT	CUTICLE COLLAGEN 34
8577	21116	34036	0.56	4.1E-02	P34687	SWISSPROT	EST84281 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9081	21617	34552	0.85	4.1E-02	AA372398.1	EST_HUMAN	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
12572	25024	30818	24.9	4.1E-02	AJ271909.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3281	19692	28371	3.71	4.0E-02	AB040904.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
3688	18466	28629	0.98	4.0E-02	L11910.1	NT	Homo sapiens PYS gene for 6-pyruvyltetrahydropterin synthase, complete cds
5266	17658	30284	0.58	4.0E-02	AB042267.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5581	18212	30661	6.51	4.0E-02	AF280107.1	NT	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:075288 075288
6362	18968	31744	1.86	4.0E-02	BF110434.1	EST_HUMAN	R28124.1.;
							Strongylocentrotus purpuratus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7678	20189	33078	6.8	4.0E-02	L23838.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33144	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33145	0.87	4.0E-02	AB000381.1	NT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8851	21180	34108	2.84	4.0E-02	P08840	SWISSPROT	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9562	22082		0.84	4.0E-02	BF676376.1	EST_HUMAN	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
9568	22088	35051	3.35	4.0E-02	AJ000941.1	NT	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9896	22392		1.28	4.0E-02	D3948.1	NT	Human mRNA for KIAA0082 gene, partial cds
11808	24051		1.62	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca ⁺⁺ ATPase
11841	24834	30768	18.69	4.0E-02	AJ001058.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1199	13762	26273	3.8	3.9E-02	BF616149.1	EST_HUMAN	UIH-BW1-enx-h-08-U151 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134.3
1390	13964	26510	1.88	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2004	14686	27145	2.97	3.9E-02	AJ403386.1	NT	M. musculus DNA for desmin-binding fragment DesD7
2728	15263		1.86	3.9E-02	4508882	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5326	17887	30303	0.6	3.9E-02	AW382417.1	EST_HUMAN	RC8-ST0268-171198-021-C08 ST0268 Homo sapiens cDNA
5344	17805	30320	1.14	3.9E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5344	17805	30321	1.14	3.9E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5687	18313	30810	0.73	3.9E-02	D50608.1	NT	Rat gene for cholesterylabin type-A receptor (CCKAR), complete cds
5687	18313	30811	0.73	3.9E-02	D50608.1	NT	Rat gene for cholesterylabin type-A receptor (CCKAR), complete cds
5906	18526	31254	1.24	3.9E-02	BE68841.1	EST_HUMAN	601849874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833842.5
6018	18637	31377	0.68	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910.5
7118	19459	32273	1.01	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830.5
7781	20324	33228	0.93	3.9E-02	BF230613.1	EST_HUMAN	601806848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779.5
8004	20548	33449	0.96	3.9E-02	AJ220041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8004	20548	33450	0.96	3.9E-02	AJ220041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11287	20289	33188	1.6	3.9E-02	P48776	SWISSPROT	ANTIGEN GOR
11691	24981		7.19	3.9E-02	AB042853.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12373	24543						Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV28S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV16S1, TCRBV15S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY9, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
12503	24902						Mus musculus chromosome X contig; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf
1995	14577	27137	64.84	3.9E-02	AL049866.2	NT	
4987	17571	30015	1.24	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215.5
4987	17571	30016	0.99	3.8E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3828757.5
5082	17635	30078	0.93	3.8E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3828757.5
5632	18261	30733	0.93	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698.5
6237	18848	31817	1.19	3.8E-02	M1128.1	NT	Human protein C gene, complete cds
19885	32748		1.07	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7359	19885	32748	1.43	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8598	21137		1.3	3.8E-02	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
10506	23000		0.47	3.8E-02	AE001329.1	NT	Chlamydia trachomatis section 56 of 87 of the complete genome
10532	23069	38082	2.17	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1026	13639	28164	3.69	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1432	14025	26553	1.15	3.7E-02	L14591.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2278	14852	27430	4.49	3.7E-02	AB84808.1	EST_HUMAN	wf85e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502.3'
2613	15175	27743	0.63	3.7E-02	AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3089	15701	28174	0.97	3.7E-02	P76944	SWISSPROT	ECMESODERMIN
3088	15703	28175	4.74	3.7E-02	BF312683.1	EST_HUMAN	601889233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126584.6'
7138	26118		0.73	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
9628	22424		0.89	3.7E-02	AA782618.1	EST_HUMAN	af55c08.s1 Saccharomyces cerevisiae, parathyroid tumor_NBHPA Homo sapiens cDNA clone 1380912.3'
11735	24139	37156	7.89	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973.6'
12435	24866	30707	3.02	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3715	16316	28784	0.82	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3723	16324	28781	0.87	3.6E-02	AL068808.1	NT	Homo sapiens genomic region containing hypervariable minisatellite chromosome 10[10q26.3] of Homo sapiens
5620	18249	30701	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pdk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5620	18249	30717	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pdk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
8808	19399	32213	5.32	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
8808	19399	32214	6.32	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7143	19876	32516	1.66	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein OY2 precursor (sgp2) gene, complete cds
7347	19873	32739	3.52	3.6E-02	AA714521.1	EST_HUMAN	hw20a05.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024.3' similar to gb:J00314.1ma2
7629	20141	33020	0.86	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8313	21827	34776	1.87	3.6E-02	U20808.1	NT	MIR0-H10159-030200-003-b08 HIT0158 Homo sapiens cDNA
8313	21827	34777	1.87	3.6E-02	U20808.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
8313	21827	34777	1.87	3.6E-02	U20808.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9530	22030	34969	0.72	3.6E-02	BF347568.1	EST_HUMAN	802020453F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156116.6'
928	13541	26059	1.57	3.5E-02	U09508.1	NT	Drosophila melanogaster tgg7/m mRNA, complete cds
1046	13654	26166	2.26	3.5E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1810	14203	28738	1.48	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1810	14203	28737	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4283	16879	26328	1.91	3.5E-02	AE001773.1	NT	Thermoplasma maritima section 86 of 138 of the complete genome
4408	16891	28435	1.18	3.5E-02	P53780	SWISSPROT	CYSTATIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6370	18974	31752	2.11	3.5E-02	J01238.1	NT	Malze actin 1 gene (MAC1), complete cds
7918	20460		0.82	3.5E-02	H28951.1	EST_HUMAN	yp4405.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:180256 5' similar to contains Alu repetitive element
8558	21097	34018	3.5	3.5E-02	BE959970.1	EST_HUMAN	601844701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
9931	22427	35401	2.44	3.5E-02	X76842.1	NT	L.lactis MG1363 grpE and dnaK genes
9977	22472	35455	0.49	3.5E-02	BE661042.1	EST_HUMAN	601344681F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877854 5'
11387	23819	36880	1.92	3.5E-02	AW891841.1	EST_HUMAN	PM1-CT0328-291288-002-H03 CT0328 Homo sapiens cDNA
11387	23819	36881	1.92	3.5E-02	AW891841.1	EST_HUMAN	PM1-CT0328-291288-002-H03 CT0328 Homo sapiens cDNA
12387	24534		1.39	3.5E-02	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV858P to TCRBV21S2A2 region
12426	24913		4.38	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543933 5'
604	13233	25708	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
604	13233	25707	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25706	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25707	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1089	13684	28703	3.22	3.4E-02	AW274020.1	EST_HUMAN	xx28407.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814263 3' similar to
1248	13845		6.54	3.4E-02	11345459	NT	SW: C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
2435	15002	27574	1.82	3.4E-02	T57180.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
3478	16084	28558	1.11	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3843	18442	28603	0.88	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3963	18591	29063	4.28	3.4E-02	AW794982.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4703	17285	29730	3.17	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5217	17782		2.81	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5237	17801	30220	1.47	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6353	18958		0.88	3.4E-02	BF131828.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
6938	18046	30468	4.83	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8204	20745		3.76	3.4E-02	AI869629.1	EST_HUMAN	wf86d04.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2433031 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8932	21221	34141	1.64	3.4E-02	AA684888.1	EST_HUMAN	nu70708.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element;
							zq04f11.s1 Stratiotes muscle 837209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
8848	21387		5.71	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDGVPLKATMRNFTEITAENLTINKESVTADAGRYEITAAANSSTTKAFINIVLDRPG
8693	22192		0.53	3.4E-02	AI092719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGSQVNTYLLKRETSTAVNTEVSATVARTMMKVMKL ...;
395	13041		11.74	3.3E-02	AA308735.1	EST_HUMAN	cd89h08.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683619 3'
1209	13809	26322	18.12	3.3E-02	AB036887.1	EST_HUMAN	z75608.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1681	14273	26806	1.29	3.3E-02	AF110763.1	NT	Cytosolus giteus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1776	14365		1.28	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2131	14709		2.05	3.3E-02	AE000700.1	NT	Aquifex acidicus section 32 of 109 of the complete genome
3406	16015	28404	0.85	3.3E-02	R08112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4256	14273	26906	2.91	3.3E-02	AF110763.1	EST_HUMAN	y33h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4566	17148	29598	2.15	3.3E-02	6755882	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
5581	19159	31656	26.84	3.3E-02	BF245985.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Ttr1), mRNA
6661	19169	31657	26.84	3.3E-02	BF245985.1	EST_HUMAN	601863910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9246	21772	34721	0.73	3.3E-02	BF119621.1	EST_HUMAN	601863910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9246	21772	34722	0.73	3.3E-02	BF119621.1	EST_HUMAN	7m92d04.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
							7m92d04.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
							ad08f09.s1 Soares NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70844_cds1
9345	21859	34807	0.59	3.3E-02	AA488202.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
9345	21859	34808	0.59	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70844_cds1
10491	22885		0.5	3.3E-02	H38109.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11000	23514	36548	3.5	3.3E-02	BF691107.1	EST_HUMAN	yp51f11.s1 Soares retina N244HR Homo sapiens cDNA clone IMAGE:190889 3'
11932	24268		2.14	3.3E-02	T98545.1	EST_HUMAN	60224717F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12089	24358		2.05	3.3E-02	M81890.1	NT	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
137	12802	25291	1.87	3.2E-02	AIJ002005.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1185	13767	26277	19.04	3.2E-02	AF066275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1185	13767	26278	19.04	3.2E-02	AF066275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1608	14398	26843	1.36	3.2E-02	AF128934.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2184	14741		1.35	3.2E-02	P28956	SWISSPROT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-18 and complete cds
2886	12802	25291	0.59	3.2E-02	AIJ002005.1	NT	LARGE TEGUMENT PROTEIN
3168	15782	26253	12.01	3.2E-02	BE687363.1	EST_HUMAN	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848727 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3778	16378	28842	1.3	3.2E-02	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4290	16885		20.05	3.2E-02	X94768.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4882	17457	28909	3.35	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5726	18352	31056	1.45	3.2E-02	X88708.1	NT	S. griseocarinum whiG-Siv gene
5728	18352	31056	1.45	3.2E-02	X88708.1	NT	S. griseocarinum whiG-Siv gene
5848	18242	32045	2.59	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W88.14
6847	19243		27.51	3.2E-02	T88397.1	EST_HUMAN	x433h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6722	19318	32119	3.78	3.2E-02	AF173845.1	NT	Alu repetitive element contains LTR1 repetitive element;
7739	20247	33140	0.85	3.2E-02	11424049	NT	Seguinus oedipus P460, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8242	20783	33702	13.08	3.2E-02	6880565	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8871	21410		0.89	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9152	21687	34630	1.06	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9152	21687	34631	1.06	3.2E-02	A1278971.1	EST_HUMAN	qm17604.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9969	22484		4.05	3.2E-02	AA719795.1	EST_HUMAN	qm17604.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10280	22765	35743	0.95	3.2E-02	U06762.1	NT	z945b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
1303	13897		1.8	3.1E-02	4503416	NT	gb108441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1348	13943	28468	1.28	3.1E-02	P18845	SWISSPROT	Mecca mullata chemokine receptor CCR5 mRNA, complete cds
1936	14520	27076	1.52	3.1E-02	6871564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
2017	14599		1.14	3.1E-02	Z50097.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5207	17772		0.87	3.1E-02	BE091869.1	EST_HUMAN	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5331	17892		0.89	3.1E-02	AL161550.2	NT	Drosophila melanogaster mRNA for headcase protein
5371	18918		3.09	3.1E-02	AU119008.1	EST_HUMAN	IL2-BT0733-130400-067-A08 BT0733 Homo sapiens cDNA
5468	18102	30421	1.13	3.1E-02	U78104.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5563	18184		2.32	3.1E-02	AA278478.1	EST_HUMAN	AU119008 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5929	18453	31178	0.8	3.1E-02	BF687742.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
9944	22439	35417	3.83	3.1E-02	AF034779.1	NT	2a81a08.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703959 5'
12667	24737		2.24	3.1E-02	AW488414.1	EST_HUMAN	602088783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4088789 5'
1684	14257		2.3	3.0E-02	AF187125.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
2821	15183	27749	0.9	3.0E-02	AA402242.1	EST_HUMAN	hs3767.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2821221 3'
3823	18228	28704	1.24	3.0E-02	MB4176.1	NT	Ptychoteles minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
						EST_HUMAN	2a85h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263 5'
						NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3714	18315	28783	3.07	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	18407		0.79	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-e09 ST0286 Homo sapiens cDNA
4021	18819		0.74	3.0E-02	AA384003.1	EST_HUMAN	EST174530 Pineal gland II Homo sapiens cDNA 5' end
5000	17573	30017	1.04	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3875503 5'
5208	17773	30195	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5208	17773	30198	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5303	17865	30289	1.1	3.0E-02	BE688917.1	EST_HUMAN	601848872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3823928 3'
5590	18221		3.82	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
8402	19005	31784	0.76	3.0E-02	N98815.1	EST_HUMAN	z339e10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294806 5' similar to contains element TAR1 repetitive element;
8402	19005	31785	0.76	3.0E-02	N98815.1	EST_HUMAN	z339e10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294806 5' similar to contains element TAR1 repetitive element;
6884	19819	32433	2.93	3.0E-02	AJ242808.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
6987	19485	32306	3.15	3.0E-02	BE888948.1	EST_HUMAN	601612206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3813848 5'
6987	19485	32307	3.15	3.0E-02	BE888948.1	EST_HUMAN	601612206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3813848 5'
7131	19471	32280	1.83	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7131	19471	32281	1.83	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7282	19810	32666	1.32	3.0E-02	M88524.1	NT	Human dystrophin gene
7583	20098		0.76	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4074548 5'
8576	21114	34033	0.78	3.0E-02	BF553889.1	EST_HUMAN	IL6-HT0704-280600-108-c04 HT0704 Homo sapiens cDNA
8726	21267		1.77	3.0E-02	AF275654.1	NT	Omithorhynchus aenatus coagulation factor X mRNA, complete cds
10357	22851	35945	1.46	3.0E-02	AE001787.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10441	22835	35944	0.46	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam tes244 (b)
11111	23821	36982	4.11	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11538	23886	37057	6.47	3.0E-02	AA483216.1	EST_HUMAN	ne87804.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12043	25076	30515	2.56	3.0E-02	R32019.1	EST_HUMAN	yh63404.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
12417	24670		18.42	3.0E-02	AW895585.1	EST_HUMAN	QV4-NN0038-270400-187-105 NN0038 Homo sapiens cDNA
12460	25069		3.53	3.0E-02	AF049887.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2478	18487	27614	1.05	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3021	15637	28114	1.11	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15637	28115	1.11	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:380595 5'
3616	16219	28698	0.84	2.9E-02	X55284.1	NT	Sheep gene for ultra high-sulphur keratin protein
4003	16601	28075	0.89	2.9E-02	HT2805.1	EST_HUMAN	y07e10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:233130 5'
5272	18016		62.36	2.9E-02	R09112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127888 5'
6213	18823	31594	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6434	19037	31824	6.5	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5'
7298	18824	32883	10.37	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7465	19979	32845	0.67	2.9E-02	D28214.1	EST_HUMAN	HUMNK282 Human epidermal keratinocyte Homo sapiens cDNA clone 282
7840	20482	33393	0.91	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schleichandalia chinensis gluconate-8-phosphate dehydrogenase (gnd) gene, partial cds
7840	20482	33394	0.91	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schleichandalia chinensis gluconate-8-phosphate dehydrogenase (gnd) gene, partial cds
9577	22077	35040	2.18	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9577	22077	35041	2.18	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9788	22286		0.59	2.9E-02	AW976587.1	EST_HUMAN	EST1388708 MAGE resequences, MAGN Homo sapiens cDNA
10247	22742	35732	0.84	2.9E-02	AP000084.1	NT	Aeropyrum pernix genome DNA, section 777
10925	19218	28698	1.73	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12046	24978		1.88	2.9E-02	AU135817.1	EST_HUMAN	AUT35817 PLACET1 Homo sapiens cDNA clone PLACE1002862 5'
591	13221		0.99	2.9E-02	AW970183.1	EST_HUMAN	EST1382234 MAGE resequences, MAGK Homo sapiens cDNA
3414	18022	28502	1.62	2.9E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3414	18022	28503	1.62	2.9E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4401	16986		0.71	2.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5337	17898	30313	0.92	2.9E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE
5679	18306	30802	11.28	2.9E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3946087 5'
6900	19634	32472	1.14	2.9E-02	T78980.1	EST_HUMAN	y21b08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108855 5'
8270	20811	33732	1.6	2.9E-02	AJ005820.1	NT	Cratogeomys planicollis mRNA for homeodomain leucine zipper protein (hb-1)
8847	21485	34407	0.74	2.9E-02	AA280762.1	EST_HUMAN	zs98c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711468 5'
9135	21670	34812	0.91	2.9E-02	AF187872.1	NT	Caixa porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9237	21783	34709	0.64	2.9E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
10488	22692	36002	1.81	2.9E-02	AF060221.1	EST_HUMAN	602039477F2 NCI_CGAP_Brr87 Homo sapiens cDNA clone IMAGE:4177287 5'
3470	18085	28559	4.18	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4280	18686	28012	1.91	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'
4280	18686	28313	1.91	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5633	18282	30734	1.11	2.7E-02	R12245.1	EST_HUMAN	y33d09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6061	18678	31420	0.7	2.7E-02	X61870.1	NT	T. aestivum pTTH20 mRNA for wheat type V thionin
6713	19307		0.9	2.7E-02	X97590.1	NT	A bisporus pgIIA gene
7127	19487	32285	2.06	2.7E-02	AA1893571.1	EST_HUMAN	cd8h03.s1 Soares fetal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1624661 3'
8295	20836					EST_HUMAN	tc28g08.x1 Soares fetal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2085982 3' similar to contains Alu repetitive element;
867	13228	26700	1.21	2.7E-02	AI377038.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
2404	14972	27544	1.52	2.6E-02	AL163282.2	NT	ab02b02.s1 Stratagene fetal retina G37202 Homo sapiens cDNA clone IMAGE:839595 3'
2406	14974	27548	2.79	2.6E-02	AA490021.1	EST_HUMAN	Mus musculus histidine rich calcium binding protein (Hic), mRNA
2406	14974	27547	7.33	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hic), mRNA
2840	15556		7.33	2.6E-02	6754241	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70L, and smRNP genes, complete cds; G7A gene, partial cds, and unknown genes
6031	17805	30049	1.17	2.6E-02	AF109008.1	NT	Chicken dorsalin-1 mRNA, complete cds
6224	17790	30208	4.74	2.6E-02	L12032.1	NT	Deinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
5264	17817	30241	1.58	2.6E-02	AE002014.1	NT	xa52b04.x1 NCL CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0089 ;
6368	18972		2.34	2.6E-02	AW241154.1	EST_HUMAN	q927f11.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6556	19154	31850	6.32	2.6E-02	AI209030.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6915	19574	32402	2.29	2.6E-02	BE921748.1	EST_HUMAN	Vaccinia virus ORF1L, strain Wyeth
6915	19574	32403	0.75	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L, strain Wyeth
6980	19488	32310	0.75	2.6E-02	Z99084.1	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
8442	20982	33887	6.45	2.6E-02	AA680848.1	EST_HUMAN	ek22f04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3'
9282	21882	34827	0.77	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9830	22130	35094	1.41	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12839(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9830	22130	35095	0.8	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12839(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10302	22768	35787	0.8	2.6E-02	AF114952.1	NT	Homo sapiens chromosome 21 segment HS21C103
11265	23783		4.1	2.6E-02	AL163303.2	NT	zs84c02.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704182 5'
11437	23887	36955	2.44	2.6E-02	AA278351.1	EST_HUMAN	U1HF-BND-ek-10-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
11965	25060	30512	1.63	2.6E-02	AW500547.1	EST_HUMAN	602015501F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150944 5'
12083	24354		1.26	2.6E-02	BF343927.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
557	13188	25668	1.26	2.6E-02	11422838	NT	on26f08.y4 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13188	25667	1.76	2.5E-02	AF03130.1	EST_HUMAN	on2606.y9 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1597827 5'
842	13458	25967	18.68	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
902	13816	26034	4.48	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2791	15344		2.84	2.5E-02	U12571.1	NT	Rattus norvegicus rebphilin-3A mRNA, complete cds
2983	16596	28078	3.52	2.5E-02	X98697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/b binding protein, Fcp1
2983	16596	28079	3.52	2.5E-02	X98697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/b binding protein, Fcp1
4119	18006	28187	0.77	2.5E-02	BE701166.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4119	18006	28188	0.77	2.5E-02	BE701166.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4284	16870	29318	5.25	2.5E-02	AW592114.1	EST_HUMAN	h38h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5939	18512	31238	0.7	2.5E-02	AF732776.1	EST_HUMAN	z83c10.x5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:3103364 3'
6340	18946		4.9	2.5E-02	BE670128.1	EST_HUMAN	7c3c609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1
6357	18981		4.3	2.5E-02	BE748888.1	EST_HUMAN	repetitive element;
6478	19078	31882	0.72	2.5E-02	L26026.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7680	20172	33068	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
7680	20172	33068	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
7820	20492	33368	0.48	2.5E-02	BE252469.1	EST_HUMAN	601108281F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
8769	21298	34219	0.93	2.5E-02	Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8804	21432	34355	0.45	2.5E-02	AW025821.1	EST_HUMAN	wo08c10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516370 3'
9979	22473		0.8	2.5E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10475	22668	35978	0.73	2.5E-02	AI147815.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1686982 3'
10889	23219	36231	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
10889	23219	36232	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-4p
10781	23285		4.04	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
11802	24045		1.73	2.5E-02	AB007546.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA
11922	24993		3.33	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12115	24855		1.53	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase MkcA (mkcA) gene, complete cds
12215	24438		2.17	2.5E-02	U60169.1	NT	Dicotyledon discoidium putative protein kinase MkcA (mkcA) gene, complete cds
12242	24454	30957	1.31	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
185	12648	25332	0.75	2.4E-02	AI375582.1	EST_HUMAN	ic72c07.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1942	14234	26768	2.09	2.4E-02	H55884.1	EST_HUMAN	y75f11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211149 5'
2088	15457	27239	2.02	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	15457	27240	2.02	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4458	17044	28487	1.89	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 26) protein mRNA, complete cds
4819	17202	28850	1.63	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4819	17202	28851	1.63	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6363	18987	31745	0.94	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:418791 3'
7273	19801	32658	1.08	2.4E-02	Z20573.1	EST_HUMAN	HSAACCKVX.T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7287	19815	32672	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7287	19815	32673	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7831	20373		0.69	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0188-230300-019-h06 ST0188 Homo sapiens cDNA
7884	20426		0.8	2.4E-02	M16780.1	NT	Human retrotropovirus 3' long terminal repeat
8379	20919		0.88	2.4E-02	H78378.1	EST_HUMAN	yui2c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element
8468	21008	33925	10.74	2.4E-02	N88442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294598 3' similar to gblK02909RATSR7K Rat (rRNA); contains A3R.b1 A3R repetitive element
8917	21455	34375	0.54	2.4E-02	AE001125.1	NT	Bartella burgdorferi (section 11 of 70) of the complete genome
							zui91c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element
8939	21477	34398	0.75	2.4E-02	AA625680.1	EST_HUMAN	
9720	22218	35193	2.78	2.4E-02	AV682954.1	EST_HUMAN	AV682954 GKC Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element
9891	22388	35368	2.9	2.4E-02	AA493894.1	EST_HUMAN	
							Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11447	23897	36982	1.9	2.4E-02	AF109905.1	NT	
							Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11447	23897	36983	1.9	2.4E-02	AF109905.1	NT	
11718	24127		3.96	2.4E-02	0627909	NT	Bacteriophage b167, complete genome
11888	24222	31044	2.48	2.4E-02	0753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
11924	24259	31013	1.38	2.4E-02	BE928869.1	EST_HUMAN	MRD-FT0175-310800-202-a08 FT0175 Homo sapiens cDNA
11984	24284	30981	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
11984	24284	31025	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9943	22438	35415	1.4	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9943	22438	35416	1.4	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10661	23183	36208	2.37	2.3E-02	P08940	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
11828	24070		1.87	2.3E-02	AF169132.1	NT	Metapneumovirus encephalitis factor 1 mRNA, complete cds
11848	24843		5.2	2.3E-02	BE278331.1	EST_HUMAN	601179859F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3646667 5'
12282	24495	30940	1.69	2.3E-02	BF628482.1	EST_HUMAN	602043828F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181454 5'
12282	24485	30941	1.59	2.3E-02	BF528482.1	EST_HUMAN	602043829F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181454 5'
12392	24552	30907	2.2	2.3E-02	U38394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12447	25100		3.04	2.3E-02	U11077.1	NT	Dictyostellium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12660	24940		1.73	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
767	13398	25885	3	2.2E-02	AF018287.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1783	14373		1.03	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2059	14639	27212	1.33	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
3482	16088		2.1	2.2E-02	AA577785.1	EST_HUMAN	nt24804.s1 NCI_CGAP_Gest1 Homo sapiens cDNA clone IMAGE:1084782 3'
3708	16309		3.58	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3920	16518	28084	1.11	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3892	16590	29062	0.85	2.2E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5225	17790	30209	0.92	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
7264	19822	32681	3.52	2.2E-02	AV689721.1	EST_HUMAN	AV689721 GKB Homo sapiens cDNA clone GKBAND03 3'
8312	20853	33778	2.58	2.2E-02	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8312	20853	33778	2.56	2.2E-02	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8744	21283	34205	0.75	2.2E-02	X79488.1	NT	P. vulgata alpha tub 2 mRNA
9574	22074	35038	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5
9574	22074	35037	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5
9604	22104	35068	1.88	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9604	22104	35067	1.88	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10106	22601		0.86	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12120	24370		3.95	2.2E-02	AA503553.1	EST_HUMAN	ne47807.s1 NCI_CGAP_Cos3 Homo sapiens cDNA clone IMAGE:800541 3' similar to contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13077		4.45	2.1E-02	AV781602.1	EST_HUMAN	AV781602 MDS Homo sapiens cDNA clone MDSADG01 5'
474	13107		6.21	2.1E-02	AF028728.1	NT	Dichotylidium discoidaleum histidine kinase C (dhkC) mRNA, complete cds
							Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1308	13900	26420	8.16	2.1E-02	U72073.1	NT	
1430	14022	26550	1.48	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1430	14022	26561	1.48	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2842	13426	25634	3.37	2.1E-02	N26286.1	EST_HUMAN	Y43307.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:284841 5'
3184	14680	27231	0.93	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3184	14680	27232	0.93	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3843	16246	28721	1.47	2.1E-02	AA461271.1	EST_HUMAN	z63309.1 Soares total fetus NB2HF8_9w Homo sapiens cDNA clone IMAGE:706121 5'
4211	16800	29249	0.77	2.1E-02	Z74283.1	NT	S cerevisiae chromosome IV reading frame ORF YOL245c
4308	16983	29428	0.83	2.1E-02	BF943655.1	EST_HUMAN	802015306F1 NCI CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4151161 5'
4540	17124	29568	1.64	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid ep32-2, erpC and erpD genes, complete cds, and unknown genes
4552	17135	29583	1.3	2.1E-02	A1768127.1	EST_HUMAN	wg81d1.1 Soares NSF_F8_BW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4820	17398	29867	5.95	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4836	17414	29867	0.67	2.1E-02	AA665737.1	EST_HUMAN	eg55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4944	17519	29861	0.83	2.1E-02	A1823432.1	EST_HUMAN	wt54905.x1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2384528 3'
							BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt)
5321	17883		1.52	2.1E-02	S82470.1	NT	
5621	18445	31167	0.8	2.1E-02	AW379528.1	EST_HUMAN	GM4-HT0244-111198-040-h05 HT0244 Homo sapiens cDNA
7126	18466	32284	0.74	2.1E-02	BF086186.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8468	20898	33914	0.66	2.1E-02	9780238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
							am83a07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element ;
9422	21831	34979	0.56	2.1E-02	AA984288.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9548	22049	35010	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9548	22049	35011	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9894	22391	35369	1.22	2.1E-02	L26324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds, and unknown genes
9973	22468	35452	0.57	2.1E-02	AA984288.1	EST_HUMAN	am83a07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element ;
12099	18030		11.53	2.1E-02	Y18213.1	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
12141	24839	30708	1.31	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12552	24655	30871	16.83	2.1E-02	AF183913.1	NT	Azoosporillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20	12699	25155	1.34	2.0E-02	BF002932.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3309888 3' similar to contains MER1.13
21	12700	25156	9.8	2.0E-02	AW895565.1	EST_HUMAN	MER1 repetitive element;
280	12697	26422	2.31	2.0E-02	6753635	EST_HUMAN	QV4-NN0038-270400-187-168 NN0038 Homo sapiens cDNA
317	12671	25480	2.42	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
831	13448	25955	1.2	2.0E-02	6753635	NT	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1128	13728	26240	1.32	2.0E-02	AL096805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1241	13839	26356	0.79	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p38.33) of Homo sapiens
1241	13839	26357	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1914	14488	27063	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
1914	14488	27054	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
2824	16378		3.19	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3115	12689	25155	1.84	2.0E-02	BF002932.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3309888 3' similar to contains MER1.13
3178	15791		1.38	2.0E-02	7305474	NT	MER1 repetitive element;
3284	16878		1.57	2.0E-02	AF095688.1	NT	Mus musculus sema domain, transmembrane domain (TIM), and cytoplasmic domain, (semaphorin) 6B
4078	16874	20135	1.54	2.0E-02	M18095.1	NT	(Sem6b), mRNA
6288	17830	30255	1.12	2.0E-02	AF183388.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
6086	18673	31414	0.87	2.0E-02	L35321.2	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7553	20072	32847	1.28	2.0E-02	AP000004.1	NT	Ajellomyces capsulatus catalase isozyme A (CATA) mRNA, complete cds
7683	20072	32848	1.28	2.0E-02	AP000004.1	NT	Dicystosellum discoideum class VII unconventional myosin (myoI) gene, complete cds
9781	22289		2.5	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
10284	22759	35748	1.63	2.0E-02	A1640342.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
10522	23080	36070	2.05	2.0E-02	Z73888.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
11250	23780	36836	2.85	2.0E-02	D88184.1	NT	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3'
11630	23878	37047	1.58	2.0E-02	10847055	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162
11530	23978	37048	1.58	2.0E-02	AA458338.1	EST_HUMAN	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11654	18034	30494	1.91	2.0E-02	AA458338.1	EST_HUMAN	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12138	19378		1.94	2.0E-02	AL161532.2	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12635	24711		8.4	2.0E-02	T80037.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
722	13342	25832	1.93	1.9E-02	AA572764.1	EST_HUMAN	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
							yd04c09.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:24875 5'
							nt18a07.s1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1
							repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1658	14251	26785	0.96	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2083	14684	27234	1.98	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
2083	14804	27235	1.98	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
2649	15113	27683	0.9	1.9E-02	AL161650.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
2830	15546	28021	8.7	1.9E-02	AA713868.1	EST_HUMAN	rw04f08.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2980	15588	28076	1.56	1.9E-02	AV648869	EST_HUMAN	AV648869 GLC Homo sapiens cDNA clone GLOBLH07 3'
3288	15909		0.75	1.9E-02	AB033811.1	NT	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3871	16272		1.09	1.9E-02	N52250.1	EST_HUMAN	y228502.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3766	16367		6.81	1.9E-02	BE738086.1	EST_HUMAN	601672682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839504 5'
4121	16714	29170	1.48	1.9E-02	AF141840.1	NT	Myoplasma imitans Vha1 precursor (vha1) and Vha2 precursor (vha2) genes, partial cds
4271	16867	29306	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	29306	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4639	17221	29875	3.21	1.9E-02	A1452889.1	EST_HUMAN	{46d04.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5157	15113	27683	2.73	1.9E-02	AL161650.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5519	18151	30585	0.83	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5660	18287	30786	1.38	1.9E-02	L47572.1	NT	Meleagris gallopavo paracetamol-2 (PON2) mRNA, complete cds
5858	18581		0.81	1.9E-02	AB019607.1	NT	Drosophila kankol gene for glyceral-3-phosphate dehydrogenase, complete cds
7158	18890	32534	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7158	18890	32535	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8508	21045		1.08	1.9E-02	U162754.2	NT	Nelusetra meningitis serogroup A strain Z2481 complete genome, segment 3/7
9254	21780	34732	0.94	1.9E-02	BF316128.1	EST_HUMAN	601888130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5'
9629	22129	35093	0.68	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9858	22463	35435	1.04	1.9E-02	BF686832.1	EST_HUMAN	601852385F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076253 5'
10054	22549	35543	0.49	1.9E-02	N39160.1	EST_HUMAN	y246h08.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:276839 3'
10151	22648	35639	0.56	1.9E-02	D84001.1	NT	Synechococcus sp. PCC6803 complete genome, 20/27, 2538000-2844794
11678	24847	30801	4.28	1.9E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament gillardin mRNA, complete cds
12477	24818		1.27	1.9E-02	L11068.1	NT	Candida albicans lambda Cas3B fragment
12587	24680	30870	1.7	1.9E-02	X68271.1	NT	H. sapiens MUC18 gene exon 16
368	13017	25500	1.84	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
714	13335	25821	2.26	1.8E-02	BF308122.1	EST_HUMAN	601894328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1202	13802	26315	1.51	1.8E-02	X17684.1	NT	H. francisci mRNA for myelin basic protein (MBP)
1484	14077	26815	2.3	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2704	15261	27828	1.22	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 526 of the complete genome
3247	15559		0.72	1.8E-02	AI805829.1	EST_HUMAN	h52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090286 3'
3956	16954	26023	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3956	16954	26024	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4160	16762		1.41	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4921	17108	29551	1.67	1.8E-02	AW836383.1	EST_HUMAN	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
5090	17683	30103	1.06	1.8E-02	O80810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6901	19635	32473	4.27	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 3 REGION
8071	20613	33527	0.81	1.8E-02	U37091.1	NT	Mus musculus carboxic anhydrase IV gene, complete cds
8404	20944	33986	0.91	1.8E-02	AW005327.1	EST_HUMAN	QV2-NN1073-220400-159-H08 NN1073 Homo sapiens cDNA
8449	20989	33907	0.76	1.8E-02	6878943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9413	21922	34870	0.46	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4105303 5'
9413	21922	34871	0.46	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4105303 5'
9560	22080		2.41	1.8E-02	AA897543.1	EST_HUMAN	482709.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394821 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
9975	22470	35463	1.72	1.8E-02	BE778274.1	EST_HUMAN	601483545F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3866983 5'
10126	22621	35611	1.12	1.8E-02	X96933.1	NT	L.stegialis mRNA for myomodulin neuropeptide precursor
11313	23011	36019	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11313	23011	36020	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11489	23930	37001	1.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (87)
11489	23938	37008	3.88	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
809	13562	28068	0.77	1.7E-02	BE394889.1	EST_HUMAN	601310826F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3832190 5'
1827	14416	26983	1.89	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;
1827	14416	26984	1.89	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;
1912	14497		3.27	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2169	14738		12.81	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for miltugumin29, complete cds
2332	14903	27474	4.64	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 381 nt. segment 1 of 2]
3028	15644	28123	0.84	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbhpU Homo sapiens cDNA clone IMAGE:1688982 3'
3562	16166		4.33	1.7E-02	AW827388.1	EST_HUMAN	hm48a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015334 3' similar to contains MER19.b1 MER19 repetitive element;
3687	16288		0.65	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	16838		1.08	1.7E-02	AA069818.1	EST_HUMAN	sec19f04.s1 Stratagene ovary (8937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element contains element MER24 repetitive element:
4278	16854		2.82	1.7E-02	R02506.1	EST_HUMAN	ye88f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124847 6'
4851	17134	28582	0.61	1.7E-02	A1305270.1	EST_HUMAN	qm08q07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4826	17209	28659	1.44	1.7E-02	AW573183.1	EST_HUMAN	h134e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2633740 3' similar to contains L1.11 L1 repetitive element:
4824	17402	28855	1.78	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4838	17611		5.59	1.7E-02	A1015076.1	EST_HUMAN	ov61e02.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3'
6274	18882	31660	1.8	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387113 3' similar to contains Alu repetitive element:
6693	18269	32091	1.98	1.7E-02	A1038280.1	EST_HUMAN	cy65h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7112	19452	32268	1.05	1.7E-02	AF190830.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7255	18783	32639	1.98	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7394	18918	32783	1.07	1.7E-02	L07889.1	NT	Human apolipoprotein (a) gene, exon 1
7394	18918	32784	1.07	1.7E-02	L07889.1	NT	Human apolipoprotein (a) gene, exon 1
7724	20232		1.7	1.7E-02	AJ010770.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase, exon 1-50
9357	20268	33195	0.97	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9615	22115	35078	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434f0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434f0314 5'
12482	26025	30619	3.35	1.7E-02	AW803482.1	EST_HUMAN	GM4-NN1030-04000-130-108 NN1030 Homo sapiens cDNA
537	13188		3.38	1.6E-02	AL021626.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1696	14289	26825	1.05	1.6E-02	Y18889.1	NT	Trepionema maltophilum flaB2, flaB3 and flid genes for flagellin subunit proteins and CAP protein homologue
2290	14864	27438	2.13	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2290	14864	27439	2.13	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2600	15182	27730	0.98	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ1 gene
2669	15227	27769	1.82	1.6E-02	AA484872.1	EST_HUMAN	ne81408.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910987
2718	15275		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3082	16688	28148	0.73	1.6E-02	AF112282.1	NT	Lasaea sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3578	16182	28664	5.61	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3914	16512	28974	0.92	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	18842		1.77	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fee-binding protein, BING1, tapasin, RIGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds, Sacm21 gene, partial>
4388	16974	28424	1.26	1.6E-02	AW875407.1	EST_HUMAN	QV2PT0012-140100-030-07 P10012 Homo sapiens cDNA
4801	17478	28922	3.99	1.6E-02	AI789132.1	EST_HUMAN	wg34b09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2368869 3'
5308	17868		0.61	1.6E-02	N80156.1	EST_HUMAN	z86607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:287444 3'
5807	18432	31153	1.26	1.6E-02	687171.5	NT	Mus musculus Gd5 antigen (Cd5), mRNA
6762	18345	32182	2	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7011	18508	32328	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7011	19509	32330	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7698	20205	33082	0.9	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8084	20808	33518	0.78	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8118	20660		1.56	1.6E-02	X05151.1	NT	Human spoc-II gene for preprocalciprotein C-II
8953	22448		2.32	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10317	22811	36806	1.17	1.6E-02	AA572818.1	EST_HUMAN	n19g03.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10317	22811	36806	1.17	1.6E-02	AA572818.1	EST_HUMAN	P28294 TELOKIN. (1):
10788	24800	36319	2.38	1.6E-02	Z94828.1	NT	n19g03.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11090	23602	36840	2.5	1.6E-02	AL161508.2	NT	P28294 TELOKIN. (1):
11090	23602	36841	2.5	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LEI0260 (=T16IIIE11))
11365	23837	36859	2.38	1.6E-02	AI373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11855	14884	27438	3.63	1.6E-02	Q84176	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11855	14884	27439	3.63	1.6E-02	Q84176	SWISSPROT	q28610.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:2042442 3'
781	13400		51.07	1.6E-02	8923734	NT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2187	14763	27332	4.38	1.6E-02	N39521.1	EST_HUMAN	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2219	14764	27367	1.78	1.6E-02	AL161594.2	NT	Homo sapiens transcription factor (HSA130884), mRNA
3097	15712	28183	0.99	1.6E-02	AJ008216.1	NT	yw27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243926 3'
3097	15712	28184	0.99	1.6E-02	AJ008216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3787	18387	28853	0.86	1.6E-02	BF082842.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
4222	18810	28257	0.88	1.6E-02	AA160867.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
5160	17729		0.78	1.6E-02	M13879.1	NT	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
5403	17963	30374	1.14	1.6E-02	AW770341.1	EST_HUMAN	z440g10.r1 Strategene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:832228 5'
							Human interleukin 2 gene, exons 1 and 2
							h76h11.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3007173 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8436	19039	31828	1.31	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7360	19888		1.92	1.5E-02	11487282	NT	Cyanophora paradoxa cyanella, complete genome
7432	19858	32821	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
7816	20368	33265	1.44	1.5E-02	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7822	20364	33273	4.16	1.5E-02	11417730	NT	Homo sapiens vely-IRNA synthetase 2 (VARS2), mRNA
8764	21303	34224	1.82	1.5E-02	BF345664.1	EST_HUMAN	602019136F1 NCL_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4164504 5'
9389	21812		0.51	1.5E-02	AF066774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9490	21849	34895	1.84	1.5E-02	D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9726	22223	35199	1.08	1.5E-02	R32687.1	EST_HUMAN	ytB4b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9726	22223	35200	1.08	1.5E-02	R32687.1	EST_HUMAN	ytB4b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10897	23227		1.71	1.5E-02	D28647.1	NT	Rice gene for thiorodoxin h, complete cds
11047	23560	36597	2.32	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12078	24892		2.25	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12636	24712		1.55	1.5E-02	AI763127.1	EST_HUMAN	w08h03.x1 NCL_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element ;
442	13076		1.41	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1187	13760	26270	4.22	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1299	13593		1.29	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1341	13836		3.36	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1564	14156		1.08	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAH11 5'
3249	15861	28342	1.91	1.4E-02	AF160869.2	NT	Bifidobacterium longum Nax/H+ antiporter (nhaB), cytosine desaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosaminidase repressor protein (nagCxyR) gene, partial cds
3445	16053	28530	0.96	1.4E-02	AW074212.1	EST_HUMAN	xb08009.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'
3531	16136	28616	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3531	16136	28617	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3571	16179	28657	0.68	1.4E-02	4503828	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3717	16318	28786	6.27	1.4E-02	6896818	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4587	17170	28614	8.88	1.4E-02	AW982898.1	EST_HUMAN	EST374761 IMAGE ressequencing, MAGG Homo sapiens cDNA
4587	17170	28615	8.88	1.4E-02	AW982898.1	EST_HUMAN	EST374761 IMAGE ressequencing, MAGG Homo sapiens cDNA
4787	17348	28787	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4787	17348	28788	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
5003	17576	30020	6.64	1.4E-02	BE733142.1	EST_HUMAN	601581403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5003	17578	30021	8.64	1.4E-02	BE733142.1	EST_HUMAN	601667403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6547	19145	31841	4.61	1.4E-02	AA558030.1	EST_HUMAN	nt11c04.s1 NCL_CGAP_B12 Homo sapiens cDNA clone IMAGE:1026980 3' similar to contains Alu repetitive element;
6547	19145	31842	4.61	1.4E-02	AA558030.1	EST_HUMAN	nt11c04.s1 NCL_CGAP_B12 Homo sapiens cDNA clone IMAGE:1026980 3' similar to contains Alu repetitive element;
8081	20623		1.97	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 68/162
8826	21368	34282	1.24	1.4E-02	M81702.1	NT	Candida bodinii methanol oxidase (AOD1) gene, complete cds
8082	21618	34553	0.99	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-9
8321	21835	34786	2.48	1.4E-02	BE444681.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10451	22945		0.81	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11765	24156	36772	12.78	1.4E-02	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12134	24387		3.62	1.4E-02	AF524985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12433	24574		2.32	1.4E-02	11426898	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1805	14490		1.18	1.3E-02	BE739283.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1898	14580	27138	2.55	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3290	15892	28343	1.91	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3250	15892	28344	1.91	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4041	16639		1.68	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
							Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmsx28orf
5455	18090	30447	1.48	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmsx28orf
5455	18090	30448	1.48	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmsx28orf
6312	18919	31694	1.4	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6345	18951	31729	0.88	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7041	18061	30449	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
7041	18061	30450	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
							ow06g05.x1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1046072 3' similar to contains Alu repetitive element;
7578	20094	32971	4.79	1.3E-02	AJ031593.1	EST_HUMAN	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
8418	20958	33876	1.63	1.3E-02	AF156961.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10108	22603	35593	1.71	1.3E-02	M63707.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10178	22673	35885	0.77	1.3E-02	AE001304.1	NT	xx44603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
10871	23392	36408	4.07	1.3E-02	AW268563.1	EST_HUMAN	xx44603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
10871	23392	36407	4.07	1.3E-02	AW268563.1	EST_HUMAN	xx44603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11742	25051		2.12	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12139	25039		2	1.3E-02	259117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2594481 to 2812870
12246	24457		2.77	1.3E-02	9833069	NT	Human herpesvirus 8B, complete genome
12438	24813		47.13	1.3E-02	AF152238.1	NT	Human sapiens V1b vesopressin receptor (VPR3) gene, complete cds
228	12888		20.25	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LAMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
377	13025	25511	3.79	1.2E-02	AA059299.1	EST_HUMAN	z05g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element 1
478	13111	25601	1.71	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3 REGION
788	13387	25886	8.37	1.2E-02	AI18322.1	EST_HUMAN	q08842.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1.H L1 repetitive element 1
2221	14788	27369	1.85	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2223	14798	27371	1.18	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2487	16052	27824	1	1.2E-02	AW172350.1	EST_HUMAN	X37608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2542	16108	27878	1.05	1.2E-02	BE539310.1	EST_HUMAN	601088408F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454808 5'
2542	15108	27879	1.05	1.2E-02	BE539310.1	EST_HUMAN	601088408F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454808 5'
3136	16749		7.58	1.2E-02	AA075418.1	EST_HUMAN	z088603.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3327	15937	28413	2.02	1.2E-02	R82805.1	EST_HUMAN	y11b08.s1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:138803 3'
4938	17513	29859	0.61	1.2E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5040	17613	30057	2.65	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
5194	17759		1.61	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
5244	17808	30230	2.01	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5927	18548	31275	1.78	1.2E-02	D76589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
7078	19850	32489	5.21	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7334	19861	32725	1.08	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:150695 3'
7353	19879	32744	19.48	1.2E-02	AV732083.1	EST_HUMAN	AV732083 HTF Homo sapiens cDNA clone HTFBJC09 5'
7939	20481	33392	2.3	1.2E-02	Q11205	SWISSPROT	GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNA-C-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA-2) (SIAT4-B)
8133	20874	33585	1.2	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8133	20874	33586	1.2	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8822	21361		1.06	1.2E-02	T76887.1	EST_HUMAN	y072c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9597	22057	35018	2.7	1.1E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9599	22089	35083	1.74	1.1E-02	AJ248003.1	NT	Homo sapiens Spast gene for spastin protein
12440	24882		4.73	1.1E-02	G18119.1	EST_HUMAN	G18119 Human placenta cDNA (TFJWZRA) Homo sapiens cDNA clone GEN-557G08 5'
1312	13906	28428	1.49	1.1E-02	AA070394.1	EST_HUMAN	zn68a11.81 Stratiogene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:530924 3'
1744	14334	28880	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1744	14334	28881	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2082	14863	27233	5.42	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4163808 5'
2802	15510		4.2	1.1E-02	N95523.1	EST_HUMAN	zn40605.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
3575	16179	28662	2.88	1.1E-02	A1653508.1	EST_HUMAN	IQ55b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPf_HUMAN
4094	16889		2.1	1.1E-02	BE144637.1	EST_HUMAN	Q92899 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4183	16773		0.81	1.1E-02	AW813786.1	EST_HUMAN	PM3-HT0175-300899-001-h08 HT0175 Homo sapiens cDNA
4658	17631	28973	2.09	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-q11 ST0197 Homo sapiens cDNA
							DKFZ588E0924_s1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZ588E0924
							Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaH (ynaH), YnaB (ynbA), YnaC (ynbC), YnaD (ynbD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH (ynaH), YnaI (ynal), YnaJ (ynal), YnaK (ynal), xylan beta-1,4-xylosyl-
6288	18906	31677	1.03	1.1E-02	U98480.1	NT	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
7694	20108	32883	2.55	1.1E-02	BE148611.1	EST_HUMAN	METALLOTHIONEIN (MT-1/MT-2)
8199	20740	33882	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8199	20740	33883	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8574	21113	34032	0.84	1.1E-02	AW698160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8756	21296	34215	0.69	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH-C4040
8833	21372	34297	7.39	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
6842	22340	35322	2.07	1.1E-02	AA082578.1	EST_HUMAN	zn24801.1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10008	22501	35492	3.79	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10858	23379	36398	3.86	1.1E-02	11435506	NT	Homo sapiens T-box 5 (TBX5), mRNA
11702	24116						ab7711.81 Stratiogene fetal retina 637202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12512	16773		2.67	1.1E-02	AA688239.1	EST_HUMAN	Alu repetitive element
7	12886	25144	1.87	1.1E-02	AW813798.1	EST_HUMAN	RC3-ST0197-120200-015-q11 ST0197 Homo sapiens cDNA
1570	14163	26694	6.97	1.0E-02	AW848120.1	EST_HUMAN	MR3-ST0176-111099-003-q10 CT0176 Homo sapiens cDNA
2608	15168		2.33	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3126	15740	28209	1.9	1.0E-02	AA086389.1	EST_HUMAN	cc22h08.81 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1350495 3'
3302	15813	28391	3.7	1.0E-02	BE834558.1	EST_HUMAN	RCO-FN0025-250500-021-h02 FN0025 Homo sapiens cDNA
			1.41	1.0E-02	BE868899.1	EST_HUMAN	801849867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3903689 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	19182		0.83	1.0E-02	AW845621.1	EST_HUMAN	MR0-CT0060-081089-003-h10 CT0060 Homo sapiens cDNA
3950	16548	28016	0.89	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4891	17468	29921	5.12	1.0E-02	0753821	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4870	17544	29988	5.03	1.0E-02	R68567.1	EST_HUMAN	yq54h01.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:189633 5'
5221	17788	30204	1.01	1.0E-02	AF218910.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced
5317	17879	30288	0.98	1.0E-02	P06599	SWISSPROT	EXTENSIN PRECURSOR
5394	17952		18.86	1.0E-02	AV723878.1	EST_HUMAN	AV723878 HTB Homo sapiens cDNA clone HTBAPF08 5'
5443	18000		3.87	1.0E-02	D34632.1	NT	Arabidopsis thaliana ecc2 gene for acetyl-CoA carboxylase, partial cds
5610	18239	30688	0.8	1.0E-02	H92881.1	EST_HUMAN	yq38h11.r1 Scores ovary tumor N3HOT Homo sapiens cDNA clone IMAGE:235941 5'
5921	18843	31269	0.7	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A1c4 (Nf1c4) gene, exons 1 and 2
6264	18872	31642	0.86	1.0E-02	AF287303.1	NT	Mus musculus synaptobrevin II (Syb2) gene, complete cds
6328	18934	31709	2.87	1.0E-02	AW877113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA
6328	18934	31710	2.87	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA
6859	19583	32425	2.22	1.0E-02	Z28842.1	NT	Z.mays U3snRNA pseudogene
8240	20781		0.48	1.0E-02	Z28107.1	NT	S. cerevisiae chromosome XI reading frame ORF YKL107w
9314	21828	34778	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
9314	21828	34778	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
11143	23851		2.17	1.0E-02	AF187559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for
11246	23776	36833	2.02	1.0E-02	AV760018.1	EST_HUMAN	AV760018 MDS Homo sapiens cDNA clone MDSBDC10 5'
11765	25110		2.18	1.0E-02	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
11847	24852	30705	4.84	1.0E-02	AW635521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
11861	24822		6.07	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12254	24898		1.53	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12422	24882		4.42	1.0E-02	X62854.1	NT	H. sapiens gene for Me49/CD63 antigen
826	13539	28057	3.16	9.0E-03	AI796126.1	EST_HUMAN	wh42709.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1307	13901		1.28	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element;
2439	18006	27578	3.82	9.0E-03	AL161559.2	NT	601470242FT NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2449	15016	27598	0.87	9.0E-03	AF096934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2831	15547	28022	0.61	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2931	16547	28023	0.61	9.0E-03	AI251744.1	EST_HUMAN	qh00709.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3731	16332	28788	0.8	9.0E-03	J05184.1	NT	qh00709.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5878	18598		1.17	9.0E-03	AI809782.1	EST_HUMAN	S. acidocaldarius thermophilin gene, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8741	18335		4.24	9.0E-03	BE745988.1	EST_HUMAN	801573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5'
7487	20010	32878	0.73	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10850 (FLJ10850). mRNA
7818	20359		0.83	9.0E-03	AL039891.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434L0412 5'
8191	20732		0.56	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9759	22257	36240	0.5	9.0E-03	P28011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
9778	22274	35258	1.26	9.0E-03	P20808	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10865	23368		1.8	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10891	23412	38431	1.71	9.0E-03	BE398380.1	EST_HUMAN	801310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3832181 5'
11505	23954	37022	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11505	23954	37023	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12001	25111		1.79	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281288-001-e09 HT0452 Homo sapiens cDNA
12221	25105		36.8	9.0E-03	BE348385.1	EST_HUMAN	hw17809.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12319	24509	30843	1.38	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
12559	24649		31.87	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281288-001-e09 HT0452 Homo sapiens cDNA
527	13159		2.87	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pined_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element
1028	13637	26152	35.57	8.0E-03	AF106856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2203	14778	27351	1.28	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3351	15859	28436	0.99	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3404	16013	28492	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3758	16339	28805	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3738	16339	28806	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4343	16930	29371	1.19	8.0E-03	BE840048.1	EST_HUMAN	QV0-FN0181-140700-304-q10 FN0181 Homo sapiens cDNA
4472	17058	29505	6.38	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-805 NN0119 Homo sapiens cDNA
5378	17937	30350	1.02	9.0E-03	U02870.1	NT	Prototheca wickerhamii 283-11 complete mitochondrial DNA
5410	17987	30376	0.88	8.0E-03	P01871	SWISSPROT	IG MU CHAIN C REGION
5714	18340	30848	2.89	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RALGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6348	24762	31730	1.34	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
6848	19496	32251	4.45	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6988	19497		1.72	8.0E-03	V01108.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7259	19787	32843	1.8	8.0E-03	M17197.1	NT	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20087		1.84	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8816	21355	34278	0.62	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
8841	21380	34304	3.73	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
8810	21448	34370	0.88	8.0E-03	0789958	NT	MR1-ST0111-11108-011-108 ST0111 Homo sapiens cDNA
8839	22358		4.76	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
10884	23385		3.01	8.0E-03	Z49552.1	NT	QV1-BT0877-040400-131-g03 BT0877 Homo sapiens cDNA
11258	23789	36845	1.97	8.0E-03	AA828817.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR182w
11259	23789	36846	1.97	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
11582	24009	37078	4.86	8.0E-03	AF084589.1	NT	cd80a09.s1 NCL_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
11713	24123		2.81	8.0E-03	M69035.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11761	24154		5.88	8.0E-03	AB038191.1	NT	Oryzodagus curvicaudus eIF-2a kinase mRNA, complete cds
723	13343	25833	14.03	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
723	13343	25834	14.03	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1012	13622	26137	5.78	7.0E-03	AF243378.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1155	13758	26268	3.21	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1408	14001		1.26	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1438	14032	26560	4.09	7.0E-03	AA689288.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HNF-2)
1550	14142	26875	3.14	7.0E-03	AW303599.1	EST_HUMAN	ab76b09.s1 Stragene fetal retina 637202 Homo sapiens cDNA clone IMAGE:953145 3'
2287	15482	27447	2.12	7.0E-03	P04829	SWISSPROT	av21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3614	16217	28696	0.58	7.0E-03	AI150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3830	18430	28892	0.91	7.0E-03	AW444463.1	EST_HUMAN	q34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3885	18483	28945	1.01	7.0E-03	AF196344.1	NT	UI-H-B13-akb-c-10-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4091	18430	28892	0.83	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4704	17266		1.1	7.0E-03	AW630888.1	EST_HUMAN	h189a05.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869836 5'
5125	17697		2.08	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5886	18605		0.79	7.0E-03	H71108.1	EST_HUMAN	y62g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:U4723 CLUSTERIN PRECURSOR (HUMAN);
6260	24760		5.32	7.0E-03	AW661059.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6456	18057	31842	1.45	7.0E-03	W68251.1	EST_HUMAN	z33310.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:342475 5'
6658	19254	32056	2.98	7.0E-03	AA327120.1	EST_HUMAN	EST30874 Cdon1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6881	19277	32080	0.92	7.0E-03	BE8857385.1	EST_HUMAN	7q34b10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TRQ13387
7139	19519	32341	2.12	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.2 TAR1 TAR1 repetitive element;
7528	20049	32921	6.78	7.0E-03	Z35839.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7529	20049	32922	6.78	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33238	0.54	7.0E-03	AJ228043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33239	0.54	7.0E-03	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8055	20597	33504	2.36	7.0E-03	BE175697.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8318	21832		0.6	7.0E-03	AF111188.2	NT	RC5-HT0582-160300-011-022 HT0582 Homo sapiens cDNA
9513	22013	34972	0.87	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9638	22136	35101	2.48	7.0E-03	P48882	SWISSPROT	y449c10.s1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248068 3' similar to contains
9638	22136	35102	2.48	7.0E-03	P48882	SWISSPROT	Alu repetitive element
10361	22875		0.93	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10708	23235	36248	3.46	7.0E-03	AB008952.1	NT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10780	23304	36311	1.81	7.0E-03	AJ004862.1	NT	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
10780	23304	36312	1.81	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10930	23448		1.86	7.0E-03	AJ242804.1	NT	Bos taurus mRNA for NDP52, complete cds
12273	25095		1.83	7.0E-03	H84065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12281	24484		1.58	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12382	24549		1.86	7.0E-03	Y17455.1	NT	Sporobolus stapianus mRNA for putative glycine and proline-rich protein
12527	25092		1.38	7.0E-03	AL183300.2	NT	y415h01.s1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12664	24734		3.16	7.0E-03	AW888110.1	EST_HUMAN	Alu repetitive element
1283	13879	26400	10.8	6.0E-03	AW511148.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
1283	13879	26401	10.8	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
2800	15352	27821	1.82	6.0E-03	AF112374.1	NT	Homo sapiens chromosome 21 segment HS21CT00
2916	15533	28004	3.54	6.0E-03	AA759135.1	EST_HUMAN	RCO-SN0052-110400-021-e04 SN0052 Homo sapiens cDNA
2916	15533	28005	3.54	6.0E-03	AA759135.1	EST_HUMAN	hd22a05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
3283	15894		2.17	6.0E-03	HT6690.1	EST_HUMAN	SW:PXK_HUMAN_076469 ORPHAN NUCLEAR RECEPTOR PXK ;
							hd22a05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
							SW:PXK_HUMAN_076469 ORPHAN NUCLEAR RECEPTOR PXK ;
							Danio rerio odorant receptor gene cluster
							ah78e11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78e11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211351 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3344	15954		0.79	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3429	16037	28518	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septiparin reductase and vasotocin genes, complete cds
3428	16037	28519	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septiparin reductase and vasotocin genes, complete cds
3600	16204		1.13	6.0E-03	W37985.1	EST_HUMAN	2213a11.1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3721	16322	28789	2.6	6.0E-03	BF510888.1	EST_HUMAN	UI-H-B14-apm-c-08-UJ1.a1 NCJ CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3757	16358	28828	1.53	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0608-260400-014-007 BT0608 Homo sapiens cDNA
3845	16444	28905	1.14	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3866	16563	28968	0.83	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240969-021-b10 CT0204 Homo sapiens cDNA
4030	16828		0.92	6.0E-03	BE250108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4419	17004		1.1	6.0E-03	N58948.1	EST_HUMAN	y42h10.s1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:278178 3'
4454	17040		1.58	6.0E-03	A016833.1	EST_HUMAN	ov3c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4805	17383	28833	8.21	6.0E-03	AA324242.1	EST_HUMAN	EST127116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5289	17852		0.92	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
6301	24781	31680	0.72	6.0E-03	9827621	NT	Varicella virus, complete genome
6908	19840	32476	0.73	6.0E-03	O14984	SWISSPROT	SYNAPSIN III
6939	18047	30469	0.72	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7642	20154	33040	0.76	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7774	20283	33180	24.22	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7799	20342	33251	6.91	6.0E-03	A1033980.1	EST_HUMAN	ov13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1846870 3' similar to contains MER10.b1 MER10 repetitive element;
7916	20457	33363	2.45	6.0E-03	AW789337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7960	20532		1.59	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
8473	21872	34821	8.46	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
8956	22451		2.15	6.0E-03	A1432661.1	EST_HUMAN	022c02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L19A;
10087	22582	35557	0.73	6.0E-03	AJ011849.1	NT	Bacillus subtilis ferD gene
10197	22892		0.91	6.0E-03	AF084555.1	NT	Homo sapiens cdc42c acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10303	22797	35788	0.63	6.0E-03	X68368.1	NT	M.thermophilicum complete plasmid pFV1 DNA
10823	23155	38168	2.04	6.0E-03	AW962184.1	EST_HUMAN	EST374237 MAGG resequences, MAGG Homo sapiens cDNA
10860	23220		2.23	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10728	23252	36269	2.16	6.0E-03	AI420786.1	EST_HUMAN	la91c12.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
10728	23252	36270	2.16	6.0E-03	AI420786.1	EST_HUMAN	la91c12.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
10881	23382		2.08	6.0E-03	U14558.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10882	23383	36401	2.4	6.0E-03	BE737895.1	EST_HUMAN	g01672746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
11630	24072	37134	1.57	8.0E-03	H70286.1	EST_HUMAN	y05101.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:8PGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;
11828	24195		3.52	6.0E-03	AF010498.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
11958	24948		5.1	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450268 (section 39 of 148) of the complete genome
12039	24914		3.02	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. retri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12088	24357		1.61	6.0E-03	Q82209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12402	24561		1.49	6.0E-03	BE768018.1	EST_HUMAN	g01482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12418	24571		1.52	6.0E-03	AJ245480.1	NT	Brassica napus elg gene for S-locus glycoprotein, cultivar T2
12556	24842		1.6	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
229	12889	25375	5.16	5.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
697	13320	25808	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
697	13320	25807	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
698	13320	25806	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
698	13320	25807	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1151	13754	28264	0.91	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2708	15283	27830	2.77	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2982	15578	28057	0.66	5.0E-03	BE286057.1	EST_HUMAN	g01184786F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3170	15784	28258	4.84	5.0E-03	T67823.1	EST_HUMAN	yc81109.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3189	15801		2.22	5.0E-03	AL181491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3202	15814	28289	1.15	5.0E-03	RT1794.1	EST_HUMAN	yf86g02.s1 Soares breast 2NIBst Homo sapiens cDNA clone IMAGE:155668 3'
3318	15928		0.86	5.0E-03	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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3728	18328	28785	5.04	5.0E-03	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
3782	18383	28831	4.88	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (pb1B) gene, complete cds
3822	18422	28884	0.88	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4043	18841		1.78	5.0E-03	AA236875.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4204	18793	29239	0.57	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4382	18978	29425	0.88	5.0E-03	H78355.1	EST_HUMAN	yJ79g10.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:240068 5'
4394	18422	28884	0.71	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4870	17252	29704	0.88	5.0E-03	U46891.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4714	17295	29739	0.8	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4828	17408	28860	1.72	5.0E-03	AI752387.1	EST_HUMAN	en15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en15c02 random
5087	17840	30083	1.02	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5391	17949	30362	0.85	5.0E-03	AF171688.1	NT	Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds
5984	18588	31320	7.68	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
8195	18805	31574	2.33	5.0E-03	O00507	SWISSPROT	Chlamydomonas reinhardtii AF39, section 62 of 94 of the complete genome
8230	18839		0.91	5.0E-03	AE00234.2	NT	600944364T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
8708	18302		10.88	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
8832	18040	30483	6.39	5.0E-03	AB026024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7108	19448		0.85	5.0E-03	AB038287.1	NT	RC3-CT0255-031099-011-007 CT0255 Homo sapiens cDNA
7595	20109		1.16	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
7744	20252	33148	7.43	5.0E-03	AB016816.1	NT	RC8-CT0281-081198-011-A08 CT0281 Homo sapiens cDNA
8182	20703	33618	1	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081198-011-A05 CT0281 Homo sapiens cDNA
8182	20703	33619	1	5.0E-03	AW855907.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8181	20722	33636	2.28	5.0E-03	P48982	SWISSPROT	Mouse complement receptor (CR2) mRNA, 3' end
8548	21087		8.38	5.0E-03	IM81132.1	NT	Escherichia coli genomic DNA, (18.1 - 19.4 min)
8742	21281	34204	1.47	5.0E-03	D80723.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
8870	21409	34333	0.69	5.0E-03	M25090.1	NT	SOF1 PROTEIN
9503	22003	34860	0.45	5.0E-03	P33750	SWISSPROT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9753	22251	35234	0.82	5.0E-03	L21710.1	NT	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
9881	22378	35354	0.77	5.0E-03	AW821888.1	EST_HUMAN	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA clone IMAGE:885587
10082	22557	35552	0.49	5.0E-03	AA533143.1	EST_HUMAN	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA clone IMAGE:885587

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10238	22731	35722	0.92	5.0E-03	7682557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10598	23133		10.33	5.0E-03	T18586.1	EST_HUMAN	894F Heart Homo sapiens cDNA clone 894
10831	23163	38175	2.28	5.0E-03	D28273.1	NT	Unknown nitrogen-fixing bacteria nifD gene encoding alpha subunit of dinitrogenase (MoFe protein)
10819	23340	36354	2.84	5.0E-03	AW170334.1	EST_HUMAN	xi59g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1 L2 L1 repetitive element;
10819	23340	36355	2.84	5.0E-03	AW170334.1	EST_HUMAN	xi59g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1 L2 L1 repetitive element;
10920	23439	36460	2.02	5.0E-03	T49163.1	EST_HUMAN	y009e04.r1 Stragene placenta (#837225) Homo sapiens cDNA clone IMAGE:70888 5'
11212	23715		3.91	5.0E-03	BE048055.1	EST_HUMAN	iz46c04.y1 NCL_CGAP_Bm82 Homo sapiens cDNA clone IMAGE:2291622 5'
11872	25054		8.12	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12111	24372		21.73	5.0E-03	AF087263.1	NT	Brugia malayi Y chromosome marker
12217	24440		1.81	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12250	24481		1.78	5.0E-03	AA46597.1	EST_HUMAN	zx75g03.s1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14885 PROBABLE DIPHEENOL OXIDASE A2 COMPONENT ;
12283	24856		5.46	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:4252002 5'
12473	24598	30883	2.21	5.0E-03	AW449109.1	EST_HUMAN	UI-H-B13-alk-4-08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
12488	24632		1.42	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
253	12913	25397	2.58	4.0E-03	AW500198.1	EST_HUMAN	UI-HF-BN0-alk-h-04-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
343	12995	25480	1.77	4.0E-03	R46482.1	EST_HUMAN	y51e04.s1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:35988 3'
488	13101	25594	0.89	4.0E-03	P54875	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
628	13256	25730	3.12	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582566 3'
910	13523	26043	1.75	4.0E-03	R46482.1	EST_HUMAN	y51e04.s1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:35988 3'
944	13557		3.19	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-r01 BT0333 Homo sapiens cDNA
1180	13781	26302	25.81	4.0E-03	AA089777.1	EST_HUMAN	z81e08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510898 5'
1211	13811	26325	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1346	13941	26463	1.4	4.0E-03	AA284374.1	EST_HUMAN	z559a01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1830	14222		1.08	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB08 5'
1778	14369	26913	2.74	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and efferent-limbic associated protein AT1-48 mRNA, complete cds
2082	14842	27217	14.12	4.0E-03	AA089777.1	EST_HUMAN	z81e08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510898 5'
2289	14863		1.62	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2317	14889	27484	2.63	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15170	27737	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2608	15170	27738	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2715	15272	27838	3.14	4.0E-03	AJ277385.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2715	15272	27839	3.14	4.0E-03	AJ277385.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2721	15277	27842	1.25	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3262	15874	28355	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3262	15874	28356	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3583	16187	28688	0.85	4.0E-03	AW188428.1	EST_HUMAN	X98F04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685279 3'
3583	16187	28670	0.85	4.0E-03	AW188428.1	EST_HUMAN	X98F04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685279 3'
3685	16286	28755	0.63	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3686	16287	28787	0.63	4.0E-03	AV648253.1	EST_HUMAN	AV648253 GLC Homo sapiens cDNA clone GLCADO2 3'
4087	16883		1.93	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
4323	16909	28350	1.88	4.0E-03	AJ768727.1	EST_HUMAN	w87a08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400274 3'
5307	17699	30291	2.1	4.0E-03	AW103719.1	EST_HUMAN	x83d03.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614489 3' similar to contains L1.11 L1 L1 repetitive element;
5354	17814	30328	1.17	4.0E-03	AA698985.1	EST_HUMAN	z189b01.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5433	17888	30395	1.19	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5480	18114	30523	1.36	4.0E-03	AF005859.1	NT	Drosophila melanogaster anion2D7 (anion2D7) mRNA, complete cds
5598	18228	30873	21.16	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5683	18585	31319	3.31	4.0E-03	P04188	SWISSPROT	(HPRG)
5965	18597	31321	1.58	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZYTE ANTIGEN PRECURSOR
6042	18661	31400	0.97	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7811014_11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7811014 5'
6235	18844		3.41	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6381	18985	31765	0.98	4.0E-03	AW580572.1	EST_HUMAN	hp48d07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2848852 3'
6451	19032	31837	1.95	4.0E-03	BE48463.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481954 5'
6775	19397	32179	1.04	4.0E-03	AA813222.1	EST_HUMAN	ap32111.s1 Soares testis_NHT Homo sapiens cDNA clone 1392045 3'
6872	19608	32440	1.51	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
7130	19470	32286	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7130	19470	32289	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7249	19778	32633	5.45	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7459	19982	32847	1.14	4.0E-03	AI681483.1	EST_HUMAN	537g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7461	19984	32849	0.96	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7883	20425	33334	0.63	4.0E-03	Q81T82	SWISSPROT	ADAM-TS 6 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
7982	20534	33438	4.22	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8145	20888	33568	1.94	4.0E-03	7682067	NT	Dictyostellium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8848	21187	34105	6.80	4.0E-03	AI553983.1	EST_HUMAN	9e49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
8821	21360		4.46	4.0E-03	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8830	21369	34293	3.12	4.0E-03	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9840	22338	35319	0.78	4.0E-03	U30864.1	EST_HUMAN	YP42g12.11 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190160 5'
10278	22773	35762	0.7	4.0E-03	AL181655.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11008	23523	36557	6.06	4.0E-03	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C008
11393	23845	36909	1.89	4.0E-03	AI208703.1	EST_HUMAN	gg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11393	23845	36910	1.89	4.0E-03	AI208703.1	EST_HUMAN	gg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11807	24050	37116	1.62	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 69 of the complete genome
11938	25071		10.45	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180900-002-b08 BN0138 Homo sapiens cDNA
11962	24284		1.62	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12047	24331		2.71	4.0E-03	AW504273.1	EST_HUMAN	UJHF-BN0-alp-p-04-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12284	24493		3.86	4.0E-03	BF224125.1	EST_HUMAN	7q74c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12341	24975		2.24	4.0E-03	AW614586.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element
12352	24532		3.01	4.0E-03	AW618141.1	EST_HUMAN	LTR5 repetitive element;
394	13040	25531	1.73	3.0E-03	AF011920.1	NT	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
912	13325	26044	5.57	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1701	14284	26828	2.85	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2298	14871		1.78	3.0E-03	AF055066.1	NT	nc73c05.s1 NCI_CGAP_Pt2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2333	14904		4.14	3.0E-03	Z32521.1	NT	Homo sapiens MHC class 1 region
2334	14805	27475	1.03	3.0E-03	U46858.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
2334	14805	27476	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2448	15015	27587	1.13	3.0E-03	AF240788.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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3022	15038		0.66	3.0E-03	Y09008.1	NT	Arabidopsis thaliana rpsM1 gene
3119	15733	28203	3.26	3.0E-03	BE376286.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609833 5'
3166	15768	28270	3.21	3.0E-03	AW602687.1	EST_HUMAN	IL2-UM0076-240300-056-003 UM0076 Homo sapiens cDNA
3464	16071	28544	2.13	3.0E-03	U34806.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3473	16076		7.31	3.0E-03	Y12900.1	NT	C.elegans semdc gene
4048	16946	29114	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4048	16946	29115	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4109	16703	28158	1.75	3.0E-03	AF792278.1	EST_HUMAN	af0409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4485	17070	28520	6.2	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4560	17143		0.71	3.0E-03	BE348739.1	EST_HUMAN	h166g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3161604 3'
4616	17169	28647	5.73	3.0E-03	AI638141.1	EST_HUMAN	ab18a08.x5 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4960	17535	28977	2.45	3.0E-03	AF32754.1	EST_HUMAN	801482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
4978	17553	29095	6.1	3.0E-03	BE787945.1	EST_HUMAN	Oryctolagus cuniculus sod gene
5069	17642	30064	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus cuniculus sod gene
5069	17642	30085	1.01	3.0E-03	AJ007044.1	NT	Homo sapiens hypodermic protein FLJ10539 (FLJ10539), mRNA
6470	18104	30423	3.56	3.0E-03	8922499	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
6744	18370	31078	1.18	3.0E-03	AJ246881.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
5809	18434	31155	13.97	3.0E-03	U35323.1	NT	Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6870	19268	32070	10.41	3.0E-03	AA458701.1	EST_HUMAN	Kluyveromyces marxianus pcp3 gene for purine-cytosine permease
7256	18764	32640	1.45	3.0E-03	AJ011419.1	NT	Oryza sativa gene for bZIP protein, complete cds
7531	20051	32824	3.37	3.0E-03	AB021736.1	NT	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7879	20421	33329	0.91	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7879	20421	33330	0.91	3.0E-03	BF333058.1	EST_HUMAN	z027004.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8097	20638	33549	4.71	3.0E-03	N92560.1	EST_HUMAN	S. cerevisiae UGA35 gene, complete cds
8257	20798		0.55	3.0E-03	ME3408.1	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8397	20937	33890	1.11	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C088
8419	20959	33877	1.31	3.0E-03	AL163268.2	NT	NONSTRUCTURAL PROTEIN V
8522	21061		1.37	3.0E-03	QB081	SWISSPROT	h180710.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.1 L1 repetitive element;
8922	21480		12.62	3.0E-03	AW613774.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8976	21613	34436	4.44	3.0E-03	AL161589.2	NT	

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8999	21536	34468	6.98	3.0E-03	AI019731.1	EST_HUMAN	0x03d12x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1
9008	21545	34474	0.92	3.0E-03	BF38078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9330	21844		1	3.0E-03	D00901.1	NT	602035880F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183838 5'
9368	20307	33210	0.96	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271800-402289
9554	22054		0.87	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071289-003-407 HT0344 Homo sapiens cDNA
9623	22123		5.92	3.0E-03	P08672	SWISSPROT	POL POLYPROTEIN[CONTAINS; PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPROTEIN[CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
9809	22307	35291	1.58	3.0E-03	P11369	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9907	22404	35379	1.3	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C103
10048	22541	35538	3.98	3.0E-03	AL163303.2	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
10728	23254		4.26	3.0E-03	5903028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11267	23787	36843	2.21	3.0E-03	AF009222.1	NT	Pneumocystis carinii kedin-like serine endoprotease mRNA, partial cds
11321	23019	36028	1.99	3.0E-03	AF268285.1	NT	Homo sapiens gadin-like protein (GLP) gene, complete cds
11354	23508	36867	3.96	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11354	23608	36868	3.98	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11707	24869		2.32	3.0E-03	AI525056.1	EST_HUMAN	promina-5.E07.7 bytumor Homo sapiens cDNA 5'
11743	24142	36783	1.31	3.0E-03	AA993154.1	EST_HUMAN	077b10.s1 Soares_tet_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to
11804	25007		1.81	3.0E-03	AB006888.1	NT	contains L1.03 MER26 repetitive element;
11868	24298	30984	2.67	3.0E-03	AJ268282.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
541	13172	25651	0.8	2.0E-03	Q04652	SWISSPROT	Rattus norvegicus mRNA for connexin38 (cx38 gene)
541	13172	25652	0.9	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
818	15429		11.05	2.0E-03	T70874.1	EST_HUMAN	RING CANAL PROTEIN (KELCH PROTEIN)
1407	14000	26526	2.25	2.0E-03	M20763.1	NT	Yd15h03.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:108341 5'
1410	14003	26531	1.35	2.0E-03	AA661605.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1418	14011	26540	20.86	2.0E-03	AF284446.1	NT	nu88f01.s1 NCL_CGAP_Am1 Homo sapiens cDNA clone IMAGE:1217593
							Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN
1638	14128	26664	1.04	2.0E-03	P48509	SWISSPROT	SFA-1) (CD151 ANTIGEN)
							Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1663	14155	26686	2.05	2.0E-03	4557836	NT	type VI) (PLOD) mRNA
1663	14166	26687	2.05	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1636	14227		5.58	2.0E-03	P28400	SWISSPROT	type VI) (PLOD) mRNA
							COLLAGEN ALPHA 5(V) CHAIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1807	14397	26942	1.01	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_tctat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1922	14507		0.89	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-061089-018-003 HT0183 Homo sapiens cDNA
2038	14820	27188	1.25	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2291	14885	27440	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2816	15177		4.13	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3463	16070	28543	4.95	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_tctat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3470	16078	28549	0.76	2.0E-03	BF568955.1	EST_HUMAN	602183680T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3728	16330	28798	6.87	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, QDB2 and RING8, 9, 13 and 14 genes
4024	16922	28084	0.89	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4191	16780	29228	2.48	2.0E-03	P03374	SWISSPROT	ENV POLYPEPTIDE [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4302	16888		12.85	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4502	17088		1.08	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4518	17102		1.34	2.0E-03	AW287380.1	EST_HUMAN	UI-H-BW0-aii-g-03-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4523	17107	28553	0.86	2.0E-03	AI084748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4844	17228	29880	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlight class 2 (shs) mRNA, complete cds
4844	17228	29881	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlight class 2 (shs) mRNA, complete cds
4821	17399		1.92	2.0E-03	R87773.1	EST_HUMAN	yc45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180880 3'
4948	17428	29878	5.2	2.0E-03	AA809488.1	EST_HUMAN	dt4f05.s1 Soares_NFL_Y_GBC_S1 Homo sapiens cDNA clone IMAGE:1523457 3'
5167	17736	30163	0.81	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5428	17985		0.9	2.0E-03	AF205087.1	NT	Desulfotribio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds
5678	18305	30767	1.16	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5810	24749	31158	2.28	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0893 protein, partial cds
5887	18510	31238	2.11	2.0E-03	U63711.1	NT	Xenopus laevis xefilin mRNA, complete cds
6258	18867	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6258	18867	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6488	19087	31869	2.38	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI)
6488	19087	31870	2.39	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI)
6488	19089	31872	7	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19121	31912	2.17	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6546	19144	31940	1.48	2.0E-03	X84451.1	NT	L. esculentum mRNA for lysyl-RNA synthetase (LysRS)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6715	18309		2.03	2.0E-03	AI991089.1	EST_HUMAN	wu38h09.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL28 HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element;
7038	18058	30480	0.89	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7104	18674	32513	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMIGC fusion partner (LHFP) mRNA
7104	18674	32514	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMIGC fusion partner (LHFP) mRNA
7141	18521	32343	3.59	2.0E-03	BE087866.1	EST_HUMAN	CMA4-BT0368-061299-054-d01 BT0368 Homo sapiens cDNA
7168	19728	32580	0.7	2.0E-03	AL289883.1	EST_HUMAN	qin89d11.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898985 3'
7335	18862	32728	0.87	2.0E-03	T88569.1	EST_HUMAN	yd77g10.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:114308 5'
7613	20128	33003	1.49	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7685	20537	33440	2.47	2.0E-03	AW582004.1	EST_HUMAN	hf37b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY.;
8159	20700	33614	5.98	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element;
8159	20700	33615	5.98	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element;
8208	20749	33682	0.52	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME 1
8228	20769	33688	0.94	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8282	20823	33743	0.82	2.0E-03	6005855	NT	Homo sapiens Ratine-derived POU-domain factor-1 (RPF-1), mRNA
8282	20823	33744	0.82	2.0E-03	6005856	NT	Homo sapiens Ratine-derived POU-domain factor-1 (RPF-1), mRNA
8307	20848	33771	0.8	2.0E-03	AU136878.1	EST_HUMAN	AU136878 PLACE1 Homo sapiens cDNA clone IMAGE:1094639 5'
8358	20898		2.04	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8123	18508	31233	0.89	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-602 UM0025 Homo sapiens cDNA
8123	18508	31234	0.69	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-602 UM0025 Homo sapiens cDNA
8164	21899	34843	0.85	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8445	21871	34920	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194288 3'
8445	21871	34921	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194288 3'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEH) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9477	21876	34823	2.57	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35049	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35050	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9839	22139	35106	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9839	22139	35106	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9828	22327	35308	0.99	2.0E-03	AW894289.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
9855	22450		4.55	2.0E-03	AA251376.1	EST_HUMAN	ze10e08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684764 3'
10894	23415		3.24	2.0E-03	M86524.1	NT	Human dystrophin gene
11361	20128	33003	2.13	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11417	23868		2.25	2.0E-03	BF330809.1	EST_HUMAN	RC9-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11424	23875	36839	13.97	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
11687	24103		3.17	2.0E-03	AB25745.1	EST_HUMAN	Y65h03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
11705	24118	37151	4.77	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
11730	24135	37155	1.94	2.0E-03	AD84325.1	EST_HUMAN	oy43g08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1688634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR. ;
11754	18032		8.98	2.0E-03	AJ245167.1	NT	Camelus dromedarius ehv19 gene for immunoglobulin heavy chain variable region
11867	25050		2.34	2.0E-03	AV697868.1	EST_HUMAN	AV697868 GK6 Homo sapiens cDNA clone GK6GX05 6'
12062	24345	30684	1.49	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12372	24542		2.06	2.0E-03	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT6, G6h, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12551	24849		5.07	2.0E-03	AV697868.1	EST_HUMAN	AV697868 GK6 Homo sapiens cDNA clone GK6GX05 5'
494	13098	25589	1.33	1.0E-03	H86471.1	EST_HUMAN	ye8c08.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
862	13477	25992	1.47	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRBT Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN ENOYL-COA HYDRATASE. ;
862	13477	25993	1.47	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRBT Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN ENOYL-COA HYDRATASE. ;
1134	13737	26246	2.21	1.0E-03	AB65788.1	EST_HUMAN	wk86a09.x1 NCL_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2422259 3'
1154	13757	26267	1.31	1.0E-03	AB54572.1	EST_HUMAN	wk83a10.x1 NCL_CGAP_Med15 Homo sapiens cDNA clone IMAGE:2561242 3'
1208	13808	26321	1.87	1.0E-03	AB692618.1	EST_HUMAN	wk86a01.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2074	14654	27227	4.05	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2199	14775	27348	9.99	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3008	15624	28102	1.45	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1261 protein, partial cds
3225	15837	28315	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

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3225	15837	28318	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3341	15951	28427	0.79	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3398	16200	28683	0.65	1.0E-03	U69061.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3398	16200	28684	0.65	1.0E-03	U69061.1	NT	Human MUC2 gene, promoter region
3727	16328		1.31	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
3987	16595	29087	0.75	1.0E-03	AW170552.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4008	16608	29080	0.81	1.0E-03	Z49649.1	NT	Contains TAR1.11 TAR1 repetitive element;
4528	17112	29558	4.29	1.0E-03	BE939182.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR149w
4574	17157	29601	5.77	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4770	17361	29803	0.83	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4950	17525	29966	2.83	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840282 3'
4950	17525	29967	2.83	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840282 3'
4951	17528		5.92	1.0E-03	BE154087.1	EST_HUMAN	PMO-HT0339-200400-010-002 HT0339 Homo sapiens cDNA
5238	17800	30219	11.45	1.0E-03	O48408	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5511	18144	30556	2.02	1.0E-03	AA290851.1	EST_HUMAN	zs44f01.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5598	18228	30678	2.74	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5647	18276	30749	1.7	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5647	18276	30750	1.7	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5761	18387	31101	0.92	1.0E-03	BE796491.1	EST_HUMAN	301569841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5768	18392	31105	1.72	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
6171	18783		2.82	1.0E-03	X07689.1	NT	Mouse nucleolin gene
6209	18819	31560	1.1	1.0E-03	BE963939.2	EST_HUMAN	301657518R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875683 3'
6338	18945		8.29	1.0E-03	11628178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6476	19077	31860	1.21	1.0E-03	T67761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116772 5'
6541	19140		1.4	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6852	19441	32266	1.31	1.0E-03	L77670.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7208	19737	32560	2.48	1.0E-03	D16828.1	NT	Human gene for fourth somatostatin receptor subtype
7498	20021		1.72	1.0E-03	AJ228042.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7635	20147	33030	1.7	1.0E-03	U62111.2	NT	Homo sapiens X28 region near ALO locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrioleukodystrophy protein >

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7684	20203	33090	3.21	1.0E-03	M83376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7734	20242	33133	1.13	1.0E-03	BE880044.1	EST_HUMAN	801491081F1 NIH_MGC_80 Homo sapiens cDNA clone IMAGE:3893278 5'
7830	20372	33279	0.57	1.0E-03	AF274591.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7891	20433	33342	6.79	1.0E-03	AJ251973.1	NT	Homo sapiens partial stearin-1 gene
8088	20827	33541	1.29	1.0E-03	AA122270.1	EST_HUMAN	zh87cd08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.L1 repetitive element:
8186	20727	33639	2.03	1.0E-03	AF163980.1	NT	Homo sapiens exocytosis-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8369	20908	33828	0.81	1.0E-03	U28387.1	NT	Rattus norvegicus plasma membrane Ca2+-ATPase isoform 3 (PMCA3) gene, 5' flanking region
8530	21069	33988	0.52	1.0E-03	AA001813.1	EST_HUMAN	zh82e08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8530	21069	33989	0.52	1.0E-03	AA001813.1	EST_HUMAN	zh82e08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8873	21412		1.29	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxopsin
8900	21438	34381	0.59	1.0E-03	AW840353.1	EST_HUMAN	CH3-LT0078-170200-092-607 LT0078 Homo sapiens cDNA
9009	21546						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9047	21884	34514	0.69	1.0E-03	U52111.2	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9047	21884	34515	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9525	22025	34982	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,8-galactosidase (aglA) gene, complete cds
9525	22025	34983	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,8-galactosidase (aglA) gene, complete cds
9734	22232	35210	0.94	1.0E-03	Q01128	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10068	22563	35558	0.57	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10073	22568		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10218	22713	35705	1.25	1.0E-03	AI024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1943175 3' similar to contains MER39.b1
10545	23082	36095	1.71	1.0E-03	AW362393.1	EST_HUMAN	MER39 MER39 repetitive element:
10545	23082	36096	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-181089-011-609 CT0278 Homo sapiens cDNA
10628	23161	36173	3.2	1.0E-03	BE170859.1	EST_HUMAN	RC1-CT0278-181089-011-609 CT0278 Homo sapiens cDNA
10703	23232		3.19	1.0E-03	AI583847.1	EST_HUMAN	QV3-HT0543-220300-130-603 HT0543 Homo sapiens cDNA
11036	23550		3.78	1.0E-03	AV758949.1	EST_HUMAN	tr73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248448 3' similar to TR-Q28195 Q28195 PVA1 GENE:
11882	24089	37149	4.46	1.0E-03	BE894488.1	EST_HUMAN	AV758949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12149	24392	30974	1.27	1.0E-03	9507208	NT	601433081F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
							Rattus norvegicus transformation related protein 63 (Trp63), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12175	25030		5.89	1.0E-03	A047355.1	EST_HUMAN	tc05h11.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12292	25052	30510	5.72	1.0E-03	BE780572.1	EST_HUMAN	601488878F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3872035 5'
6882	18484		1.83	9.0E-04	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6812	19209	32017	1.08	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9561	22061		1.56	9.0E-04	AE037203.1	NT	Glycylhistidyl glucosyltransferase mRNA for beta-amylin synthase, complete cds
1635	14127		1.05	8.0E-04	X08489.1	NT	Xlaevis mRNA for C4SR protein
4259	16845		5.17	8.0E-04	P08847	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4880	17455	28808	2.55	8.0E-04	U28785.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11024	23638		2.15	8.0E-04	AA777084.1	EST_HUMAN	zf24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11176	23682		2.5	8.0E-04	AI571089.1	EST_HUMAN	ln85608.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
12500	24828	30882	1.65	8.0E-04	AW878954.1	EST_HUMAN	PM2-H-T0353-130100-002-110 HT0353 Homo sapiens cDNA
1887	14453	27012	0.99	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2442	15008	27681	0.92	7.0E-04	U28785.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2739	15284	27681	1.75	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3319	15928	28406	1.23	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
6246	18855	31628	0.75	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:839718 similar to contains L1.b3 L1 L1 repetitive element;
8838	19232		2.83	7.0E-04	AI769331.1	EST_HUMAN	wg36108.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387209 3'
7279	19807		0.79	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
9718	22217	35191	0.57	7.0E-04	PI3487	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9719	22217	35192	0.57	7.0E-04	PI3497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11440	23690		3.42	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11463	23913	36580	2.68	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12222	24443		11.57	7.0E-04	BE077941.1	EST_HUMAN	GMT-8T0814-110300-142-b12 BT0814 Homo sapiens cDNA
12472	24597		4.94	7.0E-04	R17338.1	EST_HUMAN	y913c06.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
12505	24628		7.87	7.0E-04	6005856	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2720	15278		0.93	6.0E-04	BF341380.1	EST_HUMAN	802013339F1 NCL CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4149287 5'
4033	16831	29100	1.61	6.0E-04	AI882525.1	EST_HUMAN	wf15a11.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4163	16754	29205	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4163	16754	29208	0.8	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4264	16950	29268	3.2	6.0E-04	U46983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4538	17122	28567	0.83	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-180200-011-f09 HT0560 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4538	17122	28568	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-180200-011-09 HT0550 Homo sapiens cDNA
5413	17970	30378	0.9	6.0E-04	AI908687.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
5413	17970	30380	0.9	6.0E-04	AI908687.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
7807	20350		3.04	6.0E-04	P48408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 6, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7958	20500		0.87	6.0E-04	H82947.1	EST_HUMAN	y84c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element;
8890	22387		3.74	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
8924	22420		0.77	6.0E-04	AI858286.1	EST_HUMAN	wf35g02.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426830 3'
8982	22487	35475	2.18	6.0E-04	BE006850.1	EST_HUMAN	RC2-BN0120-230400-012-h11 BN0120 Homo sapiens cDNA
10242	22737		0.84	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoele extracellular matrix protein precursor (ECM3) mRNA, complete cds
11358	23812	36872	2.9	6.0E-04	AJ28042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11441	23891	36956	5.11	6.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-aab-b-09-0-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11495	23944		2.28	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
11869	24928		3.55	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-201189-012-c05 HT0269 Homo sapiens cDNA
12671	24739		1.81	6.0E-04	AI817088.1	EST_HUMAN	wf76g11.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
679	13303	25785	8.64	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (QRF82)
1649	14141		1.88	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3480	16067	28540	1.53	5.0E-04	AA648931.1	EST_HUMAN	nk27e11.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3778	16378	28843	1.02	5.0E-04	Q6JUP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5654	18281	30770	1.98	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6740	19334	32141	6.37	5.0E-04	AA156080.1	EST_HUMAN	zo33b08.r1 Strategene cdon (#837204) Homo sapiens cDNA clone IMAGE:588683 5'
7411	19836	32801	18.91	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium alide, complete cds
7898	20440	33346	4.97	5.0E-04	AI188382.1	EST_HUMAN	qd13f08.x1 Soares_placenta_8w9weeks_2NbhP81c5W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51802_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN)/contains Alu repetitive element;
8245	20788	33705	0.91	5.0E-04	AA814519.1	EST_HUMAN	cb86a02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9201	21718	34862	1.37	5.0E-04	AA846645.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8283	21883	34840	0.6	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
8437	21963	34912	0.65	5.0E-04	P28126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
8927	22027	34988	4.43	5.0E-04	AW270838.1	EST_HUMAN	xx08402.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10855	23376		4.52	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
11559	18291	30770	11.05	5.0E-04	AF248054.1	NT	Bos taurus mitochondrial calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11631	18936	32801	1.84	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
11808	24857		3.21	5.0E-04	AA588513.1	EST_HUMAN	nf15h02.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12353	24883		1.77	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
415	13050		0.84	4.0E-04	BF241482.1	EST_HUMAN	60187634F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4104897 5'
701	13323	25810	1.12	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
880	13494	26012	1.48	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barbaled cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
880	13494	26013	1.48	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE. ;
1514	14108	26842	9.82	4.0E-04	AW753356.1	EST_HUMAN	as70b08.x1 Barbaled cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2130	14708	27260	1.59	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023401 CT0254 Homo sapiens cDNA
2178	14758		1.34	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2658	15215	27787	1.83	4.0E-04	O96816	SWISSPROT	DKFZp434D099_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D058 5'
3200	15812	28286	2.59	4.0E-04	AF281074.1	NT	SERPIN-2 (SILK GUM PROTEIN 2)
3405	16014	28493	0.58	4.0E-04	AV586824.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3935	16533		0.94	4.0E-04	AL163267.2	NT	AV586824 GKC Homo sapiens cDNA clone GKCFH07 5'
4415	17000	29442	3.2	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C087
4415	17000	29443	3.2	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
4635	17218	28671	1.94	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5249	17812	30235	8.04	4.0E-04	BE560860.1	EST_HUMAN	zn61c08.s1 Stratiogene muscle 837209 Homo sapiens cDNA clone IMAGE:562870 3'
7312	19840	32899	1.25	4.0E-04	P48442	SWISSPROT	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3878910 5'
7541	20061		2.42	4.0E-04	AL161568.2	NT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
8473	21013	33928	1.42	4.0E-04	BF240712.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8481	21020	33935	1.85	4.0E-04	N25507.1	EST_HUMAN	601875985F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4089700 5'
							y939e12.r1 Soares melanocyte 2NH1M Homo sapiens cDNA clone IMAGE:284142 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9608	22108	35070	2.79	4.0E-04	AD26869.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
9754	22252		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(al7) mRNA, alternatively spliced, complete cds
12180	24833		2.4	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
167	12830	25316	2.71	3.0E-04	AL119428.1	EST_HUMAN	DKFZp781J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781J221 5'
209	12870	25356	3.63	3.0E-04	P48259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
913	13528	26043	1.72	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1879	14485	27022	5.5	3.0E-04	AI282100.1	EST_HUMAN	q28d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1894	14478		1.08	3.0E-04	AB98874.1	EST_HUMAN	h23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3349	15988	28434	4.85	3.0E-04	P25147	SWISSPROT	INTERALIN B PRECURSOR
4038	16834	29103	3.07	3.0E-04	P48448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4131	16723		1.37	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4197	16758		1.14	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT001.4-310599-028 HT0014 Homo sapiens cDNA
4941	17516		5.05	3.0E-04	BE153778.1	EST_HUMAN	PIM0-HT0339-190200-007-q12 HT0339 Homo sapiens cDNA
5162	17731	30168	0.57	3.0E-04	Q08472	SWISSPROT	E1A-ASSOCIATED PROTEIN P300
6292	18900		5.83	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6909	18568	32395	1.87	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7680	20105	32881	1.04	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8202	20743	33656	6.76	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9834	22332	35313	1.46	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.l1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10080	22575	35570	0.5	3.0E-04	AI982139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w175a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10356	22850	35844	8.78	3.0E-04	AA781201.1	EST_HUMAN	q124g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); nc38e04.r1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
11758	25072	30514	3.55	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12140	24909	30713	4.29	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
12574	24871		3.54	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185.1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547L185 5'
187	12848	25333	1.23	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
504	13136	25624	2.88	2.0E-04	AU148707.1	EST_HUMAN	AU148707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
940	13553	26068	5.4	2.0E-04	M86524.1	NT	Human dystrophin gene
940	13553	26070	5.4	2.0E-04	M86524.1	NT	Human dystrophin gene
1221	13821		3.94	2.0E-04	AI288021.1	EST_HUMAN	q188a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1865052 3' similar to contains MER3.b2 MER3 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	13627		1.95	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1872	14458		1.12	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Plb3 gene
2227	14802		0.8	2.0E-04	AA478980.1	EST_HUMAN	z139b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element
2610	15172	27740	6.83	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, am38c08.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3016	15632	28108	1.13	2.0E-04	AI124529.1	EST_HUMAN	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3377	16886	28484	0.78	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3483	16888	28561	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA
3983	16581	28052	0.85	2.0E-04	AW878441.1	EST_HUMAN	EST390550 MAGI resequences, MAGP Homo sapiens cDNA
4224	16812		6.34	2.0E-04	U01029.1	NT	Phaeoselin vulgaris nitrate reductase (PNR2) gene, complete cds
4776	17357	28809	1.34	2.0E-04	H98265.1	EST_HUMAN	y010111.r1 Soares pineal gland_N3HPQ Homo sapiens cDNA clone IMAGE:232556 5'
4776	17357	28810	1.34	2.0E-04	H98265.1	EST_HUMAN	y010111.r1 Soares pineal gland_N3HPQ Homo sapiens cDNA clone IMAGE:232556 5'
4913	17488		1.79	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
6216	17780	30199	1.44	2.0E-04	AB037697.1	NT	Danio rerio hector gene, exon 1 to 6, partial cds
5733	18358	31065	1.92	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCUDH10 3'
5745	18371	31078	1.87	2.0E-04	AI690862.1	EST_HUMAN	tp03611.x1 NCI CGAP_U03 Homo sapiens cDNA clone IMAGE:2207709 3'
5824	18546	31272	0.87	2.0E-04	AA266652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6102	18718	31470	1.06	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6385	18989	31769	0.81	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7281	19809		2.44	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5'
7618	20129		13.08	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7626	20138	33017	1.26	2.0E-04	P64266	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7897	20439	33344	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7897	20439	33345	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8226	20767	33585	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8226	20767	33586	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8500	21039	33660	1.77	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21217	34137	0.56	2.0E-04	X67331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9257	21783	34736	0.47	2.0E-04	AA728700.1	EST_HUMAN	al22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9340	21854	34803	0.5	2.0E-04	P18175	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF28.1
9895	22382	35357	1.4	2.0E-04	BE148303.1	EST_HUMAN	RC3-HT0264-151089-011-505 HT0264 Homo sapiens cDNA
9930	22428	35400	2.39	2.0E-04	AA403777.1	EST_HUMAN	zu66c11.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742864 5'
10731	23257	36273	6.22	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11185	23680	36737	5.43	2.0E-04	AI440282.1	EST_HUMAN	ig01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
11303	23788	36854	2.72	2.0E-04	AW138740.1	EST_HUMAN	UIH-B1T-adm-c-04-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717180 3'
769	13416	25920	1.41	1.0E-04	H88846.1	EST_HUMAN	y26c09.s1 Soares_melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:282864 3' similar to contains L1.f1 L1 repetitive element;
1113	13717	26227	2.57	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1183	13768	26285	4.04	1.0E-04	AW013847.1	EST_HUMAN	UIH-B10-aab-e-06-Q-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1153	13756	26286	4.04	1.0E-04	AW013847.1	EST_HUMAN	UIH-B10-aab-e-06-Q-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1377	13970		3.95	1.0E-04	UG2918.1	NT	Anguilla anguilla dopamine D1A1 receptor (D1A1) gene, complete cds
1689	14262	26795	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1689	14262	26798	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1801	14486	27047	2.44	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2711	15268	27835	1.09	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176388 3'
2711	15268	27836	1.09	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176388 3'
3323	15933	28410	1.1	1.0E-04	Q82203	SWISSPROT	SPUCEOSOME ASSOCIATED PROTEIN 62 (SAP 62) [SPLICING FACTOR 3A SUBUNIT 2] (SF3A66)
3798	16389	28894	2.7	1.0E-04	AI440282.1	EST_HUMAN	ig01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
4134	16726	28180	1.72	1.0E-04	MT4042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4168	16748	28201	1.27	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB004 3'
5263	17825	30250	0.95	1.0E-04	AB57156.1	EST_HUMAN	q62h04.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005875 3'
6021	18640	31380	1.5	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6598	19166	31682	0.97	1.0E-04	AA177111.1	EST_HUMAN	nc02a12.s1 NCL_CGAP_P33 Homo sapiens cDNA clone IMAGE:262

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6925	19584	32414	0.76	1.0E-04	AA584561.1	EST_HUMAN	n126a04.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:863486 3' similar to gb:M97262
7237	19767	32823	14.08	1.0E-04	A1261980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7672	19767	32823	14.23	1.0E-04	A1261980.1	EST_HUMAN	qv67d10.x1 NCL CGAP_OV42 Homo sapiens cDNA clone IMAGE:1985683 3'
7837	20478	33389	1.02	1.0E-04	A4630463.1	EST_HUMAN	qv67d10.x1 NCL CGAP_OV42 Homo sapiens cDNA clone IMAGE:1985683 3'
8280	21766	34738	2.34	1.0E-04	A1808220.1	EST_HUMAN	ab94g08.s1 Stragane lung (8637210) Homo sapiens cDNA clone IMAGE:854654 3'
9270	21768	34745	1.71	1.0E-04	Q88969	SWISSPROT	wf26e08.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9348	21860		0.78	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9584	22094	35023	2.2	1.0E-04	10803976	NT	y472c08.r1 Scores fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:113774 5'
10081	22576		2.87	1.0E-04	P08647	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10116	22811	35601	0.83	1.0E-04	P08648	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11218	23721		2.08	1.0E-04	M28587.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11503	23952	37020	1.88	1.0E-04	A8032888.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11540	23988	37086	2.1	1.0E-04	AW269081.1	EST_HUMAN	Homo sapiens mRNA for KIAA1142 protein, partial cds
11570	24017	37087	1.87	1.0E-04	Q03698	SWISSPROT	xv49g12.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2818518 3'
11670	24092		1.57	1.0E-04	BE686788.1	EST_HUMAN	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11919	24878		1.99	1.0E-04	BE676396.1	EST_HUMAN	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
727	13347	25839	1.98	9.0E-05	AA718933.1	EST_HUMAN	CMO-CT0404-130700-476-h93 CT0404 Homo sapiens cDNA
2047	14928	27198	0.92	9.0E-05	AW866218.1	EST_HUMAN	7f28a10.x1 NCL CGAP_OV42 Homo sapiens cDNA clone IMAGE:3296058 3' similar to contains L1.13 L1
8117	18733	31488	1.45	9.0E-05	Q80716	SWISSPROT	repetitive element;
9397	21820		2.71	9.0E-05	D85606.1	NT	ab45c11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1292488 3'
9398	21822	34771	2.79	9.0E-05	AF120982.1	NT	QV4-SN0023-070400-168-b04 SN0023 Homo sapiens cDNA
11017	23531	36587	2.86	9.0E-05	AW073078.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11121	23629	36671	1.89	9.0E-05	A1267878.1	EST_HUMAN	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
11483	18733	31488	3.89	9.0E-05	Q80716	SWISSPROT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11974	24939		4.28	9.0E-05	AF129756.1	NT	xx34g05.x1 NCL CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
854	13470	25881	1.21	8.0E-05	A1251646.1	NT	repetitive element;
897	13811		9.89	8.0E-05	A1251646.1	NT	qv23f08.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
						SWISSPROT	MIR repetitive element;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
							Homo sapiens MSH55 gene, partial cds; and CLIC1; DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
							Pisum sativum mRNA for beta-1,3 glucanase (gna2 gene)
							Pisum sativum mRNA for beta-1,3 glucanase (gna2 gene)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15593		0.71	8.0E-05	M5375.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4579	17162	29804	1.87	8.0E-05	AW044603.1	EST_HUMAN	wy76a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8883	21222	34142	0.49	8.0E-05	Y11688.1	NT	Mus musculus gene for heparinase II, exon 1 (end joined CDS)
11030	23544	36381	2.32	8.0E-05	M69187.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12813	24921		2.72	8.0E-05	AA276333.1	EST_HUMAN	z88h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704583 3' similar to contains Alu repetitive element contains element MSR1 repetitive element
369	13018	25501	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
369	13018	25502	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
593	13223	25697	3.82	7.0E-05	L49076.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
593	13223	25698	3.82	7.0E-05	L49076.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1093	13698	26208	1.41	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2744	15299	27865	3.67	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3194	15808	28279	4.69	7.0E-05	AB009080.1	NT	Dicotyledon discaldehyde gene for TRFA, complete cds
4482	17048	28492	1.73	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4543	17127	28570	0.58	7.0E-05	U60980.1	NT	Ceanorhabditis elegans Skp1p homolog mRNA, complete cds
8167	20708	33924	1.11	7.0E-05	AA505582.1	EST_HUMAN	nh93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:988068 3'
9472	21871	34820	3.74	7.0E-05	T07086.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#830208) Homo sapiens cDNA clone HFBED80
11040	23554		7.96	7.0E-05	10835048	NT	Homo sapiens sacroglucan, epsilon (SGCE), mRNA
2073	14853	27225	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2073	14853	27226	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2824	15188	27753	1.34	6.0E-05	AI855241.1	EST_HUMAN	wb54h08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2709	15266	27833	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10
2709	15266	27834	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10
2840	13329	25815	2.88	6.0E-05	AF03830.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5352	17912	30327	1.3	6.0E-05	AW962309.1	EST_HUMAN	EST374382 MAGG resequences, MAGG Homo sapiens cDNA
6071	18688	31432	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6071	18688	31433	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6535	19135	31928	1.45	6.0E-05	N72828.1	EST_HUMAN	y505g11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:248212 5'
7013	19511	32332	0.79	6.0E-05	AA897880.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8028	20571	33475	0.97	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H08 BT0311 Homo sapiens cDNA
8028	20571	33476	0.97	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H08 BT0311 Homo sapiens cDNA

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8381	20921	33841	0.65	6.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8395	20925	33845	2.3	6.0E-05	AW896929.1	EST_HUMAN	PM4-NN0030-310300-001-F10 NN0050 Homo sapiens cDNA
8516	21055	33978	0.82	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DEACY-ACCELERATING FACTOR PRECURSOR
9176	21753	34698	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9178	21753	34700	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9440	21968	34915	1.13	6.0E-05	T94149.1	EST_HUMAN	y628c12.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
9837	22137	35103	0.57	6.0E-05	AW627885.1	EST_HUMAN	hi37a03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10627	23159	36172	3.98	6.0E-05	R75639.1	EST_HUMAN	y69d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
11394	23848	36911	4.18	6.0E-05	AA044015.1	EST_HUMAN	zk58f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12183	24918	30716	10.28	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-F09 NT0038 Homo sapiens cDNA
1449	14041	26589	18.37	6.0E-05	AW392088.1	EST_HUMAN	QV4-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA
1903	14488		1.75	6.0E-05	8923891	NT	Homo sapiens 22kDa peroxidase membrane protein-like (LOC55886), mRNA
4051	16848	29116	3.89	6.0E-05	AJ251894.1	NT	Homo sapiens partial SL C22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5718	18342	30848	11.28	6.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6144	18758	31516	2.97	6.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA08 3'
6316	18923	31700	0.97	6.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7370	19698		1.22	6.0E-05	AB037864.1	NT	Mus musculus gene for calretinin, exon 1
11971	24460		5.73	6.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12249	24460		9.18	6.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2833	12908		3.49	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4590	17163	26605	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4580	17163	26606	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5166	17735	30182	0.58	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7020	19518	32340	0.76	4.0E-05	U01947.1	NT	Micaca mulatta haptoglobin (HP) gene, 5' region
9442	21968		7.28	4.0E-05	AF202835.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
9912	22408	35384	0.55	4.0E-05	P11369	SWISSPROT	ENDONUCLEASE
10305	22769	35790	0.73	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)(ACID BETA-GALACTOSIDASE)
10848	23180	36193	5.05	4.0E-05	AW627948.1	EST_HUMAN	hi36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974390 3' similar to contains element MIR repetitive element;
11850	24210	31041	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
11929	24204		1.38	4.0E-05	AW117580.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
709	13330	25817	0.64	3.0E-05	AI248061.1	EST_HUMAN	qh84c10.x1 Soares_fetal_liver_aplees_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1097	13702	26212	1.49	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1170	13772	26260	1.51	3.0E-05	BF037898.1	EST_HUMAN	601481463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3885142 5'
1170	13772	26261	1.51	3.0E-05	BF037898.1	EST_HUMAN	601481463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3885142 5'
2748	15301	27887	1.17	3.0E-05	Q62234	SWISSPROT	SKLEMIN
3331	15941						q91g11.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4471	17057	29503	0.69	3.0E-05	AI288919.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN. ;
4471	17057	29503	7.22	3.0E-05	BE199211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4955	17148	29504	7.22	3.0E-05	BE168211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4955	17148	29504	1.09	3.0E-05	AA388679.1	EST_HUMAN	EST76996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4565	17148	29505	1.06	3.0E-05	AA388679.1	EST_HUMAN	EST76996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4692	17274		0.71	3.0E-05	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4728	17307	28751	0.75	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4963	13330	25817	0.65	3.0E-05	AI248061.1	EST_HUMAN	qh84c10.x1 Soares_fetal_liver_aplees_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
5748	18372	31080	1.73	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myc2p), mRNA
6854	19442	32257	1.28	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6854	19442	32258	1.28	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7639	20381	33286	1.9	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8263	20334	33756	1.29	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8824	21963	34288	1.78	3.0E-05	AW770982.1	EST_HUMAN	h194608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
8928	21387	34261	1.22	3.0E-05		NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8932	21371	34286	0.47	3.0E-05	P43391	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9058	21595		0.88	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9244	21770	34718	1.3	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9581	22081		2.97	3.0E-05	AI769331.1	EST_HUMAN	wg36709.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10428	22922	35925	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10428	22922	35926	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12055	24338		1.48	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12387	25101		1.52	3.0E-05	AW518689.1	EST_HUMAN	xs83d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2778811 3'
2362	14933	27506	1.55	2.0E-05	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
2619	15181	27747	10.26	2.0E-05	MI13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2738	15283		6.78	2.0E-05	AA180562.1	EST_HUMAN	zq48a12.r1 Sryetogene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
3171	15785	28257	1.59	2.0E-05	BE068036.1	EST_HUMAN	RC3-BT0319-120200-014-008 BT0319 Homo sapiens cDNA
3391	15989	28477	0.63	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3418	16024	28506	1.04	2.0E-05	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
3541	16146		0.72	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3880	16478		0.87	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681084_r1 568 (synonym: hfxd2) Homo sapiens cDNA clone DKFZp5681084 5'
5010	17383	30028	0.63	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5178	17743		2.42	2.0E-05	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5933	18555	31282	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6125	18740	31492	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6125	18740	31493	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6305	18912	31886	0.73	2.0E-05	AJ149272.1	EST_HUMAN	qc72a2.x1 Soares_placenta_8t6weeks_2NbpHP8b6W Homo sapiens cDNA clone IMAGE:1715114 3'
6738	19330	32136	2.12	2.0E-05	AA714330.1	EST_HUMAN	mw08a12.x1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6982	19480	32301	2.2	2.0E-05	Y08928.1	NT	P.falciparum mRNA for AARP1 protein, partial
6984	19492	32313	1.34	2.0E-05	AJ492960.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711
7002	19500		8.08	2.0E-05	AI881025.1	EST_HUMAN	Q02711 PRO-POL-DUTPASE POLYPROTEIN ;
							wu35h07.x1 Soares_Dieckgrafe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7207	19738	32591	2.2	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7207	19738	32592	2.2	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7403	19928		0.91	2.0E-05	AF128947.1	NT	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
7826	20368	33276	1.41	2.0E-05	AJ381040.1	EST_HUMAN	ig20h05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2108369 3'
9191	21708	34651	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9191	21708	34652	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9837	22335	35317	0.48	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10041	22638	35532	0.74	2.0E-05	BF056939.1	EST_HUMAN	7175g09.y1 NCI_CGAP_Bn20 Homo sapiens cDNA clone IMAGE:3340576 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10482	22878	35984	2.82	2.0E-05	N41751.1	EST_HUMAN	yw01a06.r1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10482	22878	35985	2.82	2.0E-05	N41751.1	EST_HUMAN	yw01a06.r1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10524	19500		2.44	2.0E-05	A1891025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgrafe_colon_NHOD Homo sapiens cDNA clone IMAGE:2522077 3'
11327	23025	36034	2.74	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11983	24844		4.91	2.0E-05	BE348228.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2;
12080	25018		13.02	2.0E-05	AW074604.1	EST_HUMAN	xa88a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element;
12144	24831		2.54	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12955	24727		2.35	2.0E-05	A1200970.1	EST_HUMAN	qf88g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1756236 3'
2719	15475	27841	1.45	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3711	16312	28780	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lamba 120 Suppressor of Hairless (Su(H)) gene, partial cds
4039	18637	28105	11.8	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LON
4262	18840	29289	0.98	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4364	16951	28391	1.89	1.0E-05	AA431119.1	EST_HUMAN	zw68g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781484 5'
4876	17550	28992	2.24	1.0E-05	AW418134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5395	17953		0.94	1.0E-05	A1733568.1	EST_HUMAN	os84d07.x3 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1610125 3' similar to contains Alu repetitive element;
5426	17983	30389	0.91	1.0E-05	L27595.1	NT	Mus musculus bradykinin B2 receptor (B2R) gene, complete cds
6848	19438	32252	1.32	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7140	19520	32342	3.98	1.0E-05	AA641848.1	EST_HUMAN	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.H1 L1 L1 repetitive element;
7142	18675	32515	14.32	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7655	20167	33054	0.76	1.0E-05	BF222848.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3849945 3' similar to contains MER10.b3 MER10 repetitive element;
7754	20282		2.22	1.0E-05	P18474	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8848	21385		2.56	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8990	21528	34457	2.18	1.0E-05	AA452578.1	EST_HUMAN	z6c5h12.s1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9211	21728	34871	13.74	1.0E-05	AA236110.1	EST_HUMAN	z3d5e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:884332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
9288	21888	34834	0.6	1.0E-05	AV732180.1	EST_HUMAN	AV732180 HTF Homo sapiens cDNA clone HTFBIH01 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9752	22260	35232	0.76	1.0E-05	AW510802.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFFR.H1 OFR repetitive element;
9762	22260	35233	0.76	1.0E-05	AW510802.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFFR.H1 OFR repetitive element;
9830	22328	35309	1.58	1.0E-05	AW281521.1	EST_HUMAN	UI-H-BI2-epk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9830	22328	35310	1.58	1.0E-05	AW281521.1	EST_HUMAN	UI-H-BI2-epk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10087	22582		1.73	1.0E-05	AW468985.1	EST_HUMAN	hd07e10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.L2 L1 repetitive element;
10789	23322	36332	2.32	1.0E-08	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10789	23322	36333	2.32	1.0E-08	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12493	25011	30616	1.67	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2696	15253	27824	4.74	9.0E-08	AI583811.1	EST_HUMAN	tt73a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248386 3'
3130	15744	28213	5.23	9.0E-06	AI218983.1	EST_HUMAN	gg11b08.x1 Soares_placenta_8to9weeks_2Nbl-P8b8W Homo sapiens cDNA clone IMAGE:1759181 3'
3870	18271		3.37	9.0E-08	M81755.1	NT	Human diaphanous-related protein 1 (DPR1) gene, exons 1 and 2
6064	18881	31423	2.25	9.0E-06	L23418.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6947	19524	32346	0.84	9.0E-08	BE085042.1	EST_HUMAN	RC1-BT0313-110500-017-g07 BT0313 Homo sapiens cDNA
7468	19888	32853	0.85	9.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7751	20259	33166	12.47	9.0E-06	AI034370.1	EST_HUMAN	ox20q01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1856912 3' similar to contains Alu repetitive element;
8400	20940	33853	1.18	9.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8813	21451	34372	2.48	9.0E-08	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8813	21451	34373	2.48	9.0E-08	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9149	21884	34828	4.6	9.0E-08	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10818	23339	36353	3.76	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2569	15489	27701	1.48	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
10424	22918	35918	0.84	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10424	22918	35920	0.84	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1015	13825		1.71	7.0E-06	AA889728.1	EST_HUMAN	ab00110.a1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1487	14080	28819	3.38	7.0E-06	7882177	NT	MER20.11 MER20 repetitive element ; Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2177	14754	27324	1.55	7.0E-06	AW593215.1	EST_HUMAN	hg11b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845278 3' similar to gb:X82048_cds1 WEE1-LIKE PROTEIN KINASE (HUMAN);
2897	15514		7.94	7.0E-06	AI368252.1	EST_HUMAN	qw18g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1881286 3' similar to contains Alu repetitive element;
3820	16223		1	7.0E-06	AA385542.1	EST_HUMAN	EST186205 Thyrid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5874	18498		5.81	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0082-250400-173-H01 OT0082 Homo sapiens cDNA
5872	18593	31327	0.94	7.0E-06	N98845.1	EST_HUMAN	y95507.1 Soares_multiple_sclerosis_2N5bHMSP Homo sapiens cDNA clone IMAGE:278412 5'
8724	21283	34183	0.72	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
8814	22312		2.32	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11710	25043	30508	1.82	7.0E-06	BF215972.1	EST_HUMAN	801881622F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4083972 5'
2942	15558	28032	1.29	8.0E-06	BE089188.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4865	15584	28085	2.03	8.0E-06	Q01458	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4875	17450	28901	1.47	8.0E-06	AI040099.1	EST_HUMAN	ac08602.x1 Soares_fetal_liver_epilepsy_INFLS_S1 Homo sapiens cDNA clone IMAGE:1865738 3' similar to contains MER8.12 MER8 repetitive element ;
5552	18184	30589	1.3	8.0E-06	AF187441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5605	18234	30685	1.15	8.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9770	22268		1.87	8.0E-06	AW801912.1	EST_HUMAN	IL6-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12602	24888	30881	1.47	8.0E-06	11418157	NT	Homo sapiens cadmium channel, voltage-dependent, alpha 11 subunit (CAGNA11), mRNA
5361	17921	30335	1.02	5.0E-06	AL183268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6211	18821	31592	3.73	5.0E-06	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6479	19080	31883	2.04	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7284	19812	32688	1.11	5.0E-06	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds
10013	22508	35498	6.57	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10408	22800	35895	0.54	5.0E-06	P06881	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12482	24615	30890	13.8	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
875	13289	25780	8.05	4.0E-06	R18287.1	EST_HUMAN	y848c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
879	13493	26011	8.94	4.0E-06	AW103354.1	EST_HUMAN	xc88g12.x1 NCI_CGAP_Eco2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379	13972	28499	3.92	4.0E-06	AI934928.1	EST_HUMAN	ib33608.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2068168 3'
1379	13972	28500	3.92	4.0E-06	AI934928.1	EST_HUMAN	ib33608.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2068168 3'
1522	14114	28651	3.17	4.0E-06	BF395612.1	EST_HUMAN	QV2-NT0049-200800-250-H07 NT0048 Homo sapiens cDNA
2305	14878	27454	1.88	4.0E-06	AW016401.1	EST_HUMAN	U1H-B10-aut-f-05-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3099	15714	28168	1.26	4.0E-06	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
3983	18561	28030	1.35	4.0E-06	AW848285.1	EST_HUMAN	IL3-CT0214-150200-074-803 CT0214 Homo sapiens cDNA
4930	17505	29651	1.88	4.0E-06	AI895939.1	EST_HUMAN	wf94c10.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2432682 3' similar to contains element MER22 repetitive element:
5053	17628	30070	2.12	4.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
8438	20978	33890	0.53	4.0E-06	O16393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
8735	21274	34195	2.89	4.0E-06	AF008690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TORBV12S2 region
9824	22124	35088	1.11	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11324	23022	36031	3.84	4.0E-06	AB007855.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
2208	14784	27357	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_splice_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2208	14784	27358	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_splice_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2307	14878		1.54	3.0E-06	AF202635.1	NT	Homo sapiens PPI200 mRNA, complete cds
2948	15584	28038	1.02	3.0E-06	AA888218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408252 3' similar to contains LTR1.13 LTR1 repetitive element:
3304	15915		2.41	3.0E-06	AI857778.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN, contains L1.12 L1 repetitive element:
3851	18449	28911	1.08	3.0E-06	BE047094.1	EST_HUMAN	h984d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3851	18449	28912	1.08	3.0E-06	BE047094.1	EST_HUMAN	h984d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4573	17158	28600	0.88	3.0E-06	T50268.1	EST_HUMAN	y078b10.r1 Stratiogene ovary (8837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4881	17243	28697	4.82	3.0E-06	X54916.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
5045	17618	30083	0.94	3.0E-06	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
5045	17618	30084	0.94	3.0E-06	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
6308	18915	31689	0.78	3.0E-06	AU158412.1	EST_HUMAN	AU158412 THYROT1 Homo sapiens cDNA clone THYROT1001602 3'
7280	18808		2.79	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8027	20569	33473	0.72	3.0E-06	BE562984.1	EST_HUMAN	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3890314 5'
8818	21157	34070	0.88	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12162	24394		13.37	3.0E-08	AW385262.1	EST_HUMAN	RCO-LT0001-281189-011-A03 LT0001 Homo sapiens cDNA
216	12877		2.91	2.0E-08	P94368	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1814	14207		4.46	2.0E-08	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2418	14888	27560	2.2	2.0E-08	AI872138.1	EST_HUMAN	w804a03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30.b1 MER30 repetitive element;
2508	15070	27843	1.79	2.0E-08	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2601	15163	27731	1.34	2.0E-08	P08719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3570	16174	28656	1.04	2.0E-08	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3825	16425	28897	1.85	2.0E-08	AA173518.1	EST_HUMAN	ZP02605.r1 Strategene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:595232 5'
3836	16435	28897	0.83	2.0E-08	AW450215.1	EST_HUMAN	U1-H-B13-alky-g-05-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3'
3844	16443	28904	1.74	2.0E-08	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6239	18848		0.70	2.0E-08	AA974632.1	EST_HUMAN	on34h01.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:1868609 3' similar to contains Alu repetitive element;
6267	18875	31643	0.87	2.0E-08	AI539448.1	EST_HUMAN	ts51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080241 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
6570	19168	31965	4.94	2.0E-08	AI19424.1	EST_HUMAN	wj90b04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7658	20400		0.89	2.0E-08	AW669223.1	EST_HUMAN	MR3-SN0087-120400-002-f02 SN0087 Homo sapiens cDNA
8033	20575	33480	0.75	2.0E-08	T12238.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8770	21309		0.59	2.0E-08	AA772497.1	EST_HUMAN	Z127c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
8782	21321	34245	1.54	2.0E-08	H82051.1	EST_HUMAN	y437c04.r1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9143	21678	34621	0.91	2.0E-08	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9143	21678	34622	0.91	2.0E-08	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9817	22117	35080	0.72	2.0E-08	N30576.1	EST_HUMAN	yw69e03.s1 Soares_placenta_8to9weeks_2NbIP8to9W Homo sapiens cDNA clone IMAGE:257212 3'
9833	22331		0.83	2.0E-08	AV748968.1	EST_HUMAN	AV748968 NPC Homo sapiens cDNA clone NPCAXD05 5'
12052	26046	30508	1.01	2.0E-08	P23249	SWISSPROT	PROTEIN MOV-10
12210	24434		6.63	2.0E-08	BE326232.1	EST_HUMAN	hs9202.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144698 3' similar to contains L1.12 L1 repetitive element ;
36	12715	25174	1.77	1.0E-08	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
685	13309	25794	1.45	1.0E-08	AF084394.1	NT	Mus musculus DBMSE protein (D8Mm5e) mRNA, complete cds
1500	14062	26631	2.08	1.0E-08	P08125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1671	14184	26695	1.12	1.0E-08	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1827	14220		1.54	1.0E-08	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2037	14619	27186	8.38	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2037	14619	27187	8.38	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4459	17045	29488	14.7	1.0E-08	U07581.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5299	17831	30256	0.99	1.0E-08	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5299	17831	30257	0.99	1.0E-08	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5494	18128	30536	4.64	1.0E-08	BF33015.1	EST_HUMAN	MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA
5518	18150	30563	1.08	1.0E-08	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5518	18150	30564	1.08	1.0E-08	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5887	18284	30774	1.13	1.0E-08	C60813	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6954	19531	32359	5.98	1.0E-08	P02871	SWISSPROT	FIBRINOGEN ALPHA1A-E CHAIN PRECURSOR
7943	20486		0.68	1.0E-08	AA912823.1	EST_HUMAN	d28c08.s1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8216	20757	33671	1.21	1.0E-08	A1347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
8425	20985	33879	1.23	1.0E-08	A1287878.1	EST_HUMAN	qy23f06.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9228	21950	34899	0.98	1.0E-08	N74635.1	EST_HUMAN	MIR repetitive element;
9301	21901	34850	0.5	1.0E-08	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9600	22100	35082	3.34	1.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9600	22100	35083	3.34	1.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9843	22143	35111	4.38	1.0E-08	AA132811.1	EST_HUMAN	z017e08.f1 Strabagene cdon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9703	22202		3.84	1.0E-08	AA449257.1	EST_HUMAN	z04d11.s1 Scores_total_Nh2HF8_9w Homo sapiens cDNA clone IMAGE:765493 3' similar to
10382	22876		1.61	1.0E-08	AL163203.2	NT	gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11502	23951		8.24	1.0E-08	AW890941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12087	24356	30866	7.83	1.0E-08	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12185	14618	27186	1.67	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12195	14619	27187	1.67	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12803	14220		1.38	1.0E-08	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
383	13030	25518	2.01	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
383	13030	25519	2.01	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8346	20887		0.57	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11126	23634	36675	2.95	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4895	17460	28912	6.02	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4895	17460	28913	6.02	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6047	18698		7.49	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7944	20498		8.81	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11486	23635		8.73	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBEN89
11690	24106		7.99	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1908	14491	27052	1.14	7.0E-07	AF187341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5710	18336	30841	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5710	18336	30842	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
10842	23174	36186	1.59	7.0E-07	BE076848.1	EST_HUMAN	7133g01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286496 3' similar to TR:Q98897 Q98897
1956	14540	27098	2.56	8.0E-07	AW85558.1	EST_HUMAN	ENDOGENOUS RETROVIRUS-K, LTR U5 AND GAG GENE. ; CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2534	19098	27871	2.3	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes.>
4044	18642		1.76	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
8068	21605	34538	1.94	6.0E-07	BF001887.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L. ;
11825	24067	37131	1.83	6.0E-07	AF792950.1	EST_HUMAN	cm8705.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1554177 5'
11949	24989		2.85	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-260300-121-f12 NN1029 Homo sapiens cDNA
348	12989		1.19	5.0E-07	AI831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1095	13700		2.21	5.0E-07	AA380630.1	EST_HUMAN	EST183615 Supt cells Homo sapiens cDNA 5' end
3068	15681		0.64	5.0E-07	AI831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4751	17332	29775	1.32	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6268	18876	31644	1.13	5.0E-07	U65087.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7124	18494	32261	1.56	5.0E-07	AB393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7124	19484	32282	1.56	5.0E-07	AB393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7398	18912	32776	16.07	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:U15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8217	20758	33872	0.82	5.0E-07	Q8WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8427	20987		1.08	5.0E-07	P09583	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10270	22765	35752	4.46	5.0E-07	A080587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
10542	23079	36083	1.56	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11391	23843	36907	4.94	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11452	23902		2.43	5.0E-07	A1271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12391	24889		2.85	5.0E-07	AW982537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4071	16867	28128	1.94	4.0E-07	AW009602.1	EST_HUMAN	we84h05.x1 NCL CGAP_Oc3 Homo sapiens cDNA clone IMAGE:2504697 3'
7230	18761		0.88	4.0E-07	A1272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7311	19839	32697	1.35	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7311	19839	32698	1.35	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7863	20405	33312	0.65	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8981	21519	34445	5.37	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10228	22723	35715	0.5	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10817	23338	36351	4.05	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
10817	23338	36352	4.05	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
11100	23810		2.08	4.0E-07	BE001828.1	EST_HUMAN	PMT-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
469	13100	25591	4.51	3.0E-07	U19718.1	NT	Human microtubulin-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
609	13237	25711	2.84	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1417	14010	26539	1.65	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1667	14260		1.95	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2090	14870		3.87	3.0E-07	AA526763.1	EST_HUMAN	n56b08.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element;
2327	14898	27471	1.72	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2508	15072	27845	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2508	15072	27846	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3069	15884	28156	0.78	3.0E-07	T84704.1	EST_HUMAN	yd50f12.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:111695 5'
3195	15807	28260	2.03	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4768	17368		0.58	3.0E-07	P20740	SWISSPROT	OVESTATIN PRECURSOR (OVOMACROGLOBULIN)
4834	17412	28865	7.74	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCC001 3'
4878	17453	28905	0.71	3.0E-07	A1787236.1	EST_HUMAN	we8db12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347687 3'
5222	17787	30205	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h06.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5222	17787	30208	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h08.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5947	18471	31197	12.79	3.0E-07	O88807	SWISSPROT	qb-M82882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6128	18743	31498	0.71	3.0E-07	O42280	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6804	18985		5.41	3.0E-07	AA816175.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
7519	20039	32908	3.22	3.0E-07	AW787188.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7659	20171		1.6	3.0E-07	AI591065.1	EST_HUMAN	cc04c10.s1 NCJ_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1339890 3'
11373	23825		1.88	3.0E-07	BE439409.1	EST_HUMAN	QV1-JM0038-200300-115-g02 UM0036 Homo sapiens cDNA
12641	24718		6.74	3.0E-07	AJ132362.1	NT	tw28f11.x1 NCJ_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element/contains element MSR1 MSR1 repetitive element ;
31	12710	25168	3.36	2.0E-07	AF282988.1	NT	HTM1-025F1 HTM1 Homo sapiens cDNA
165	12828	25314	7.91	2.0E-07	L77569.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
165	12828	25315	7.91	2.0E-07	L77569.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
184	12854	25338	45.53	2.0E-07	U38849.1	NT	Homo sapiens D(George syndrome critical region, telomeric end
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Homo sapiens D(George syndrome critical region, telomeric end
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic(vesicular) actin gene, complete cds
791	13409		0.91	2.0E-07	P11389	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
979	13591	26106	2.56	2.0E-07	AA223280.1	EST_HUMAN	zr08b07.s1 Strategene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650889 3' similar to gb:U31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
980	13592	26107	6.66	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:80760 3' similar to contains L1 repetitive element ;
1205	13805	26318	0.76	2.0E-07	Q28768	SWISSPROT	I/6 AUTOANTIGEN
1644	14236	26771	1.88	2.0E-07	Q08701	SWISSPROT	HYPOTHETICAL 72.6 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3679	16280		0.85	2.0E-07	BF131397.1	EST_HUMAN	601818918F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3751	16352	28820	22.38	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5647	18179	30593	1.81	2.0E-07	AW889086.1	EST_HUMAN	RC3-NN0068-280400-021-g11 NN0068 Homo sapiens cDNA
6769	19362	32171	1.59	2.0E-07	AI208716.1	EST_HUMAN	qg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8405	20046		3.57	2.0E-07	AV726390.1	EST_HUMAN	AV726390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8628	21167	34082	1.1	2.0E-07	AA035198.1	EST_HUMAN	zkt27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
9878	22175		2.27	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10168	22663	35658	5.85	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10383	22877	35868	0.76	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10383	22877	35869	0.75	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11842	24603		2.67	2.0E-07	BE153717.1	EST_HUMAN	PMO-HT0339-260100-008-H07 HT0339 Homo sapiens cDNA
11734	24890		3.56	2.0E-07	AI732492.1	EST_HUMAN	zn65h11.x6 Streptococcus pneumoniae 21 segment HS21C082
1141	13744		1.17	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C013
2013	14595	27157	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2013	14595	27158	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2424	14892	27565	0.93	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2854	14162	26893	2.94	1.0E-07	P09266	SWISSPROT	GLYCOPROTEIN GPV
3807	13744		1.22	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4380	16987	29413	2.75	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4380	16987	29414	2.76	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6827	19223	32028	1.57	1.0E-07	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6950	19527	32349	4.57	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6950	19527	32350	4.57	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7604	20028	32890	8.82	1.0E-07	N55081.1	EST_HUMAN	yz43c07.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:245484 3'
7644	20156	33042	0.82	1.0E-07	BF375808.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7644	20156	33043	0.82	1.0E-07	BF375808.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7669	20181	33068	1.35	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8157	20668	33611	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8157	20668	33612	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8894	21422	34347	2.7	1.0E-07	AA693576.1	EST_HUMAN	z51e10.s1 Soares_fetal_liver_spleen_TNFSL S1 Homo sapiens cDNA clone IMAGE:434348 3'
8184	21711	34654	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9535	22035	34995	0.49	1.0E-07	BE327843.1	EST_HUMAN	hu28h08.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9849	22347	35328	2.51	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element:
9855	22353	35334	1.19	1.0E-07	AA388311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
10362	22866		3.53	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C082

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12013	24880	30704	2.42	1.0E-07	BE048770.1	EST_HUMAN	h35c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 O95722 DJ1163J1.1
7325	19852	32714	0.87	9.0E-08	AI59362.1	EST_HUMAN	ssd1b08.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
9802	22300	35285	2.1	9.0E-08	AV734818.1	EST_HUMAN	AV734819 cda Homo sapiens cDNA clone cdABF808 5'
11081	23573	36610	3.41	9.0E-08	AI591052.1	EST_HUMAN	wn30e07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12 OFR repetitive element:
11519	23967	37039	4.51	9.0E-08	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
11861	24283		2.98	9.0E-08	AJ251973.1	NT	Homo sapiens partial stefin-1 gene
635	15420		2.27	8.0E-08	AI511352.1	EST_HUMAN	wd18b05.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
1088	13693		0.79	8.0E-08	BE786489.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
3568	16202		1.05	8.0E-08	BE795489.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
8674	21213	34133	3.54	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8674	21213	34134	3.54	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9545	22045	35008	3.32	8.0E-08	AW970693.1	EST_HUMAN	EST392776 MAGE resequences, MAGK Homo sapiens cDNA
11124	23632		2.81	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
84	12760	25243	2.82	7.0E-08	Q02387	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1405	13958	26527	11.08	7.0E-08	X04808.1	NT	Rat mRNA for ribosomal protein L31
3636	16238	28713	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3635	16238	28714	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16900	26073	0.89	7.0E-08	P01608	SWISSPROT	IG KAPPA CHAIN V-J REGION OU
4002	16900	26074	0.89	7.0E-08	P01608	SWISSPROT	IG KAPPA CHAIN V-J REGION OU
10683	23223		6.5	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 contam Homo sapiens cDNA 3'
11523	23971	37041	6.1	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12450	16238	28713	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12450	16238	28714	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
850	13498	25874	3.81	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
850	13498	25875	3.81	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2401	14988	27543	2.01	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0166-191189-004-909 HT0166 Homo sapiens cDNA
4334	16921	26363	1.14	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7892	20434		0.68	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9251	21777		0.6	6.0E-08	AA827075.1	EST_HUMAN	ds58c05.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11283	23745	36802	2.81	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11407	23858		1.77	6.0E-08	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C009
88	12764	25247	2.33	5.0E-08	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2277	14851	27429	1.23	5.0E-08	AA463851.1	EST_HUMAN	nt03b09.s1 NCL_CGAP_Thyl1 Homo sapiens cDNA clone IMAGE:843183 similar to contains Alu repetitive element;
11692	24107		7.32	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11888	24233	31004	1.48	5.0E-08	AW851678.1	EST_HUMAN	QV0-CT0225-131089-034-a12 CT0225 Homo sapiens cDNA
1797	14387	26831	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1787	14387	26932	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2910	15527		1.49	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0428_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0428 5'
3100	15718		1.01	4.0E-08	AI078417.1	EST_HUMAN	cc25d02.x1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1674498 3' similar to contains Alu repetitive element;
3986	16584	29055	0.87	4.0E-08	U82968.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6537	19136	31928	1.14	4.0E-08	P82624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8733	21272	34182	0.57	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
6068	21803	34533	0.92	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9583	22063		0.87	4.0E-08	P08847	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10233	22728		0.71	4.0E-08	AI016342.1	EST_HUMAN	α78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622803 3'
10287	22782	35774	3.59	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
10782	23308		1.7	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
10968	23483	36510	3.7	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
10968	23483	36511	3.7	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
11697	25022		1.4	4.0E-08	W76159.1	EST_HUMAN	z085g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
12378	24546		3.48	4.0E-08	AI343353.1	EST_HUMAN	tb95a11.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2082078 3' similar to contains MER18.b3
5795	18420	31136	3.12	3.0E-08	BE018348.1	EST_HUMAN	MER18 MER18 repetitive element ;
7052	18071	30482	3.77	3.0E-08	AI02737.1	EST_HUMAN	bb7de10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z158 Q8Z158 SYNTAXIN 17. ;
7545	20065	32839	1.41	3.0E-08	AL163246.2	NT	q376f11.y5 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:1844045 5'
							Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7730	20238		4.17	3.0E-08	AI438352.1	EST_HUMAN	th83h09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
8812	22310		0.51	3.0E-08	AF05086.1	NT	Homo sapiens MHC class I region
11682	24087		38.68	3.0E-08	R18420.1	EST_HUMAN	ygo2f04.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30848 5' similar to contains Alu repetitive element
220	12881		6.74	2.0E-08	AW302886.1	EST_HUMAN	xt87f06.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2787139 3'
247	12607		6.48	2.0E-08	AA425688.1	EST_HUMAN	zaw8f07.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
622	13164	26837	2.59	2.0E-08	AF188348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
688	13312	25786	10.89	2.0E-08	AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
688	13312	25797	10.99	2.0E-08	AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1027	13838		22.68	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138883 5'
1387	13881	26508	2.09	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1777	14387		1.3	2.0E-08	BE734871.1	EST_HUMAN	601670463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845189 5'
1895	14480		4.65	2.0E-08	AW270271.1	EST_HUMAN	xp43711.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2482	15029	27597					rw04h01.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1261409 3' similar to contains L1.L3 L1 repetitive element;
2580	15143		0.97	2.0E-08	AA731948.1	EST_HUMAN	Sheep Hls-RNA-GUG
3243	15855	26337	2.21	2.0E-08	K00216.1	NT	WNT-14 PROTEIN PRECURSOR
3243	15855	26338	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3826	16524		1.93	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161089-012-b03 ST0197 Homo sapiens cDNA
4162	16744	28188	0.57	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4494	17079		1.74	2.0E-08	AA458040.1	EST_HUMAN	aa28c07.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.L2 L1 repetitive element;
5092	17665		3.83	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5817	18441	31183	0.87	2.0E-08	AA813204.1	EST_HUMAN	el80h11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3'
5898	18618	31354	0.87	2.0E-08	AW088824.1	EST_HUMAN	xd32c04.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595482 3' similar to contains MER18.b3
7948	20486	33398	1.07	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8054	20598	33503	1.2	2.0E-08	AA480121.1	EST_HUMAN	POL POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9014	21551		1.41	2.0E-08	AU139878.1	EST_HUMAN	ab02g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839874 3'
							AU139878 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	22807	35904	0.78	2.0E-08	N78097.1	EST_HUMAN	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contig
10413	22907	35905	0.78	2.0E-08	N78097.1	EST_HUMAN	LTR1.B3 LTR1 repetitive element;
11882	24283		1.74	2.0E-08	AL163284.2	NT	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.B3 LTR1 repetitive element;
12559	25079		1.44	2.0E-08	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C084
1812	14402	26947	0.89	1.0E-08	AF125348.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2095	14874		2.74	1.0E-08	BE141858.1	EST_HUMAN	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5785	18410	31128	4.23	1.0E-08	AJ010770.1	NT	PM2-HT0130-150889-001-f12 HT0130 Homo sapiens cDNA
7746	20254	33148	1.14	1.0E-08	P19474	SWISSPROT	Homo sapiens hyperion gene, exons 1-50
7978	20520	33428	0.55	1.0E-08	AL163302.2	NT	62 KD RO PROTEIN (SUGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8070	20612	33525	0.85	1.0E-08	AF224686.1	NT	Homo sapiens chromosome 21 segment HS21C102
8070	20612	33525	0.85	1.0E-08	AF224686.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8484	21023	33940	1.84	1.0E-08	A015304.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9132	21687	34608	0.75	1.0E-08	BE072572.1	EST_HUMAN	cd35a05.a1 Soares_basils_NHT Homo sapiens cDNA clone IMAGE:1618738 3'
9878	22373	35350	1.18	1.0E-08	P79110	SWISSPROT	PM2-BT0546-210100-004-002 BT0548 Homo sapiens cDNA
10449	22943	35953	0.64	1.0E-08	P88083	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
11195	23700	36761	3.79	1.0E-08	AF044083.1	NT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (BMP-1)
12081	24353		2.27	1.0E-08	X61755.1	NT	BONE MORPHOGENETIC PROTEIN 1 (BMP-1)
4327	16913	26356	3.93	9.0E-09	AL163278.2	NT	Homo sapiens major histocompatibility locus class III region
4327	16913	26357	3.93	9.0E-09	AL163278.2	NT	Human lambda-immunoglobulin constant region complex (germline)
9874	22459		0.49	9.0E-09	T87060.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7309	19536	32694	8.53	8.0E-09	AI193900.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7942	20484	33398	2.88	8.0E-09	AW000159.1	EST_HUMAN	y68a12.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
8919	21457		2.77	8.0E-09	AA838892.1	EST_HUMAN	q442a07.x1 Soares_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
3687	16288		1.87	7.0E-09	D88842.1	NT	GM0-NN1004-100300-273-008 NN1004 Homo sapiens cDNA
4090	16878		1	7.0E-08	U90871.1	NT	op74d09.a1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
							Homo sapiens DNA for 3-kebabacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
							Human familial Alzheimer's disease (STM2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7843	20385		0.5	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
7691	20533		0.78	7.0E-09	AA259200.1	EST_HUMAN	z60c05.r1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:881992 5' similar to contains L1.12 L1 repetitive element;
9184	21701	34644	2.89	7.0E-09	LD9709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10086	22581	35574	1.3	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10248	22743		0.63	7.0E-09	AA058626.1	EST_HUMAN	z758e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381168 3' similar to contains L1.12 L1 repetitive element;
10552	23088		2.78	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121818 3'
2188	14774		1.18	6.0E-09	AL040438.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434C0514 5'
5118	17688	30128	5.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5246	17810	30232	1	6.0E-09	AW593471.1	EST_HUMAN	hg18112.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:X63743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5246	17810	30233	1	6.0E-09	AW593471.1	EST_HUMAN	hg18112.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:X63743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5582	18213	30882	12.11	6.0E-09	AW195784.1	EST_HUMAN	1. ISOFORM C PRECURSOR (HUMAN);
8512	21051	33973	0.81	6.0E-09	BE161653.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
9103	21838	34578	2.37	6.0E-09	4503710	NT	MR3-HT0448-280300-201-h12 HT0448 Homo sapiens cDNA
10177	22872		3.89	6.0E-09	AF200923.2	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10610	23143	36154	1.68	6.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
1480	14052	28584	3.95	6.0E-09	BE148264.1	EST_HUMAN	RC2-HT0232-120200-014-h10 HT0232 Homo sapiens cDNA
1893	14478	27038	0.83	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6542	19141	31833	2.28	5.0E-09	AA359454.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
8521	21080	33983	0.59	6.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10007	22502	35469	2.27	5.0E-09	AW789807.1	EST_HUMAN	PM2-UM0053-240300-008-c09 UM0053 Homo sapiens cDNA
547	13178		1.69	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1000	13811		1.98	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1518	14110	26646	1.81	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038189), mRNA
2473	15040	27608	4.54	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
7788	20331	33237	0.72	4.0E-09	AA495747.1	EST_HUMAN	zw04c08.r1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:768288 5'
8459	20899	33915	0.82	4.0E-09	T64842.1	EST_HUMAN	yd11a07.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:88804 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10986	23510		1.73	4.0E-08	AA185142.1	EST_HUMAN	z334412.11 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:565278 5' similar to gb:L07807 DYNAMIN-1 (HUMAN);
2390	14958	27530	6.63	3.0E-08	BE222239.1	EST_HUMAN	hu09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
2589	15151	27717	0.95	3.0E-08	BE222239.1	EST_HUMAN	hu09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
2677	15235	27802	1.22	3.0E-08	P23249	SWISSPROT	PROTEIN MOV-10
3372	15980	28457	1.05	3.0E-08	BE222239.1	EST_HUMAN	hu09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
3423	16031		3.13	3.0E-08	AA442272.1	EST_HUMAN	z54404.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4172	16763		3.64	3.0E-08	X16874.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4517	17101	29548	5.18	3.0E-08	AF175326.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4910	17193	29639	1.52	3.0E-08	Q8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
7841	20363	33287	1.28	3.0E-08	BE465780.1	EST_HUMAN	hu03002.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091 O55091 IMPACT PROTEIN. ;
10148	22641	35631	1.88	3.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10800	23420	38437	3.87	3.0E-08	BF109843.1	EST_HUMAN	7172c08.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
10800	23420	38438	3.87	3.0E-08	BF109843.1	EST_HUMAN	7172c08.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
845	13461		1.01	2.0E-08	X16874.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1301	13895	28417	6.02	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1688	14291		10.31	2.0E-08	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2364	14935	27507	2.79	2.0E-08	Q8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
4011	16609	29082	4.13	2.0E-08	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4083	16678	29139	0.94	2.0E-08	AI263476.1	EST_HUMAN	gi07309.x1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
6876	19910		0.74	2.0E-08	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' and similar to EST containing L1 repeat
7474	19998	32961	8.48	2.0E-08	AA461430.1	EST_HUMAN	z683108.r1 Scores_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:798187 5' similar to contains Alu repetitive element;
7532	20052	32925	0.88	2.0E-08	W28934.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8848	21185	34104	1.72	2.0E-08	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11634	24074		1.72	2.0E-08	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
12238	13461		27.08	2.0E-08	X16874.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12310	25094		2.25	2.0E-08	AA226070.1	EST_HUMAN	nc11c02.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1032	13642		1.14	1.0E-09	W78152.1	EST_HUMAN	zsf78d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
1148	13751	26260	2.3	1.0E-09	5031624	NT	gb1.02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1148	13751	26261	2.3	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2814	15531	28003	1.74	1.0E-09	U80017.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2852	15568	28042	3.98	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
2852	15568	28043	3.98	1.0E-09	M28699.1	NT	protein (nlp) and survival motor neuron protein (smn) genes, complete cds
3073	15688	28160	0.77	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
4818	17491		5.48	1.0E-09	AA719297.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
5684	18320	30819	0.87	1.0E-09	AL163283.2	NT	601056802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446177 5'
5998	18616	31352	1.48	1.0E-09	U07000.1	NT	zsf35b03.s1 Soares_pituitary_gland_N3HPQ Homo sapiens cDNA clone IMAGE:414028 3' similar to contains
6293	18801	31671	3.17	1.0E-08	P28694	SWISSPROT	Alu repetitive element; contains element MER22 repetitive element ;
8329	20870	33794	0.87	1.0E-09	AI688474.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
10218	22711		2.57	1.0E-09	AL163283.2	NT	Human breakpoint cluster region (BCR) gene, complete cds
12136	25032	30820	3.3	1.0E-09	11418127	NT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
12583	24944		1.82	1.0E-09	AF260225.1	NT	wd39b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
1352	13947	26471	1.48	9.0E-10	AW867740.1	EST_HUMAN	MER25.t1 MER25 repetitive element ;
2880	15479	27955	6.87	9.0E-10	AI870071.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
6822	19581	32410	4.35	9.0E-10	AI452892.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
158	12821	25309	10.47	8.0E-10	U53530.2	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3388	15985	28472	0.59	8.0E-10	BE080748.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
4278	16965	28311	4.11	8.0E-10	AA378932.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
9375	22372		2.34	8.0E-10	U36308.2	NT	SW:RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
730	13350	25844	24.84	7.0E-10	7708225	NT	t48b09.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
730	13350	25845	24.84	7.0E-10	Q13342	SWISSPROT	TR:000372 000372 PUTATIVE P150. ;
1663	14258	26791	2.13	7.0E-10	P08548	SWISSPROT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
2087	14947		1.31	7.0E-10	P08548	SWISSPROT	QV1-8T0631-150200-071-01 B70631 Homo sapiens cDNA
2594	15158		13	7.0E-10	P08547	SWISSPROT	EST88564 Small intestine Homo sapiens cDNA 5' and
							Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
							Homo sapiens TPA inducible protein (LOC51568), mRNA
							Homo sapiens TPA inducible protein (LOC51568), mRNA
							LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3124	15738	28206	2.84	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
6332	18938	31714	5.28	7.0E-10	A343820.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
7448	19970	32838	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-012 HT0619 Homo sapiens cDNA
7852	20184		1.43	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7916	20458	33364	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
7916	20458	33365	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10212	22707	35701	0.57	7.0E-10	L08895.1	NT	Homo sapiens MAD5MEF2-family transcription factor (MEF2C) mRNA, complete cds
11511	23959	37030	1.54	7.0E-10	AW778769.1	EST_HUMAN	ho12p02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element/contains MER7.b1 MER7 repetitive element ;
949	13559	26072	3.68	6.0E-10	AJ400877.1	NT	Homo sapiens ASC13 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2702	15258	27827	1.89	6.0E-10	A1424405.1	EST_HUMAN	h02d07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2095021 3'
4847	17426		2.16	6.0E-10	AW863719.1	EST_HUMAN	RC3-CT0254-031089-012-g12 CT0254 Homo sapiens cDNA
8718	21257	34177	0.94	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
8718	21257	34178	0.94	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2) (CD82E)
9592	22052	35015	0.52	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
11731	24138		1.47	6.0E-10	AW971823.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR(ENTEROKINASE)
792	13410		5.2	6.0E-10	AL048804.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
3522	16127	28607	0.98	6.0E-10	Q01033	SWISSPROT	DKFZp434N219.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219.5'
5002	17575	30018	1.05	6.0E-10	AW028877.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
5002	17575	30018	1.05	6.0E-10	AW028877.1	EST_HUMAN	w97b03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542061 3' similar to contains MER10.11
5128	17700	30134	1.37	5.0E-10	AF181897.1	NT	MER10 repetitive element ;
7383	19889		1.84	5.0E-10	BF105159.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
9455	21931	34832	1.65	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9455	21931	34833	1.65	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
116	12787		1.02	4.0E-10	A1221083.1	EST_HUMAN	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
607	13235	25709	0.73	4.0E-10	AA515280.1	EST_HUMAN	qg09f08.x1 Soares placenta_8tcbwks_2NbhP8b9W Homo sapiens cDNA clone IMAGE:1756049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
2039	14821	27189	1.17	4.0E-10	AW594709.1	EST_HUMAN	m64a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924848 3'
							hg68g03.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2848844 3' similar to contains Alu repetitive element

PCT/US01/00669

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15171	27738	4.19	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7228	19759	32614	22.35	4.0E-10	AF224688.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10067	22592	35584	0.82	4.0E-10	AW263243.1	EST_HUMAN	U1-H-B12-ah1-e-07-q-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10342	22836	35831	1.01	4.0E-10	AI267342.1	EST_HUMAN	sq33h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
948	13560	26074	1.95	3.0E-10	N38113.1	EST_HUMAN	y42208.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272883 3' similar to contains L1 H L1 repetitive element
1395	13989		4.43	3.0E-10	AY005160.1	NT	Homo sapiens extracellular glycoprotein lectin precursor, gene, complete cds
4633	17216	28667	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4633	17216	28668	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5646	18274	30748	0.92	3.0E-10	N50109.1	EST_HUMAN	y211g08.s1 Soares_multiple_sclerosis_2N6HMSHP Homo sapiens cDNA clone IMAGE:282782 3'
6350	18655	31734	1.87	3.0E-10	P20350	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
6482	18083	31877	2.86	3.0E-10	BE302970.1	EST_HUMAN	bat7d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2868319 5'
7737	20245	33136	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7737	20245	33137	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8685	21204	34122	1.08	3.0E-10	H87208.1	EST_HUMAN	y674b12.s1 Soares retina N264HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER28 repetitive element
8978	21517	34442	1.61	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
8978	21517	34443	1.61	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9284	21790		0.86	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
10359	22853		2.13	3.0E-10	T64691.1	EST_HUMAN	yc11612.r1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:80398 5'
10485	22879		1.71	3.0E-10	AA768294.1	EST_HUMAN	nz26g03.s1 NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:1289808 3'
12415	24568	30911	3.44	3.0E-10	BE178617.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
38	12717	25176	92.79	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
38	12717	25177	92.78	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1942	14526		2.33	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
3015	15631		0.66	2.0E-10	BF675047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5971	18592		7.24	2.0E-10	Q28640	SWISSPROT	(HPRG)
6398	18001	31779	1.42	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7414	19839	32803	7.79	2.0E-10	BE781082.1	EST_HUMAN	601596208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7856	20498	33407	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7956	20498	33408	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8228	21742		0.85	2.0E-10	BF434566.1	EST_HUMAN	7a78d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3842303 3' similar to contains L1.13 L1
1556	14149		2.28	1.0E-10	AW867797.1	EST_HUMAN	repetitive element;
1650	14242	28776	2.41	1.0E-10	AV652123.1	EST_HUMAN	MRO-SN0038-280300-001-01 SN0038 Homo sapiens cDNA
2818	15180		1.78	1.0E-10	AW852001.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
3548	16152	28634	0.73	1.0E-10	AW832912.1	EST_HUMAN	QV0-CT0225-191199-058-008 CT0225 Homo sapiens cDNA
3560	16187		0.82	1.0E-10	AL041685.1	EST_HUMAN	QV2-TT0003-181189-013-q10 TT0003 Homo sapiens cDNA
3911	16197		0.89	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: hta3) Homo sapiens cDNA clone DKFZp434N1317 5'
4087	16883		6.83	1.0E-10	AF213884.1	NT	DKFZp434N1317_1 434 (synonym: hta3) Homo sapiens cDNA clone DKFZp434N1317 5'
							Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4207	16786	28243	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4207	16786	29244	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4214	16803	28253	1.95	1.0E-10	AB031088.1	NT	Homo sapiens POCX1 mRNA for protein containing CXXC domain 1, complete cds
4248	16837		2.53	1.0E-10	M30829.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5343	17804		1	1.0E-10	AI797745.1	EST_HUMAN	we82704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains
8182	20723	33637	1.06	1.0E-10	AW408860.1	EST_HUMAN	MER31.11 MER31 repetitive element;
8589	21128		1.03	1.0E-10	AI268340.1	EST_HUMAN	fb_8A4 Fetal brain library Homo sapiens cDNA
10103	22598		4.16	1.0E-10	AA081888.1	EST_HUMAN	qnt04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.1 L1
10783	23316	36325	3.47	1.0E-10	AO38280.1	EST_HUMAN	repetitive element;
11672	18038		1.58	1.0E-10	XB7344.1	NT	zn23g06.r1 Stratagene neuroepithelium NT2BAMI 837234 Homo sapiens cDNA clone IMAGE:548314 5'
283	12639	26425	0.98	9.0E-11	BE145800.1	EST_HUMAN	cy65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1872681 3'
2152	14729	27302	6.73	9.0E-11	AL134395.1	EST_HUMAN	Hi.sapiens DMA, DMB, HLA-Z1, IIP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DQ82 and RING8, 9, 13 and 14 genes
2162	14729	27303	6.73	9.0E-11	AL134395.1	EST_HUMAN	IL2-HT0203-281099-016-c08 HT0203 Homo sapiens cDNA
3430	18038	28520	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
							DKFZp547D225_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
							DKFZp547D225_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	18038	28521	2.33	9.0E-11	AL134386.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
4598	17182	28629	0.89	9.0E-11	AA775985.1	EST_HUMAN	aa7801.s1 Striatum echino brain S11 Homo sapiens cDNA clone IMAGE:870287 3'
6763	18389		3.77	9.0E-11	BE078780.1	EST_HUMAN	RC8-B10827-140200-Q11-E08 B10827 Homo sapiens cDNA
10058	22553	35548	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10058	22553	35549	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12059	24342	30889	3.62	9.0E-11	C18638.1	EST_HUMAN	C18635 Clontech human acris polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-506B08 5'
3150	15784		9.38	8.0E-11	H19971.1	EST_HUMAN	Yn53f1.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element
4035	16833	29102	0.88	8.0E-11	AI478817.1	EST_HUMAN	tm54609.xt NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2181838 3'
4117	18711	29165	5.2	8.0E-11	N23712.1	EST_HUMAN	Yw46608.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3'
1487	14089	28629	2.84	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
3839	16537	28004	0.84	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8435	20975	33889	2.91	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22824		1.1	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
12206	24430		1.52	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBABC09 5'
437	13070	25568	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
437	13070	25567	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6822	18412	32229	1.03	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7680	20191	33080	3.29	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8305	20848	33769	3.25	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCA5C08 5'
12	12891	25147	0.8	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3411	12891	25147	1.29	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4312	18898	28343	1.04	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6639	19235	32037	3.02	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7537	20057	32831	12.3	5.0E-11	11418708	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1448	14038		1.41	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2818	15368	27837	8.36	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
2897	15613	28093	1.17	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4725	17306	29750	0.93	4.0E-11	D44886.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6602	19198	32005	3.5	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7409	19634		4.08	4.0E-11	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8316	21830		1.44	4.0E-11	BE149425.1	EST_HUMAN	RC1-H10258-210100-013-008 HT0258 Homo sapiens cDNA
8590	22080	35045	0.91	4.0E-11	AI609753.1	EST_HUMAN	H82g12.x1 NCL_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2108830 3' similar to WP:ZK353.1
12275	24478	30837	1.36	4.0E-11	11846732	NT	CE00385
1538	14130	26868	3.79	3.0E-11	8876077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4363	16950		1.47	3.0E-11	AA309248.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
995	13607	26121	1.64	2.0E-11	AI150502.1	EST_HUMAN	EST160120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1227	13828	26342	5.04	2.0E-11	R24807.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:35144 5'
1227	13828	26343	5.04	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1855	14247	26760	6.04	2.0E-11	L17432.1	NT	y943e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1655	14247	26761	6.04	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and erythrocyte-like protein (COR3/beta) (COR3/beta) genes, complete cds
1659	14252	26768	1.08	2.0E-11	AI128371.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and erythrocyte-like protein (COR3/beta) (COR3/beta) genes, complete cds
3230	15942	28323	6.98	2.0E-11	P10283	SWISSPROT	gc5tc10.x1 Soares_pregnant_uterus_Nb1PU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02882 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.t1 L1 repetitive element
3368	16978	28453	0.76	2.0E-11	AI478617.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3409	18018	28497	0.65	2.0E-11	Q10473	SWISSPROT	tm54c08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
3544	18148		1.01	2.0E-11	AF020503.1	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
4339	17123		0.89	2.0E-11	BE065537.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4711	17263		0.85	2.0E-11	AL163227.2	NT	RC3-BT0316-170200-014-605 BT0316 Homo sapiens cDNA
5070	17643		1.37	2.0E-11	BE092558.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521C027
6284	18982	31651	1.2	2.0E-11	AW877808.1	EST_HUMAN	QV2-BT0258-261068-014-601 BT0258 Homo sapiens cDNA
6452	18053	31838	2.02	2.0E-11	AA581028.1	EST_HUMAN	QV2-P70073-280300-109-008 PT0073 Homo sapiens cDNA
7248	19775	32632	0.78	2.0E-11	BF592945.1	EST_HUMAN	nc83h05.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR18_YEAST
7623	20385		0.66	2.0E-11	P37072	SWISSPROT	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
							J97cd3.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:342565 3'
							OLFATORY RECEPTOR-LIKE PROTEIN COR8

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9150	21886		1.27	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10184	22679	35871	4.6	2.0E-11	Q13808	SWISSPROT	OLFACTORY RECEPTOR 61 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10409	22903	35898	0.79	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10409	22903	35900	0.79	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10992	23506	36538	2.41	2.0E-11	AA035389.1	EST_HUMAN	zK27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
10992	23508	36539	2.41	2.0E-11	AA035389.1	EST_HUMAN	zK27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11805	25020		2.8	2.0E-11	AA704195.1	EST_HUMAN	zK27g02.s1 Soares_fetal_liver_INFIL_S1 Homo sapiens cDNA clone IMAGE:480824 3'
11836	24200		2.49	2.0E-11	AW642143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
11880	24218	31043	2.25	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070800-372-g01 TN0140 Homo sapiens cDNA
12136	24388		2.03	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12283	24492		5.24	2.0E-11	P08847	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12629	24707		3.57	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13325	25812	2.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
816	13434	25939	0.84	1.0E-11	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
1259	13856	26372	2.86	1.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
1546	14138		1.68	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2171	14748	27317	2.61	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3546	16150	28630	0.83	1.0E-11	BE004315.1	EST_HUMAN	GM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
4905	17480		0.97	1.0E-11	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5535	18167	30581	15.03	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5997	18817	31353	0.8	1.0E-11	BF222848.1	EST_HUMAN	7p57d01.x1 NCL_GAP_P228 Homo sapiens cDNA clone IMAGE:3849945 3' similar to contains MER10.b3
8143	20884	33598	3.16	1.0E-11	4885646	NT	MER10 repetitive element
8517	21058	33979	4.89	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8978	21516	34440	1.38	1.0E-11	BF385119.1	EST_HUMAN	Y73d08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28168 5'
8978	21516	34441	1.38	1.0E-11	BF385119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA
11167	23674	36721	2.48	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA
2879	15595	28075	0.87	9.0E-12	P20742	SWISSPROT	802154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
9713	22211	35184	5.63	9.0E-12	AL163300.2	NT	PREGNANCY ZONE PROTEIN PRECURSOR
9713	22211	35185	5.63	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9261	21767		1	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
11911	24249		4.51	8.0E-12	AJ271736.1	NT	IL5-BT0578-130300-038-G12 BT0578 Homo sapiens cDNA
4766	17347	28796	1.68	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 2/2 34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	23759	38815	12.18	7.0E-12	AA704735.1	EST_HUMAN	z23g01.e1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3601	18205		0.72	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4440	17026	29468	10.25	6.0E-12	AA732618.1	EST_HUMAN	n288f11.e1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
8926	21484	34380	0.82	6.0E-12	AF003249.1	NT	Marone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9395	21818		1.8	6.0E-12	AA847698.1	EST_HUMAN	cd10g11.a1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER29.12
1081	13888	28188	2.66	6.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element
3437	16045	28526	1.19	5.0E-12	BE047779.1	EST_HUMAN	ES104462 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBDDV33
3780	16390	28855	6.69	5.0E-12	AJ271736.1	NT	tz42b05.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2281217 5'
6172	18784	31550	6.69	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6172	18784	31551	5.59	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6617	19214	32019	6.62	5.0E-12	AW974760.1	EST_HUMAN	EST388850 MAGIE resequences, MAGN Homo sapiens cDNA
7089	19448	32284	1.12	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_e1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7108	19448	32284	1.14	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_e1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8171	20712	33829	1.43	5.0E-12	AA033745.1	EST_HUMAN	z01g12.e1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:376718 3' similar to contains L1.13 L1 repetitive element
8602	21141		0.7	5.0E-12	AW887037.1	EST_HUMAN	RC1-O10085-220300-011-b07 OT0088 Homo sapiens cDNA
8925	21483		0.56	5.0E-12	AL078581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9037	21674	34504	2.42	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9344	21859	34806	1.04	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E)(OLFACTORY RECEPTOR 17-4)(OR17-4)
10176	22671		4.17	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10266	22761	35748	0.67	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10481	22935	35968	2.12	5.0E-12	6978754	NT	Rettus narvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
285	12923	25409	3.53	4.0E-12	AA700328.1	EST_HUMAN	z74g11.e1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460878 3'
266	12923	25409	4.43	4.0E-12	AA700328.1	EST_HUMAN	z74g11.e1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460878 3'
4727	17308	29752	0.82	4.0E-12	AI888984.1	EST_HUMAN	bx2h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE
7815	20128		0.7	4.0E-12	BF445140.1	EST_HUMAN	ned21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3386077 3' similar to contains MER7.b2
8185	20726		2.2	4.0E-12	AF109607.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8621	21160	34075	1.2	4.0E-12	AB042815.1	NT	Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10861	23476	35501	4.25	4.0E-12	AJ228043.1	NT	Homo sapiens 858 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12180	24416		1.61	4.0E-12	U78027.1	NT	Homo sapiens Brubin's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
644	13287	25744	2.73	3.0E-12	AW341683.1	EST_HUMAN	hdf13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR:O14517
644	13287	25745	2.73	3.0E-12	AW341683.1	EST_HUMAN	hdf13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR:O14517
5643	18272	30748	1.18	3.0E-12	AF111168.2	NT	O14517 SMRP. ;
8316	20857	33783	0.52	3.0E-12	O35453	SWISSPROT	Homo sapiens serine peptidyl transferase, subunit II gene, complete cds; and unknown genes
9035	21572	34501	0.58	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10535	23072	36085	3.26	3.0E-12	U37672.1	NT	SERINE PROTEASE HEPSIN
10535	23072	36088	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1693	14286	28820	1.05	2.0E-12	AW802131.1	EST_HUMAN	Human prostate specific antigen gene, 5' flanking region
3513	16118	28598	0.67	2.0E-12	BT54495	NT	IL5-UM0071-120400-065-005 UM0071 Homo sapiens cDNA
4192	16781	29229	0.8	2.0E-12	J01884.1	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4192	16781	29230	0.8	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4512	17086		2.98	2.0E-12	BE063509.1	EST_HUMAN	Rat U3A small nuclear RNA
6603	19200		1.54	2.0E-12	AW971857.1	EST_HUMAN	CMO-BT0281-031186-087-003 BT0281 Homo sapiens cDNA
7227	19768	32613	2.97	2.0E-12	T08188.1	EST_HUMAN	EST383948 MAGE resequences, MAGI Homo sapiens cDNA
7382	19908	32773	1.21	2.0E-12	BE173035.1	EST_HUMAN	EST080660 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
7656	20168	33055	2.38	2.0E-12	11422226	NT	MRO-HT0559-200400-015-008 HT0559 Homo sapiens cDNA
7894	20436		0.8	2.0E-12	AV683827.1	EST_HUMAN	Homo sapiens Ac-like transposable element (ALTE), mRNA
9232	21954		2.18	2.0E-12	AF168884.1	NT	AV683827 GKC Homo sapiens cDNA clone GKC7B04 5'
9898	22393		11.42	2.0E-12	BE165980.1	EST_HUMAN	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10408	22802	35898	0.69	2.0E-12	AI334130.1	EST_HUMAN	MR3-HT0487-150200-113-001 HT0487 Homo sapiens cDNA
11820	24180		2.46	2.0E-12	AL163283.2	NT	qq0702.x1 Soares_NH-MPU_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR:Q13538
128	12788	25282	2.78	1.0E-12	AW627874.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN. ;
2031	14613		1.53	1.0E-12	AI871726.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
3108	15721	28191	1.33	1.0E-12	AF000891.1	NT	h90808.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11
3108	15721	28192	1.33	1.0E-12	AF000891.1	NT	MER18 repetitive element ;
3943	18541	29007	38.65	1.0E-12	AU132248.1	EST_HUMAN	hm51607.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439463 3' similar to contains L1.b3 L1 repetitive element ;
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	16541	28008	38.66	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 6'
6121	18736		1.85	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6192	18802		1.85	1.0E-12	Q872G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0981
6653	19249	32051	0.7	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
7170	19702	32549	1.74	1.0E-12	AF106884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7204	19735	32587	9.7	1.0E-12	AI248533.1	EST_HUMAN	qb:186804.x1 Sceres fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7204	19735	32588	9.7	1.0E-12	AI248533.1	EST_HUMAN	qb:186804.x1 Sceres fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8426	20666	33880	0.54	1.0E-12	U69059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8639	21178	34099	1.18	1.0E-12	AA782323.1	EST_HUMAN	ec28406.x1 Strati gene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
11723	24130	37164	4.65	1.0E-12	AW982164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
11941	24273		1.6	1.0E-12	AI738592.1	EST_HUMAN	w331h08.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
12097	24990		2.72	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
12424	24609		2.02	1.0E-12	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4019	16617	26092	0.91	8.0E-13	AB026900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 6
9519	22019		3.1	9.0E-13	N89653.1	EST_HUMAN	za26b06.x1 Sceres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
746	13366	25860	4.58	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
746	13366	25861	4.58	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1878	14464	27021	3.95	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8056	20598	33505	0.68	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8056	20598	33506	0.68	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10051	22546		2.58	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11600	24052	37117	2.51	8.0E-13	U68080.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
8178	20717		0.63	7.0E-13	Q65155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12212	24435		37.61	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3868613 5'
12448	24583		1.71	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2149	14728	27299	6.02	6.0E-13	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3394	15972		0.78	5.0E-13	R76336.1	EST_HUMAN	y8264.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3444	16052		1.84	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element :
6958	19536	32369	0.68	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10739	23264	36278	2.49	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1908	14493		3.69	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2500	15084		1.71	4.0E-13	AF003528.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
4858	17436		1.03	4.0E-13	AA454054.1	EST_HUMAN	z48d07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:785469 5'
5774	18399	31113	5.09	4.0E-13	BE189131.1	EST_HUMAN	PM3-HT0520-230200-002-e08 HT0520 Homo sapiens cDNA
7257	19785	32641	1.07	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7607	20120	32987	0.81	4.0E-13	AA431528.1	EST_HUMAN	z476g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA.;
7706	20214		1.84	4.0E-13	N44291.1	EST_HUMAN	y33g05.r1 Soares melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 A32995 t complex sterility protein - mouse ;
8775	21314	34236	0.84	4.0E-13	AL043810.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: h1a33) Homo sapiens cDNA clone DKFZp434A0128 5'
9833	22429	35403	4.28	4.0E-13	AI289831.1	EST_HUMAN	q32d05.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element;
11049	23559	36595	1.91	4.0E-13	AA435819.1	EST_HUMAN	z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11048	23559	36596	1.91	4.0E-13	AA435819.1	EST_HUMAN	z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
192	12852		4.5	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
898	13512		4.67	3.0E-13	AA430310.1	EST_HUMAN	z468d08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2408	14978	27550	1.08	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
2519	15083		6.72	3.0E-13	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2887	15245	27812	2.75	3.0E-13	BF372682.1	EST_HUMAN	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3221	15833		3.1	3.0E-13	AA745844.1	EST_HUMAN	cd18402.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3551	16155	28637	1.04	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3551	16155	28638	1.04	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5730	18356	31060	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6730	18356	31061	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6143	18757	31515	0.68	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2585890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN;
7824	20366	33274	9.59	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8021	20563	33484	0.66	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re- reactive factor
8021	20563	33485	0.66	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re- reactive factor
10556	23092		4.07	3.0E-13	AI084788.1	EST_HUMAN	HA0538 Human fetal liver cDNA library Homo sapiens cDNA
10924	23443	36484	2.91	3.0E-13	BE063509.1	EST_HUMAN	GM0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
11489	23919	36986	2.49	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
161	12824	25312	2.58	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
260	12919	25408	2.22	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1313	13807	28427	8.84	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3038	15654	28133	0.58	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3038	15654	28134	0.58	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3320	15930	28407	1.2	2.0E-13	BF431899.1	EST_HUMAN	nab70605.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3555	16159	28642	1.14	2.0E-13	AF109607.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4168	16776		1.9	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6271	18879	31647	5.27	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6903	19839	32476	7.42	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
10355	22849	35843	4.58	2.0E-13	5031888	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
11893	24238		20.31	2.0E-13	AW892155.1	EST_HUMAN	GM0-NIN001-100300-274-s11 NIN001 Homo sapiens cDNA
313	12987	25456	1.8	1.0E-13	S74128.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
821	13534	26052	4.35	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1381	13974	26502	1.01	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2068	14648	27220	1.8	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4118	16710		2.21	1.0E-13	AA324394.1	EST_HUMAN	EST27235 Ceraballum II Homo sapiens cDNA 5' end similar to EST containing L1 repeat
4898	17278	28724	1.61	1.0E-13	BF340987.1	EST_HUMAN	602038008F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4185898 5'
7851	20393	33298	0.77	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1094801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
7851	20393	33297	0.77	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1094801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10002	22497		0.9	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10202	22697	35691	0.52	1.0E-13	AF300701.1	NT	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds
11256	23788	36842	15.07	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;
11714	24124		1.87	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12393	24553		4.28	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
355	13004	25488	4.61	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
359	13005	25489	2.07	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2545	15108		3.84	9.0E-14	AW891577.1	EST_HUMAN	RC4-CT0322-080100-013-009 CT0322 Homo sapiens cDNA
2627	15189	27757	1.41	9.0E-14	AJ13127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2627	15189	27758	1.41	9.0E-14	AJ13127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2782	15335	27805	3.29	9.0E-14	AB038182.1	NT	Homo sapiens TFF gene cluster for Trefol factor, complete cds
3145	15759	28225	4.32	9.0E-14	AW513268.1	EST_HUMAN	xs54h05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3275	13004	25488	0.71	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3866	16484	28928	7.24	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4870	17448	28897	1.77	9.0E-14	AJ002153.1	NT	Sequinus oedipus gene for seminal vesicle secreted protein semenogelin I

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3545	16149		0.97	8.0E-14	BE489263.1	EST_HUMAN	h271c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4029	16827		3.29	8.0E-14	R76289.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
9369	20308	33211	38.57	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9479	21878	34826	4.61	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Strategene fetal retina 637202 Homo sapiens cDNA clone IMAGE:628670 3'
11310	23803		4.45	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA
12106	24388	30972	2.07	8.0E-14	A1698118.1	EST_HUMAN	wc92h08.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1671	15447		2.78	7.0E-14	AW151673.1	EST_HUMAN	x87e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
8851	21390		0.54	7.0E-14	AL163285.2	NT	MER10 repetitive element ; Homo sapiens chromosome 21 segment HS21C085
390	13036	25526	14.21	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9736	22234	35212	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9736	22234	35213	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
846	13289	25747	5.28	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2)(CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5209	17774	30197	1.53	5.0E-14	AW073791.1	EST_HUMAN	xb03b05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2576185 3' similar to contains L1.12 L1 repetitive element ;
5724	18350	31053	4.91	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1162	15434		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1920	14505	27082	3.86	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3816	16416		0.84	4.0E-14	AA045502.1	EST_HUMAN	zkb7a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 6'
4379	16866	29412	0.9	4.0E-14	N46328.1	EST_HUMAN	y773c12.s1 Soares_multiple_sclerotic_2NbHMP Homo sapiens cDNA clone IMAGE:278190 3' similar to contains L1.13 L1 repetitive element ;
7899	20441		0.49	4.0E-14	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
11633	24073	37135	1.91	4.0E-14	P05548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12457	25107		4.37	4.0E-14	AJ886224.1	EST_HUMAN	wrm08c03.x1 NCL_CGAP_Ux4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element ;
986	13697	28110	1.26	3.0E-14	X93468.1	NT	R.norvegicus mRNA for CP32 protein
5059	17632	30075	0.74	3.0E-14	AW265354.1	EST_HUMAN	xp48f12.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element ; contains element MER9 repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8832	19422	32237	1.08	3.0E-14	A1420786.1	EST_HUMAN	ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.1
8832	19422	32238	1.08	3.0E-14	A1420786.1	EST_HUMAN	ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.1
8722	21281	34181	0.88	3.0E-14	N42165.1	EST_HUMAN	yy07b10.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270523 5' FATTY ACID AMIDE HYDROLASE.1
10872	23393	38408	2.75	3.0E-14	BE88016.1	EST_HUMAN	601511930F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5' FATTY ACID AMIDE HYDROLASE.1
11116	17632	30076	0.84	3.0E-14	AW285354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12369	24964		1.84	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
413	13048	25539	2.61	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
413	13048	25540	2.51	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
719	15422	25828	0.8	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2431	14988		1.48	2.0E-14	AW372888.1	EST_HUMAN	RC5-BT0377-091288-031-D12 BT0377 Homo sapiens cDNA
2504	15088		1.07	2.0E-14	7657520	NT	Homo sapiens hbbdd tumor deletion region protein 1 (RTDR1), mRNA
2567	15131	27689	1.03	2.0E-14	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
2689	15266		0.88	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5715	18341	30847	0.95	2.0E-14	BF380681.1	EST_HUMAN	IL2JUT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5804	18428	31148	0.8	2.0E-14	A1512351.1	EST_HUMAN	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5895	18517	31242	2.86	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6963	19540		0.88	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-408 BN0072 Homo sapiens cDNA
7326	19856	32719	1.12	2.0E-14	P56103	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7518	20038	32808	20.34	2.0E-14	BE168781.1	EST_HUMAN	IL2-HT0397-071288-024-D04 HT0397 Homo sapiens cDNA
7518	20038	32807	20.34	2.0E-14	BE168781.1	EST_HUMAN	IL2-HT0397-071288-024-D04 HT0397 Homo sapiens cDNA
9831	22328	35311	0.54	2.0E-14	A1978795.1	EST_HUMAN	wr58g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element
10659	23101	38208	4.65	2.0E-14	AW139800.1	EST_HUMAN	ULH-B11-actw-a-10-0-U1.e1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12366	24968		3.3	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
12617	15088		1.89	2.0E-14	7657520	NT	Homo sapiens hbbdd tumor deletion region protein 1 (RTDR1), mRNA
1105	13709	28218	1.89	1.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
1452	14044	28572	6.89	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1452	14044	28573	6.89	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
2044	14626	27185	7.63	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2228	14803	27374	5.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2433	15020	27591	5.89	1.0E-14	AF001688.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2971	15587	28089	1.51	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
3203	15816	28290	3.91	1.0E-14	BF336227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3203	15815	28291	3.91	1.0E-14	BF336227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3935	16553	28022	2.1	1.0E-14	AA682894.1	EST_HUMAN	aa89c12.a1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4572	17155	29596	1.71	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5977	18597	31332	2.03	1.0E-14	AF129145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6778	24770	32183	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6778	24770	32184	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1620	14213	28744	1.19	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2217	14792		1.39	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor 1 (GIM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -
7507	20020	32892	3.77	9.0E-15	P21416	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7959	20501	33410	1.38	9.0E-15	BE603559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960168 5'
12580	24690		1.78	9.0E-15	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2837	13138		1.17	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7233	19783	32619	1.29	7.0E-15	BF030327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
10331	22825		2.53	7.0E-15	AW241958.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element:
11776	24184		1.78	7.0E-15	AA284465.1	EST_HUMAN	zs57d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:U21834 STEROL
1031	13841	26156	6.29	6.0E-15	AJ271735.1	NT	O-ACYLTRANSFERASE (HUMAN); contains L1.1f L1 repetitive element:
6077	18694	31440	1.18	6.0E-15	X73482.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6077	18694	31441	1.18	6.0E-15	X73482.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11182	25128		1.88	6.0E-15	AW839843.1	EST_HUMAN	O.aries mRNA for hair keratin cysteine-rich protein
12848	24722		1.3	6.0E-15	BF432200.1	EST_HUMAN	QV1-LT0038-150200-070-c10 LT0038 Homo sapiens cDNA
435	13068	25563	5.19	5.0E-15	AL163208.2	NT	nab81c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
							Homo sapiens chromosome 21 segment HS21C008
2789	15342	27912	2.35	5.0E-15	U091328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rcr1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
3515	16120		1.08	5.0E-15	AW296817.1	EST_HUMAN	UIH-BWO-qlp-g-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219 3'

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5288	17881		1.28	5.0E-15	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10555	23091		2.72	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 8'
452	12681	25137	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6771	18384	32173	0.78	4.0E-15	AB007870.1	NT	Homo sapiens chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
10940	20287	33184	2.94	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10940	20287	33185	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4287	18883		7.28	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5060	17633		0.57	3.0E-15	P92485	SWISSPROT	NADH-BIQUINONE OXIDOREDUCTASE CHAIN 5
5179	17746	30176	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5179	17746	30176	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6904	18638		1.41	3.0E-15	Q84626	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7323	18850	32711	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7323	18850	32712	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9839	22337		2.32	3.0E-15	AA807128.1	EST_HUMAN	oc38607 at NCI_CGAP_GDB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11
10673	23205	38218	3.36	3.0E-15	AB026898.1	NT	MER19 repetitive element;
12114	24997		1.36	3.0E-15	AJ271735.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
271	12928	25415	4.1	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
391	13037	26526	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25527	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2410	14978	27552	1.44	2.0E-15	BE350127.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2410	14978	27553	1.44	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3
3558	18163	28845	0.73	2.0E-15	AF223391.1	NT	MER29 repetitive element;
3559	18163	28846	0.73	2.0E-15	AF223391.1	NT	MER28 repetitive element;
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4142	16734	28168	0.95	2.0E-15	AW238489.1	EST_HUMAN	XP2801.x1 NCL_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element ;
4729	17310		2.72	2.0E-15	AB06335.1	EST_HUMAN	W07008.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR:Q81043 Q81043 NINEIN. ;
5332	17893	30306	0.93	2.0E-15	P13993	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5332	17893	30307	0.93	2.0E-15	P13993	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
6329	18935	31711	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
6329	18935	31712	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 6'
7168	19700		1.37	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7315	19842	32703	2.51	2.0E-15	AA704195.1	EST_HUMAN	z77603.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7427	19951	32816	4.49	2.0E-15	W05004.1	EST_HUMAN	za76410.r1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
8837	21378	34300	2.62	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9002	21539	34468	0.87	2.0E-15	AA397758.1	EST_HUMAN	z77608.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9002	21539	34468	0.87	2.0E-15	AA397758.1	EST_HUMAN	z77608.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9325	21839	34780	1.13	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201099-078-e12 HT0244 Homo sapiens cDNA
9325	21839	34781	1.13	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201099-078-e12 HT0244 Homo sapiens cDNA
10718	23246		3.59	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12487	16183	28845	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12487	16183	28846	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2803	15355		2.08	1.0E-15	AF699984.1	EST_HUMAN	b2805.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3046	15682	28143	1.24	1.0E-15	BE043584.1	EST_HUMAN	hk40602.y1 NCL_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 5'
3176	15789	28281	1.05	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6510	19110	31806	1.71	1.0E-15	T95763.1	EST_HUMAN	y40610.s1 Scores_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER8 repetitive element ;
7080	19652		1.91	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-q05 BT0569 Homo sapiens cDNA
7109	19445	32282	0.77	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8174	20715	31631	0.89	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8359	20899	33819	4.97	1.0E-15	A1200976.1	EST_HUMAN	qf88h08.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8359	20899	33820	4.97	1.0E-15	A1200976.1	EST_HUMAN	qf88h08.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8689	21607	34428	0.51	1.0E-16	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8972	21510	34432	1.89	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9171	21748	34891	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9550	22050	35012	1.18	1.0E-15	AA664633.1	EST_HUMAN	h37c03.s1 NCL_CGAP_K148 Homo sapiens cDNA clone IMAGE:1469872 3' similar to contains L1.13 L1
10698	23228	36242	6.86	1.0E-16	AF044083.1	NT	repetitive element;
12684	24820	30782	9.36	1.0E-16	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4417	17002		0.63	9.0E-16	BF689487.1	EST_HUMAN	602120192F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277422 5'
4602	17185	29832	1.11	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
10873	23394	38409	2.68	9.0E-16	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
5880	18502	31228	0.73	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7379	19905	32769	1.38	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7379	19905	32770	1.38	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12509	24916		33.75	7.0E-16	T94149.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
2186	14762		29.26	8.0E-16	AW972811.1	EST_HUMAN	ye28c12.r1 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:119062 5'
5436	17991	30397	0.94	8.0E-16	BF365702.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1539	14131	28687	1.21	6.0E-16	AJ251154.1	NT	QV2-NT0048-160800-316-412 NT0048 Homo sapiens cDNA
2705	15262	27829	2.6	6.0E-16	AA962176.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
11396	23848	36914	3.76	6.0E-16	BF217368.1	EST_HUMAN	0180c04.s1 Soares_tad1_fetus_Nb2HF8_9W Homo sapiens cDNA clone IMAGE:1623078 3' similar to
12606	24690		4.86	5.0E-16	11418127	NT	contains element L1 repetitive element;
2281	14855	27561	1.23	4.0E-16	AB001523.1	NT	601865734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2419	14987	27562	1.68	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2419	14987	27562	1.68	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3503	18108	28584	6.73	4.0E-16	Q18653	SWISSPROT	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4223	18111	29258	4.28	4.0E-16	BE083875.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4223	18111	29259	4.28	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
7688	20207	33094	37.48	4.0E-16	AL163284.2	NT	PM4-B10650-010400-002-g09 B10650 Homo sapiens cDNA
9219	21736	34678	1.44	4.0E-16	11423191	NT	PM4-B10650-010400-002-g09 B10650 Homo sapiens cDNA
11098	23608	36648	1.68	4.0E-16	AV730030.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
							AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11800	24180		1.34	4.0E-16	P08848	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11887	24232		13.78	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
11897	24238	31006		4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12178	24414		1.8	4.0E-16	R18591.1	EST_HUMAN	Y06b11.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 6'
138	12803	25282	0.83	3.0E-16	AW022882.1	EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2488378 5'
138	12803	26293	0.93	3.0E-16	AW022882.1	EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2488378 5'
491	13124		1.24	3.0E-16	AL048445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434P037 5'
501	13133		2.35	3.0E-16	AF135448.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1501	14093	26632	1.81	3.0E-16	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
3004	16820	28097	4.2	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (NA) (CONTAINS: GLYCOPROTEIN GP220)
4007	16805	29079	0.81	3.0E-16	T08189.1	EST_HUMAN	EST060660 Infant Brain, Berto Scores Homo sapiens cDNA clone HIBBA13 5' end
4031	16828		1.07	3.0E-16	U03987.1	NT	Human BXP20 gene
4899	17271	28720	0.87	3.0E-16	AW160828.1	EST_HUMAN	au76b08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782183 5' similar to SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5077	17850	30091	1.14	3.0E-16	AV681393.1	EST_HUMAN	AV681393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5482	18118		0.9	3.0E-16	AA077226.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5801	18428	31144	1.57	3.0E-16	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8692	21131	34047	4.08	3.0E-16	AU002836.1	EST_HUMAN	am88h05.s1 Strangene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR_b2 THR repetitive element;
9805	22303		0.84	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332032 5'
10027	22522	35518	5.15	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12637	25078	30516	0.33	3.0E-16	AL043288.2	EST_HUMAN	DKFZp434L1823_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L1823 5'
1007	13818		1.38	2.0E-16	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2428	14998		1.01	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Scores_tastis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2713	15270		1.53	2.0E-16	J03091.1	NT	Human SSAN-related endogenous retroviral LTR-like element
4267	16843	29282	1.34	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
5370	17830	30344	0.57	2.0E-16	BE061178.1	EST_HUMAN	RC3-BT0046-131189-003-H12 BT0046 Homo sapiens cDNA
6839	19429	32245	0.89	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7701	20210	33097	0.78	2.0E-16	AI470723.1	EST_HUMAN	H168t11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
7908	20450	33357	1.81	2.0E-16	AI732837.1	EST_HUMAN	nz47f06.x6 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280847 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7 repetitive element.;

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8099	20840	33551	0.7	2.0E-16	BE58028.1	EST_HUMAN	782h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8099	20840	33552	0.7	2.0E-16	BE58028.1	EST_HUMAN	782h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8484	21004	33921	0.6	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-401 PT0034 Homo sapiens cDNA
8484	21004	33922	0.6	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-401 PT0034 Homo sapiens cDNA
10808	23331	36343	2.71	2.0E-16	5902146	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
197	12857	28339	2.99	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
405	13080		20.83	1.0E-16	AA828592.1	EST_HUMAN	af39g11.81 Scores: total_tctus_Nb2HF8_0w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element:
2014	14596	27159	1.78	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-410 BN0148 Homo sapiens cDNA
5896	18518	31243	0.85	1.0E-16	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19163		27.66	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6688	18284	32087	2.77	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7556	19163		6.98	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
8207	21724	34987	1.15	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-405 PT0012 Homo sapiens cDNA
3802	19402	28868	2.48	9.0E-17	AW800048.1	EST_HUMAN	CM1-NN1003-200300-153-601 NN1003 Homo sapiens cDNA
6824	19414		1.84	9.0E-17	AI392884.1	EST_HUMAN	tg22c11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108624 3' similar to contains MER28.12 MER28 repetitive element:
8052	20594		4.65	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2830950 3' similar to contains OFR.12 OFR repetitive element:
10124	22819		2.1	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1056	13681		1.59	8.0E-17	AW880701.1	EST_HUMAN	QV0-O10032-080300-155-401 O10032 Homo sapiens cDNA
3681	18559		0.7	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5771	24748	31111	3.55	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0556-060300-003-604 HT0556 Homo sapiens cDNA
7319	18846		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1505	14097		3.4	7.0E-17	8753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBc2), mRNA
5526	18158		2.97	7.0E-17	AF216850.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6789	19380	32186	7.16	7.0E-17	AF22843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
217	12878	25365	7.43	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
6455	19056	31841	1.68	8.0E-17	AW682772.1	EST_HUMAN	h181d04.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878895 3' similar to contains L1.12 L1 repetitive element:
10192	22887	35680	0.52	8.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP87)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
446	12675	25131	2.78	5.0E-17	T64110.1	EST_HUMAN	yc05H08.r1 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:78839 5'
7866	20101	32978	1.82	5.0E-17	T81043.1	EST_HUMAN	yc28b04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:109327 5'
9284	21884	34829	1.12	4.0E-17	AW129185.1	EST_HUMAN	x120a04.x1 NCI_CGAP_K18 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element ;
11365	23817	36878	2.17	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11816	24188		2.38	4.0E-17	A1073546.1	EST_HUMAN	Q16530 PMS3 mRNA ; contains MER10.12 MER10 repetitive element ;
1540	14132		1.03	3.0E-17	D14547.1	NT	Human DNA, SINE repetitive element
2148	14723	27265	1.28	3.0E-17	AW119123.1	EST_HUMAN	xd89c09.r1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3227	15839		1.41	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3704	16305	28773	1.24	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181898 3'
3704	16306	28774	1.24	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181898 3'
5181	17747		1.02	3.0E-17	BF511266.1	EST_HUMAN	UI-H-B14-ec-c-09-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
8212	20753	33667	1.09	3.0E-17	N68451.1	EST_HUMAN	za14b02.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:282481 3' similar to contains PTR5.13 PTR5 repetitive element ;
9818	22118	35081	4.54	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10282	22777	35767	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10282	22777	35768	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11775	24163		3.77	3.0E-17	11417988	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
375	13024	25510	3.38	2.0E-17	A1270080.1	EST_HUMAN	qt03a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element;
378	13024	25510	2.68	2.0E-17	A1270080.1	EST_HUMAN	qt03a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element;
1025	13636		1.12	2.0E-17	AA722832.1	EST_HUMAN	zq81d04.s1 Soares_Fetal_Heart_NbHH19W Homo sapiens cDNA clone IMAGE:368751 3'
2490	15055	27627	2.43	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2490	15055	27628	2.43	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2858	15572	28049	8.08	2.0E-17	P12038	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5569	18200	30848	1.57	2.0E-17	M27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5569	18200	30849	1.57	2.0E-17	M27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
8410	19013		1.8	2.0E-17	AF055098.1	NT	Homo sapiens MHC class 1 region
6816	19213		1.58	2.0E-17	AL134881.1	EST_HUMAN	DKFZp782J0610_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782J0610 5'
7773	20282	33178	0.85	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8028	20570	33474	1.64	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8394	20934	33866	1.16	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
9783	22281	35267	2.45	2.0E-17	BE298888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980615 5'
9818	22316	35297	3.38	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9818	22316	35298	3.38	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10160	22655	35650	7.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10281	22776	35785	0.58	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10281	22778	35786	0.58	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10308	22800	35791	0.63	2.0E-17	A1788902.1	EST_HUMAN	w64504.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10308	22800	35792	0.63	2.0E-17	A1788902.1	EST_HUMAN	w64504.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
780	13399	25902	3.38	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1746	14336		1.2	1.0E-17	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1804	14394	26839	2.89	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2162	14739	27309	2.11	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2373	14943	27616	1.86	1.0E-17	U78410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3825	16228		0.89	1.0E-17	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4217	16806		8.48	1.0E-17	R09942.1	EST_HUMAN	y30607.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128388 5'
6759	18352	32161	1.55	1.0E-17	A185842.1	EST_HUMAN	q66503.x1 Soares_fetal_lung_NbHL16W Homo sapiens cDNA clone IMAGE:1743825 3'
6759	18352	32162	1.55	1.0E-17	A185842.1	EST_HUMAN	q66503.x1 Soares_fetal_lung_NbHL16W Homo sapiens cDNA clone IMAGE:1743825 3'
7148	18878	32520	1.28	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
6528	21087	33886	1.23	1.0E-17	BE082744.1	EST_HUMAN	QV0-BT0263-101289-072-d07 BT0263 Homo sapiens cDNA
9919	22415	35390	0.94	1.0E-17	AW988538.1	EST_HUMAN	QV3-BN0046-220300-128-c10 BN0046 Homo sapiens cDNA
11285	23747	36805	1.82	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2510	15074	27847	1.13	8.0E-18	AA174078.1	EST_HUMAN	zp18g12.a1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
9418	21927		3.03	9.0E-18	AI472167.1	EST_HUMAN	y86403.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3854	16452	28915	1.58	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
371	13020	25504	32.68	7.0E-18	AW316878.1	EST_HUMAN	xx10604.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20888 60S
371	13020	25505	32.68	7.0E-18	AW316878.1	EST_HUMAN	xx10604.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20888 60S
7489	19891	32854	0.98	7.0E-18	AW887542.1	EST_HUMAN	RC9-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12308	13020	25504	5.28	7.0E-18	AW318976.1	EST_HUMAN	xc10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
12308	13020	25508	6.28	7.0E-18	AW318976.1	EST_HUMAN	xc10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3334	15944	28419	1.36	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdnfr-1 gene for glia-derived neuroprotease modin 1, enhancer region
4857	17435		3.95	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8182	20733		2.75	6.0E-18	11428158	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC634448), mRNA
8289	20830	33751	0.6	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11014	23528	36964	1.87	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11209	23713	36767	1.9	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
11591	24034		2.22	6.0E-18	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
12041	24328	30985	2.24	6.0E-18	U87829.1	NT	Human acetylase hydratase (ACO2) gene, exon 4
1187	13788	26289	11.3	5.0E-18	AI280214.1	EST_HUMAN	qm85g11.x1 Soares_placenta_8to9weeks_2Nbl-P8b9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
5284	17848	30273	0.94	5.0E-18	D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-411F05 5'
5477	18111	30520	1.03	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8854	21193	34111	4.92	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c08 HT0161 Homo sapiens cDNA
10857	23378	36396	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10857	23378	36397	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12170	24409		6.5	5.0E-18	AW887182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
12531	24944		51.19	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
130	12797	25283	1.96	4.0E-18	BE044076.1	EST_HUMAN	hc36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28 b3 MER29 repetitive element;
130	12797	25284	1.96	4.0E-18	BE044076.1	EST_HUMAN	hc36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28 b3 MER29 repetitive element;
1754	14344	26880	8.14	4.0E-18	AA621814.1	EST_HUMAN	nc24f11.s1 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M28328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1933	14517		0.92	4.0E-18	AI738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2392095 3' N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N- ACETYLGLUCOSAMINYL TRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2242	14817	27360	1.23	4.0E-18	C06430	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N-ACETYLGLUCOSAMINYL TRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2242	14817	27391	1.23	4.0E-18	Q06430	SWISSPROT	cu23a06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5568	18197	30843	2.32	4.0E-18	A0107595.1	EST_HUMAN	cu23a06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5568	18197	30844	2.32	4.0E-18	A0107595.1	EST_HUMAN	cu23a06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7787	20330		0.81	4.0E-18	AA745811.1	EST_HUMAN	rx34a08.s1 NCL_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1266988 similar to contains L1.12 L1 repetitive element;
10884	23405	36424	7.68	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
882	13498	26015	18.02	3.0E-18	AA814198.1	EST_HUMAN	P-46782 40S RIBOSOMAL PROTEIN S6.;
885	13578	26091	2.25	3.0E-18	BE088834.1	EST_HUMAN	CMO-BT0690-210300-268-g07 B.T0690 Homo sapiens cDNA
4022	18020	29083	1.25	3.0E-18	AL103247.2	NT	Homo sapiens chromosome 21 segment H921C047
6917	18578	32405	6.98	3.0E-18	BE001871.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
2454	24504	18508	8.85	3.0E-18	AW022015.1	EST_HUMAN	df31h12.Y1 Morton Felal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
12312	19576	25416	2.57	2.0E-18	AW839820.1	EST_HUMAN	QV1-LT0038-150200-070-e07 LT0038 Homo sapiens cDNA
272	12829		197.1	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
1192	13793		1.15	2.0E-18	Q36975	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
3157	15771	28238	3.99	2.0E-18	AA898810.1	EST_HUMAN	ak53a07.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1409852 3' similar to TR:O14577
5606	18235		3.18	2.0E-18	D14547.1	NT	Q14577 BAG CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.;
5687	18323	30823	3.18	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5687	18323	30824	3.18	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
6038	18657		1.98	2.0E-18	BF347729.1	EST_HUMAN	602021164F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4196870 5'
6313	18920	31695	1	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6313	18920	31696	1	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
8424	19027	31810	0.84	2.0E-18	BF352940.1	EST_HUMAN	IL3-H70816-220700-222-C12 HT0819 Homo sapiens cDNA
			7.53	2.0E-18	AW665693.1	EST_HUMAN	h194g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879884 3' similar to contains MER19.12 MER19 repetitive element;
6460	19061	31847	1.39	2.0E-18	AW151673.1	EST_HUMAN	xf67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12 MER10 repetitive element;
9960	22455	35437	1.39	2.0E-18	AW151673.1	EST_HUMAN	xf67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12 MER10 repetitive element;
8960	22455	35438	1.39	2.0E-18	AW151673.1	EST_HUMAN	he33d08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
10954	23275	26204	4.96	2.0E-18	AW470791.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11578	24026	37083	5.24	2.0E-18	AW151289.1	EST_HUMAN	xp47e08.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MERB.b2
11970	13793		20.18	2.0E-18	BE250097.1	EST_HUMAN	MERB repetitive element ; 601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4507	17091		0.85	1.0E-18	T95408.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:120538 5' similar to contains L1 repetitive element ;
5558	18190	30608	1.91	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCCKE11 3'
6759	18385	31099	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5759	18385	31100	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6582	19180	31890	1.37	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8380	20920	33840	1.22	1.0E-18	AI148288.1	EST_HUMAN	cd8d009.x1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.11 L1 repetitive element ;
9813	22311	35283	4.45	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11918	24255	31011	4.39	1.0E-18	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
571	13202	25684	3.33	9.0E-19	AA281981.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
572	13202	25684	2.68	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element ;
7760	20333		5.93	9.0E-19	F08688.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
8922	21181	34076	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8822	21181	34077	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11007	23521	36556	3.92	9.0E-19	AB032669.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11878	13202	25684	28.32	9.0E-19	AA281981.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
1086	13691		1.38	8.0E-19	AW974902.1	EST_HUMAN	MER19 repetitive element ;
8090	20831	33544	1	8.0E-19	BE168936.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
2287	14881	27436	1.72	7.0E-18	4758139	NT	MRO-HT0404-210200-001-q08 HT0404 Homo sapiens cDNA
6584	19182	31982	1.91	7.0E-18	AF092090.1	NT	Homo sapiens DEAD/H (Aap-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
7341	18898	32732	0.95	7.0E-18	P26444	SWISSPROT	Rattus norvegicus cp151 mRNA, partial cds
9925	22421	35395	0.47	7.0E-19	AI344651.1	EST_HUMAN	BETA CRYSTALLIN A2
11823	25088		2.85	7.0E-19	AA705884.1	EST_HUMAN	tb01c08.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2052302 3'
3847	16446		1.21	6.0E-19	AW852930.1	EST_HUMAN	z180b01.s1 Soares fetal_liver_spliced_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
							PMO-CT0248-131088-001-p01 CT0248 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4582	17145	25592	1.39	6.0E-19	P34996	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4582	17145	25593	1.39	6.0E-19	P34996	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4919	17494		1.15	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6019	18638	31378	5.29	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6385	18989	31747	0.79	5.0E-19	AW663302.1	EST_HUMAN	h177606.v1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2868787 5'
10322	22816	35812	0.66	5.0E-19	AJ287689.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11412	23863	35924	7.61	5.0E-19	AW183725.1	EST_HUMAN	x187b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element
12544	24823		1.36	5.0E-19	U66060.1	NT	Human gametone T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S8A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
590	13210	25698	0.95	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2707	15264	27631	1.25	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4267674 5'
5593	18223	30672	1.1	4.0E-19	AF224989.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3919	16517	28982	1.58	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3919	16517	28983	1.58	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4373	16960	29405	0.9	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4373	16960	29406	0.9	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4544	17128	29571	1.33	3.0E-19	AV708138.1	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADGAMA11 5'
5484	18118		0.8	3.0E-19	AF223487.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7418	18942		1.83	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9380	20319	33220	1.2	3.0E-19	X89885.1	NT	M.musculus mRNA for TPCR33 protein
12084	24347		18.44	3.0E-19	AF165520.1	NT	Homo sapiens parvalbumin 1 protein (PBI) mRNA, complete cds
2595	15157	27725	7.09	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4542	17128		1.28	2.0E-19	AJ311783.1	EST_HUMAN	POLENV GENE;
8272	20813	33735	8.35	2.0E-19	AA012654.1	EST_HUMAN	z934c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
9823	22321	35308	0.91	2.0E-19	Q85155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
507	13140		1.65	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2209	14785	27358	1.48	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2743	15268		2.16	1.0E-19	D38044.1	NT	Human gene for AII-receptor, exon 7-9
2873	15491		5.99	1.0E-19	4786977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3448	16055	28531	1.37	1.0E-19	AA834987.1	EST_HUMAN	aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5322	17894		2.47	1.0E-19	AW117377.1	EST_HUMAN	xd88h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804739 3' similar to contains L1.b2 L1.L1 repetitive element;
6225	18834	31607	3.54	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6366	26116		0.74	1.0E-19	AA595627.1	EST_HUMAN	rh22d03.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.11 L1 repetitive element;
7824	20137	33015	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
7824	20137	33016	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8387	20927	33847	1.79	1.0E-19	M84857.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
8676	21215		2.48	1.0E-19	T69920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
10090	22585	35578	25.84	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191089-031-b05 S10174 Homo sapiens cDNA
10099	22894	35597	1.89	1.0E-19	N44631.1	EST_HUMAN	yy31e09.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:272872 5'
11353	23807		2.24	1.0E-19	AW023137.1	EST_HUMAN	df49h01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5'
11594	24037	37108	1.84	1.0E-19	U83163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
6754	18347	32155	2.39	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6754	18347	32156	2.39	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7527	20047	32917	1.4	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7527	20047	32918	1.4	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3314	15924	28402	0.78	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0098-050900-003-a04 AN0098 Homo sapiens cDNA
7088	18087	30443	5.61	7.0E-20	AL138120.1	EST_HUMAN	DKFZp447D092.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp447D092 5'
8433	20973	33887	9.45	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
8433	20973	33888	9.45	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
11551	24008		9.21	7.0E-20	6912333	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3611	16214	28694	4.64	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4359	16946	26388	4	6.0E-20	BE922434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4700	17282		1.11	5.0E-20	AV726123.1	EST_HUMAN	AV726123 HTC Homo sapiens cDNA clone HT08TA01 6'
7188	19701	32548	1.33	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library/Homo sapiens cDNA clone HA0250
7888	20428	33336	4.79	5.0E-20	W90526.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
7886	20428	33337	4.79	5.0E-20	W90526.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
8047	20589	33498	0.79	5.0E-20	BE18980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8789	21308	34231	1.53	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
8788	21308	34232	1.53	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9386	20305		1.08	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
5830	18454		0.82	4.0E-20	Q68880	SWISSPROT	HISTONE H2B C (H2B/C)
7886	20408		5.58	4.0E-20	AB74352.1	EST_HUMAN	tz84g03.x1 NCI_CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2283398 3'
10383	22887	35882	1.36	4.0E-20	AW637489.1	EST_HUMAN	QV3-DT0043-080200-080-c04 DT0043 Homo sapiens cDNA
2184	14760	27330	1.11	3.0E-20	U03888.1	NT	Human BXP21 gene
4288	16874	26323	1.49	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4408	16983	26436	0.67	3.0E-20	AF230376.1	NT	Meriones ungulicatus prestin (Pres) mRNA, complete cds
4731	17312	28755	0.83	3.0E-20	AA037616.1	EST_HUMAN	z436b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ;
8865	21404		2.94	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10223	22718	35708	0.82	3.0E-20	BF185284.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10543	23080		1.84	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11387	23839	36802	2.42	3.0E-20	A1284244.1	EST_HUMAN	q170d02.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element ;
11387	23839	36803	2.42	3.0E-20	A1284244.1	EST_HUMAN	q170d02.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element ;
11839	24202	31039	17.42	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915622 5'
863	13478		23.08	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:3915622 5'
1160	13763	26282	2.92	2.0E-20	AA516335.1	EST_HUMAN	P97481 40S RIBOSOMAL PROTEIN S6 ;
							ng68h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS6_MOUSE
							G1224068 ORF2: FUNCTION UNKNOWN ;
							ng68h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224068
1150	13763	26283	2.92	2.0E-20	AA516335.1	EST_HUMAN	G1224068 ORF2: FUNCTION UNKNOWN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2843	13478		16.26	2.0E-20	AW303888.1	EST_HUMAN	x24e10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2761068 3' similar to SW:RS5_MOUSE
5081	17854	30094	4.35	2.0E-20	Q28983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5 ;
5081	17854	30095	4.35	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5328	17888		1.43	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8081	20803	33514	0.97	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9118	21854	34595	5.33	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9118	21854	34596	5.33	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
11822	24064	37128	1.76	2.0E-20	AA768755.1	EST_HUMAN	MER4 repetitive element ;
11822	24064	37129	1.76	2.0E-20	AA768755.1	EST_HUMAN	MER4 repetitive element ;
12236	24808	30789	2.84	2.0E-20	H65371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2058	15396	27211	3.02	1.0E-20	AA281861.1	EST_HUMAN	z11d08.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
4533	17117	29583	1.18	1.0E-20	BF115158.1	EST_HUMAN	repetitive element ;
6975	19551	32378	0.72	1.0E-20	AFO49587.1	EST_HUMAN	AFO49587 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
9090	21826	34582	2.48	1.0E-20	11418491	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11427	23878	36943	3.02	1.0E-20	AF223381.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11968	24288		6.39	1.0E-20	AA420453.1	EST_HUMAN	nc80g08.r1 NCI CGAP_P71 Homo sapiens cDNA clone IMAGE:745894 similar to contains L1.13 L1
11681	24098		3.9	9.0E-21	AW898188.1	EST_HUMAN	repetitive element ;
8748	21285		1.77	8.0E-21	AW874891.1	EST_HUMAN	RC3-NN0088-090500-021-503 NN0088 Homo sapiens cDNA
11413	23884	36925	4.8	8.0E-21	AA809411.1	EST_HUMAN	bc30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
11852	24212		5.02	8.0E-21	O21330	SWISSPROT	O85169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
2113	14691	27258	1.61	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2113	14691	27259	1.61	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3784	18365	28832	0.58	7.0E-21	AL168300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4341	16928		4.31	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6584	19182	31860	0.78	7.0E-21	AL163218.2	NT	z667a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
							Homo sapiens chromosome 21 segment HS21C018

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8327	20868	33761	1.47	7.0E-21	AJ277567.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
8810	21149	34084	10.47	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10022	22517	35512	0.73	7.0E-21	AW868922.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
10575	23110	36123	3.18	7.0E-21	AA723404.1	EST_HUMAN	zq73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:U14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR13 OFR repetitive element ;
11147	23686	36697	1.94	7.0E-21	7706698	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4179	16770	29219	0.89	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9083	21600		0.58	6.0E-21	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
980	13571	26087	0.82	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4453	17039	29482	3.12	5.0E-21	BE688830.1	EST_HUMAN	601848871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4922	17497	29848	5.67	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6860	19584		0.83	5.0E-21	AW440884.1	EST_HUMAN	h006e10.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2818154 3'
7086	19857	32496	1	5.0E-21	BE5859503.1	EST_HUMAN	783d11.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11 OFR repetitive element ;
10486	22860	35970	0.79	5.0E-21	Q81690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10486	22860	35971	0.79	5.0E-21	Q81690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11768	24157		1.49	5.0E-21	AA393574.1	EST_HUMAN	z72d04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1769	14359	26904	1.24	4.0E-21	AA970713.1	EST_HUMAN	cc88d08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TRQ16530 Q16530 PMS3 MRNA ; contains OFR.11 OFR repetitive element ;
6953	19530	32355	3.04	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9696	22194	35187	0.61	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
1877	14463	27020	5.92	3.0E-21	AA218891.1	EST_HUMAN	zq15d08.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628771 3'
2313	14885	27460	1.2	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3116	15730	28200	3.35	3.0E-21	AJ007873.1	NT	Homo sapiens LGMD2B gene
5691	18317	30816	0.97	3.0E-21	AJ277567.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5691	18317	30817	0.97	3.0E-21	AJ277567.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5913	18535		0.75	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLCGOA10 3'
6326	18932		60.27	3.0E-21	BF184739.1	EST_HUMAN	601844485F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7128	19489	32287	7.35	3.0E-21	BF361083.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9609	22108	35071	0.98	3.0E-21	AW897760.1	EST_HUMAN	CMI-NN0003-280400-203-h08 NN0003 Homo sapiens cDNA
12359	25013	30817	2.75	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
167	12820		19.17	2.0E-21	BE163247.1	EST_HUMAN	QV9-HT0458-170200-000-g12 HT0458 Homo sapiens cDNA
870	13581	26083	0.71	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
970	13581	26094	0.71	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1258	13853		2	2.0E-21	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
2695	15223	27795	2.45	2.0E-21	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
2695	15223	27796	2.45	2.0E-21	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
5875	18302	30794	1.81	2.0E-21	A1824592.1	EST_HUMAN	ts30903.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5765	18391	31103	0.91	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 61.1 KD PROTEIN
5765	18391	31104	0.91	2.0E-21	AA027211.1	EST_HUMAN	z897a12.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8304	20845	33788	5.08	2.0E-21	BE141785.1	EST_HUMAN	z897a12.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8757	21298	34216	3.84	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
10937	23454		2.2	2.0E-21	BE3560127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005032 5'
11199	23704	36754	2.24	2.0E-21	BE973829.1	EST_HUMAN	h05g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148266 3' similar to contains MER29.b3
11199	23704	36755	2.24	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element
12072	24351		10.78	2.0E-21	AF179816.1	NT	601880036F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3951008 5'
1298	13892	28415	1.54	1.0E-21	AA557657.1	EST_HUMAN	601880036F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3951008 5'
1448	14040		3.58	1.0E-21	AB01264.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
5397	17855	30386	14.37	1.0E-21	P08548	SWISSPROT	nl46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
6613	19210		2.59	1.0E-21	AL079782.1	EST_HUMAN	MER29 repetitive element
7243	19772	32829	4.58	1.0E-21	A1223104.1	EST_HUMAN	ar85d12.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
10477	22971		1.45	1.0E-21	5730038	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12485	24816		2.48	1.0E-21	AF049133.1	NT	DKFZp434i0830_r1 434 (synonym: hbes3) Homo sapiens cDNA clone DKFZp434i0830 5'
4500	17084	29534	2.78	8.0E-22	A102438.1	EST_HUMAN	qq47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM
8540	21078	33988	1.2	9.0E-22	AL163201.2	NT	PROTEIN (HUMAN);
8540	21078	33989	1.2	9.0E-22	AL163201.2	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10670	23202	36215	5.06	9.0E-22	AV761874.1	EST_HUMAN	Homo sapiens chromosome Xp22 410-8
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001
							AV761874 MDS Homo sapiens cDNA clone MDSOCC05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11553	24001	37073	3.44	9.0E-22	AL140358.1	EST_HUMAN	AL140358 PLACE2 Homo sapiens cDNA clone PLACE2000384 5'
884	13568		4.18	8.0E-22	BE144748.1	EST_HUMAN	CMO-HT0179-281089-076-h08 HT0179 Homo sapiens cDNA
7837	20378		3.26	8.0E-22	AA046502.1	EST_HUMAN	2657a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
693	13318	25801	5.27	7.0E-22	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
4370	18957	29398	2.55	7.0E-22	Q81838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5190	17755	30184	1.12	7.0E-22	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8824	21163		1.99	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8766	21305	34227	3.39	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCF07
9520	22020	34977	1.83	7.0E-22	AF008880.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8184	20725		2.87	6.0E-22	AW029123.1	EST_HUMAN	w025g07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2642812 3'
6840	19236	32038	2.82	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10221	22716	35707	7.63	5.0E-22	U00822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12314	24508		2.92	5.0E-22	BF476511.1	EST_HUMAN	nea27b06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3255688 3' similar to contains Alu repetitive element
3698	18289		0.93	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
8048	20391	33498	0.53	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAU12 5'
8352	25122		3.38	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C082
10801	23135	36149	2.85	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12492	24621		3.39	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
994	13806		0.99	3.0E-22	AH489879.1	EST_HUMAN	hm14h10.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element;
3735	16336		1.44	3.0E-22	D14718.1	NT	Human chromosomal protein HMG1 related gene
4921	17488	28947	3.04	3.0E-22	AI060125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8172	20713		1.07	3.0E-22	BE156613.1	EST_HUMAN	QVG-HT0368-080200-099-112 HT0368 Homo sapiens cDNA
8177	20718	33833	2.55	3.0E-22	BE098841.1	EST_HUMAN	RCS-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8301	20842	33782	1	3.0E-22	X60860.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
8301	20842	33783	1	3.0E-22	X60860.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
1898	14578		2.49	2.0E-22	N24842.1	EST_HUMAN	yv73d05.s1 Soares_melanocytes_2NBHM Homo sapiens cDNA clone IMAGE:287369 3'
2664	15128	27697	1.81	2.0E-22	P24816	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3467	16074	28547	5.3	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4310	18898	29340	1.35	2.0E-22	AW817784.1	EST_HUMAN	PM1-ST0262-261189-001-d12 ST0262 Homo sapiens cDNA
6015	24753	31372	1.95	2.0E-22	W39456.1	EST_HUMAN	zo20f01.r1 Soares_sarcomatous_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6324	18930	31706	3.3	2.0E-22	BF092116.1	EST_HUMAN	RCO-TN0078-150900-025-h12 TN0078 Homo sapiens cDNA
8819	22119	35082	1.59	2.0E-22	A1276522.1	EST_HUMAN	q178h08.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains MER28.b3 MER28 repetitive element :
9712	22210	35182	0.69	2.0E-22	AA716315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219268 3'
9712	22210	35183	0.69	2.0E-22	AA716315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219268 3'
11595	24038	37107	2.33	2.0E-22	AW418960.1	EST_HUMAN	hs24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
11844	24605	30886	2.57	2.0E-22	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1821	14508	27083	1.59	1.0E-22	AW85517.1	EST_HUMAN	PM4-SN0020-010400-008-h02 SN0020 Homo sapiens cDNA
2820	15182	27748	1.88	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3457	18084	28539	1.45	1.0E-22	D14847.1	NT	Human DNA, SINE repetitive element
7723	20231	33120	1.29	1.0E-22	BE084687.1	EST_HUMAN	MRO-BT0869-220200-002-h07 BT0869 Homo sapiens cDNA
10446	22940	35850	0.84	1.0E-22	A1365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020881 3' similar to contains MER28.b2 MER28 repetitive element :
10446	22940	35851	0.84	1.0E-22	A1365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020881 3' similar to contains MER28.b2 MER28 repetitive element :
12540	24650		12.67	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0078-070400-001-F11 UM0078 Homo sapiens cDNA
3629	18232	28707	0.84	8.0E-23	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
3352	18960		2.37	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAW007 3'
10818	23437	36458	4.4	7.0E-23	5031932	NT	Homo sapiens Nci58 (D. melanogaster)-like protein (NOT58L) mRNA
3481	16087		1.83	6.0E-23	AF198333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4355	16942	28384	1.1	6.0E-23	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
11790	24173	31026	3.44	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11790	24173	31027	3.44	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11980	24300	30885	4.29	6.0E-23	A1209130.1	EST_HUMAN	q959c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE_P23249 PROTEIN MOV-10 :
5835	18264	30736	5.78	5.0E-23	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
6396	24763	31770	3.66	5.0E-23	AF179818.1	NT	Pongo pygmaeus effector receptor (PPY118) gene, partial cds
7483	24763	31770	3.02	5.0E-23	AF179818.1	NT	Pongo pygmaeus effector receptor (PPY118) gene, partial cds
5375	17834	30348	0.92	3.0E-23	AW846839.1	EST_HUMAN	QV3-CT0184-031189-004-f08 CT0184 Homo sapiens cDNA
6698	19187	31863	1.01	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6669	19167	31964	1.01	3.0E-23	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7760	20323	33228	4.27	3.0E-23	AA130165.1	EST_HUMAN	z55g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER28 12 MER29 repetitive element;
9173	21760	34694	2.69	3.0E-23	Z70864.1	NT	Human endogenous retroviral element HC2
9173	21750	34695	2.69	3.0E-23	Z70864.1	NT	Human endogenous retroviral element HC2
10219	22714		1.23	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-001 NN0066 Homo sapiens cDNA
10689	23503		1.54	3.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
894	13317	25802	3.65	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1182	15361		4.01	2.0E-23	M65270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2821	15373	27942	1.47	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2821	15373	27943	1.47	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3418	18026		1.36	2.0E-23	AI201458.1	EST_HUMAN	q573f11.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:1843757 3' similar to TR:Q13537 Q13537
3779	18378		3.93	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE..;
4048	16845	28112	3.01	2.0E-23	H59931.1	EST_HUMAN	MIR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4048	16845	28113	3.01	2.0E-23	H59931.1	EST_HUMAN	y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
7814	20357		4.59	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8777	21316	34238	1.05	2.0E-23	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11772	24161		3.5	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12328	24512		4.44	2.0E-23	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12454	25017		1.35	2.0E-23	AJ133931.1	EST_HUMAN	AL133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4627	17210	29660	1.72	1.0E-23	AL183252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4881	17458		5.35	1.0E-23	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6821	19411		4.93	1.0E-23	BE378471.1	EST_HUMAN	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
8297	20838	33766	4.53	1.0E-23	AA448097.1	EST_HUMAN	zw82c08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12 PTR5 repetitive element;
678	13208		1.48	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:EI9822 EI9822 CA PROTEIN.;
4753	17334	28777	1.16	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4753	17334	28778	1.16	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6576	19174	31873	1.08	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3941	16539		1.23	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-808 DT0047 Homo sapiens cDNA
5345	17908		18.11	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.1_134 (synonym: hla3) Homo sapiens cDNA clone DKFZp434A2311.6'
10518	23057		2.8	7.0E-24	AW303317.1	EST_HUMAN	xy1703.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
735	13355		2.28	6.0E-24	AB001421.1	NT	Macaca fascicularis mRNA for Testis-Specific Protein Y (TSPY), complete cds
871	13488	28001	12.95	6.0E-24	AL183249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4042	16840	28107	9.12	6.0E-24	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7735	20243	33134	0.9	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6087	18703	31451	3.17	4.0E-24	AA594178.1	EST_HUMAN	nm31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN;
8615	21154	34088	1.37	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-106 ST0197 Homo sapiens cDNA
11059	23571	36608	1.65	4.0E-24	BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484488 5'
12165	24405	30980	4.77	4.0E-24	AB028016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12428	24611	30889	1.37	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8382	20902		2.57	3.0E-24	AW614971.1	EST_HUMAN	h88e-08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2887860 3' similar to contains MER29.b2 MER29 repetitive element;
8414	20984		1.51	3.0E-24	AW952076.1	EST_HUMAN	EST374149 MAGE resequences, MAGG Homo sapiens cDNA
8388	21808	34760	3.79	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12247	24458	30989	2.85	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053396 5'
2394	14953	27525	3.07	2.0E-24	AA187539.1	EST_HUMAN	zp1169.r1 Stratiotes fetal retina 637202 Homo sapiens cDNA clone IMAGE:609161 5'
3897	16485		0.82	2.0E-24	AW898189.1	EST_HUMAN	RC3-NN0088-090500-021-603 NN0088 Homo sapiens cDNA
7480	20013	32879	1.14	2.0E-24	AF088824.1	NT	Mus musculus hdnra-interacting citron kinase (Cik) mRNA, complete cds
8675	21214	34135	2.59	2.0E-24	AL119159.1	EST_HUMAN	DKFZp761L1712_r1_761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
8712	21251		0.87	2.0E-24	H89214.1	EST_HUMAN	yr92b09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element;
9768	22266	35250	0.82	2.0E-24	AI521759.1	EST_HUMAN	877609.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2136008 3'
9768	22266	35251	0.82	2.0E-24	AI521759.1	EST_HUMAN	877609.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2136008 3'
12080	25082		13.88	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1734	14325	28887	3.18	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2687	15284		1.43	1.0E-24	AW820184.1	EST_HUMAN	QV0-ST0284-100400-185-c10 ST0284 Homo sapiens cDNA
3055	15671	28147	0.76	1.0E-24	DB8423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4357	16844		1.97	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7551	20070	32848	4.06	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7713	20222	33109	0.8	1.0E-24	BE144528.1	EST_HUMAN	MRO-HT0166-271199-005-d09 HT0166 Homo sapiens cDNA
7885	20427	33335	1.38	1.0E-24	AW801184.1	EST_HUMAN	CMO-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
11545	23093	37084	1.58	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG1), mRNA
8443	17888		2.05	8.0E-25	6138972	NT	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA
5138	17708	30140	2.99	7.0E-25	AA483044.1	EST_HUMAN	ne52a10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911764 similar to contains MER1.b2
8160	20701	33816	5.07	7.0E-25	AA488948.1	EST_HUMAN	ne08a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
11547	23885	37087	9.93	7.0E-25	AA583540.1	EST_HUMAN	m25h08.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7065	18084	26628	4.4	6.0E-25	W87623.1	EST_HUMAN	P38105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.;
7708	20215	33103	10.77	8.0E-25	7306390	NT	z65h07.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
11198	23701	38782	4.55	5.0E-25	AW978107.1	EST_HUMAN	Mus musculus clogelin (Clog), mRNA
1486	14088	26628	2.75	4.0E-25	T88107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
3449	18058		3.2	4.0E-25	AW887871.1	EST_HUMAN	yes6h04.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3974	18572	28042	1.42	4.0E-25	AF00368.1	NT	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4407	18992		4.05	4.0E-25	BE170967.1	EST_HUMAN	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
3362	18970	28447	3.73	3.0E-25	8823321	NT	QV3-HT0543-140400-149-s11 HT0543 Homo sapiens cDNA
3362	15970	28448	3.73	3.0E-25	8823321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5022	17596	30039	0.68	3.0E-25	P28822	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
8728	18322	32127	0.84	3.0E-25	AA603590.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8278	20820	33739	3.84	3.0E-25	AL163210.2	NT	np27b02.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1117616 3' similar to gb:M61868 ZINC FINGER PROTEIN 85 (HUMAN);
10911	23430	38450	2.02	3.0E-25	AA578013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1392	13888	26513	9.82	2.0E-25	5032158	NT	repetitive element;
2347	14918	27492	7.6	2.0E-25	BE888016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2858	15142	27711	3.84	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4268	18554	28301	2.04	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S18
4268	18554	28302	2.04	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S18
5680	22179	35154	1.9	2.0E-25	AL448573.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S18
387	13033	25522	0.71	1.0E-25	AL040229.1	EST_HUMAN	AL448573 Homo sapiens Testis (Starvies GS) Homo sapiens cDNA
1291	13886		1.67	1.0E-25	8835487	NT	DKFZp434H0313_r1 434 (synonym: hss5) Homo sapiens cDNA clone DKFZp434H0313 5'
							Human endogenous retrovirus, complete genome

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2478	16046	27613	1.13	1.0E-26	Q06035	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4894	17558	30001	3.09	1.0E-26	BE162737.1	EST_HUMAN	PM1-HT0494-080100-002-H09 HT0454 Homo sapiens cDNA
6883	19276		0.86	1.0E-26	AA189080.1	EST_HUMAN	z44508.s1 Stratiogene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element
6890	24775	32460	3.08	1.0E-26	AA582690.1	EST_HUMAN	nt54h11.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
7855	20397	33303	4.27	1.0E-26	AA708076.1	EST_HUMAN	z46904.s1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains
9485	21890	34846	0.68	1.0E-26	X60660.1	NT	PTRE.13 PTR5 repetitive element
9489	21890	34847	0.68	1.0E-26	X60660.1	NT	R. retus RY2G5 mRNA for a potential ligand-binding protein
10849	23370	36399	3.71	1.0E-26	U93163.1	NT	R. retus RY2G5 mRNA for a potential ligand-binding protein
11787	24171	36777	1.9	1.0E-26	D14547.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11787	24171	36778	1.9	1.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2523	16087	27660	1.57	9.0E-26	AL163218.2	NT	Human DNA, SINE repetitive element
11645	24828		1.69	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C018
5872	18484		1.55	8.0E-26	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C085
1621	14214	26745	0.92	7.0E-26	AF003628.1	NT	Human DNA, SINE repetitive element
4052	16649	28117	1.18	7.0E-26	X89211.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4238	16827	29276	2.04	7.0E-26	AW340163.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
5819	18443	31165	0.86	7.0E-26	AL163202.2	NT	h02a12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808366 3'
11520	23968		8.46	7.0E-26	AA115895.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
12378	24644		3.49	7.0E-26	AW954569.1	EST_HUMAN	z33008.r1 Stratiogene neuroepithelium NT2RAMI 637234 Homo sapiens cDNA clone IMAGE:648943 5' similar to gb-M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); EST366828 MAGE resequences, MAGE Homo sapiens cDNA
2287	14841	27418	2.32	6.0E-26	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3300	16988	28478	1.37	6.0E-26	AA208131.1	EST_HUMAN	z52h04.r1 Stratiogene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:645271 5'
10428	22920	35922	0.48	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10428	22920	35923	0.48	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11531	23978	37049	5.92	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1219	13819	26334	3.55	5.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barstead acia HPLRB8 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1218	13818	26335	3.55	5.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barstead acia HPLRB8 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1591	14184		2.25	4.0E-26	AA329548.1	EST_HUMAN	EST33448 Embryo, 12 week II Homo sapiens cDNA 5' end
9333	21847		3.53	4.0E-26	7657870	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10538	23078	36900	3.69	4.0E-26	BE268187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536210 5'
1798	14386	26930	1.2	3.0E-26	D14847.1	NT	Human DNA, SINE repetitive element
2046	14828	27187	1	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434i086_j1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i086 5'
2077	14857		2.22	3.0E-26	AA115895.1	EST_HUMAN	z330408.r1 Stratiens neuroepithelium NT2RAM1 637234 Homo sapiens cDNA clone IMAGE:548943 5'
3846	16445	28906	1.48	3.0E-26	AA152484.1	EST_HUMAN	similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3846	16445	28906	1.48	3.0E-26	AA152484.1	EST_HUMAN	G895374 THYROID RECEPTOR INTERACTOR ;
3846	16445	28907	1.48	3.0E-26	AA152484.1	EST_HUMAN	z33010.r1 Stratiens cdon (6637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
6991	19489	32311	6.04	3.0E-26	BF245498.1	EST_HUMAN	G895374 THYROID RECEPTOR INTERACTOR ;
10604	23138		1.87	3.0E-26	AF039405.1	NT	601804963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11442	23892	36957	2.58	3.0E-26	AW875651.1	EST_HUMAN	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11442	23892	36958	2.58	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11472	23922	36992	13.09	3.0E-26	AA583173.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
12566	24605		2.21	3.0E-26	AW073434.1	EST_HUMAN	nr37403.s1 NCL CGAP_GCS Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
12661	24732	30857	1.48	3.0E-26	AF165520.1	NT	OFR repetitive element ;
710	13331	26818	6.38	2.0E-26	AL163282.2	NT	xa57b09.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2670873 3' similar to contains MER30.11
1908	14494		2.42	2.0E-26	AL036099.2	EST_HUMAN	MER30 repetitive element ;
3268	16980	28363	4.94	2.0E-26	X86894.1	NT	Homo sapiens phospholipase 1 protein (PL1) mRNA, complete cds
10633	23166		3.35	2.0E-26	D87676.1	NT	Homo sapiens chromosome 21 segment HS21C082
11098	23607	36847	5.24	2.0E-26	AB01412.1	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hnf42) Homo sapiens cDNA clone DKFZp566L171 3'
11298	23748		2.17	2.0E-26	AF056066.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-16
11694	24237		1.65	2.0E-26	AB037859.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12101	25005	30612	3.03	2.0E-26	11435947	NT	ts89a01.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2186416 3' similar to contains Alu
142	12807	25295	13.71	1.0E-26	BE170371.1	EST_HUMAN	repetitive element; contains element MER20 MER20 repetitive element ;
2091	14671	27241	1.5	1.0E-26	AL039363.2	EST_HUMAN	Homo sapiens MHC class 1 region
2588	15160	27728	1.48	1.0E-26	BE814995.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2710	15267		6.31	1.0E-26	AF261085.1	NT	QV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
6927	19566		2.52	1.0E-26	BE165890.1	EST_HUMAN	DKFZp434H1810_j1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1810 5'
							MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10772	23266		2.98	1.0E-28	AL038487.1	EST_HUMAN	DKFZp568C2148_r1_668 (synonym: hfk42) Homo sapiens cDNA clone DKFZp568C2148 5'
12151	25084		2.78	1.0E-28	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
12825	24703		1.27	1.0E-28	AW408742.1	EST_HUMAN	U1-HF-BM0-adv-d-10-U1 r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'
7684	20058		1.17	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9227	21949		4	9.0E-27	U93183.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11848	24080		6.15	9.0E-27	BF445556.1	EST_HUMAN	ncs03c07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3283844 3' similar to contains OFR.t1 OFR repetitive element:
11	12680	25148	3.07	8.0E-27	A1831482.1	EST_HUMAN	w49cd04.x1 NCL_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element:
583	13213		3.38	8.0E-27	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1481	14053	26586	28.2	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):
1481	14053	26588	28.2	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):
2212	14787	27382	1.48	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-#07 SN0018 Homo sapiens cDNA
3219	15831	28310	1.89	8.0E-27	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3388	18004	28485	0.59	8.0E-27	AF181887.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5873	18495	31221	1.14	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB08 5'
7054	18073		2.9	8.0E-27	BE928580.1	EST_HUMAN	MR4-BT0398-260800-204-#08 BT0398 Homo sapiens cDNA
7111	18451	32287	2.49	8.0E-27	N94970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9138	21871	34613	1.35	8.0E-27	AW857679.1	EST_HUMAN	GM1-CT0315-091289-063-#07 CT0315 Homo sapiens cDNA
9138	21871	34614	1.35	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-063-#07 CT0315 Homo sapiens cDNA
712	13333		1.39	7.0E-27	Z70864.1	NT	Human endogenous retroviral element HC2
5252	17815		2.68	7.0E-27	AW629172.1	EST_HUMAN	h15h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O78040 O78040 ORF2: FUNCTION UNKNOWN.:
8791	21330		0.77	7.0E-27	D88984.1	NT	Human mRNA for KIAA0231 gene, partial cds
10828	23160		4.39	7.0E-27	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12288	24485		3.27	7.0E-27	AV723385.1	EST_HUMAN	AV723385 HTB Homo sapiens cDNA clone HTBAHE02 5'
10805	23139	36151	11.92	6.0E-27	M26897.1	NT	Human nuclear protein (B23) mRNA, complete cds
11821	24083	37127	2.33	6.0E-27	U93183.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7752	20260		0.78	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C03
10136	22831	35819	2.88	5.0E-27	BF686814.1	EST_HUMAN	602121491F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278827 5'
10136	22831	35820	2.88	5.0E-27	BF686814.1	EST_HUMAN	602121491F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278827 5'
2423	14981	27684	4.88	4.0E-27	D25303.1	NT	Human mRNA for Integrin alpha subunit, complete cds
6842	19432	32247	1.37	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
7880	20422		1.14	4.0E-27	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C09
7825	20467		1.22	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9659	22158	35130	0.8	4.0E-27	AW880859.1	EST_HUMAN	QV6-OT0033-070300-182-b10 OT0033 Homo sapiens cDNA
11473	23923	36883	2.38	4.0E-27	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
2085	14686	27237	6.19	3.0E-27	X80858.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4358	16945	28387	1.58	3.0E-27	BE071824.1	EST_HUMAN	PMO-BT0527-080100-001-d11 BT0527 Homo sapiens cDNA
5548	18181	30588	6.22	3.0E-27	AA077705.1	EST_HUMAN	7844C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7844C08
9226	21951	34900	3.87	3.0E-27	BF036327.1	EST_HUMAN	601458631F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3682088 5'
45	12724	25185	28.89	2.0E-27	AF094187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1940	14524		12.18	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886.60S
3143	15757		12.54	2.0E-27	AW829172.1	EST_HUMAN	h15h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875878 3' similar to TR:O76040
3261	15873	28363	1.74	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3261	15873	28354	1.74	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6778	18370	32185	0.88	2.0E-27	H02865.1	EST_HUMAN	X86601.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8034	20576	33481	1.24	2.0E-27	AIB66347.1	EST_HUMAN	SP-HMGC_MOUSE Q02691 HOMEOBOX PROTEIN ;
9193	21710		2.25	2.0E-27	AA551527.1	EST_HUMAN	m28g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426288 3'
9707	22205	35178	1	2.0E-27	X80858.1	NT	nh08h05.s1 NCL_CGAP_Thyl1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1 L3 L1
9948	22443	35421	1.03	2.0E-27	M78580.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
9948	22443	35422	1.03	2.0E-27	M78580.1	EST_HUMAN	EST00738 Fetal brain, Strabagene (cat8639208) Homo sapiens cDNA clone HFBCF07
10834	23355	36370	3.38	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Strabagene (cat8639208) Homo sapiens cDNA clone HFBCF07
11360	14624		16.88	2.0E-27	AA565345.1	EST_HUMAN	ALU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
481	13085		1.17	1.0E-27	AL163246.2	NT	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886.60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C046

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1034	13644	26157	1.25	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4155	18747		1.02	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER20.b3
6885	19281	32085	6.88	1.0E-27	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6852	19529	32353	1.88	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
6852	19529	32354	1.88	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
8548	21085	34008	0.7	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8916	21454		1.89	1.0E-27	BE076780.1	EST_HUMAN	RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
9638	22138	35104	2.68	1.0E-27	DB7449.1	NT	Human mRNA for KIAA0260 gene, partial cds
11551	23999	37071	3.65	1.0E-27	AF111093.1	NT	Bos taurus letraphilin 3 splice variant bbah mRNA, complete cds
148	12810		2.02	9.0E-28	BE348399.1	EST_HUMAN	hwt1c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
333	12985	25472	2.19	9.0E-28	AU128280.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313 ;
11732	24137		4.71	9.0E-28	BF377859.1	EST_HUMAN	CM2-TNC140-070900-372-g01 TNC140 Homo sapiens cDNA
12066	24923		4.41	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to
1223	13823	28338	16.9	7.0E-28	AU142750.1	EST_HUMAN	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element ;
11066	23578	36616	3.08	7.0E-28	11417885	NT	AU142750 Y78AA1 Homo sapiens cDNA clone Y78AA1000824 5'
11888	24104		2.37	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8850	21389		1.04	6.0E-28	AF018052.1	NT	AV735348 CB Homo sapiens cDNA clone CBFACA12 5'
12346	24527		12.5	6.0E-28	AA504562.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
340	12992		2.28	5.0E-28	AI921003.1	EST_HUMAN	aa60d03.1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
4081	16877	29137	1.79	5.0E-28	R79782.1	EST_HUMAN	repetitive element; contains element PTR5 repetitive element ;
2654	15213	27786	1.12	4.0E-28	AW195066.1	EST_HUMAN	w018c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:24555892 3' similar to contains THR.b1
3005	15621	28088	0.78	4.0E-28	4503316	NT	THR repetitive element ;
3142	15756	28223	3.13	4.0E-28	BE409100.1	EST_HUMAN	y68f10.1r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148443 5'
7368	19894	32757	1.79	4.0E-28	AI198941.1	EST_HUMAN	xs33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2865504 3' similar to SW:GG96_HUMAN
10745	23269		4.9	4.0E-28	AF029308.1	NT	Q08379 GOLGIN-95 ;
							Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3835305 5'
							qf66f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M18503 LINE-1
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
							Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypanogen gene families

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23406		25.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10804	19894	32757	3.33	4.0E-28	A108941.1	EST_HUMAN	qf66f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1785019 3' similar to gb:M18503 LINE-1
12116	24375		1.71	4.0E-28	AW854244.1	EST_HUMAN	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12657	24728		72.51	4.0E-28	AW157571.1	EST_HUMAN	RC3-CT0264-240400-210-112 CT0254 Homo sapiens cDNA
1326	13920		1.96	3.0E-28	AF155382.1	NT	au83r08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to
8761	21300	34221	3.77	3.0E-28	BF354030.1	EST_HUMAN	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element ;
10815	23336	36349	2.08	3.0E-28	U63588.1	EST_HUMAN	Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
12147	24390		2.53	3.0E-28	A831091.1	EST_HUMAN	MR3-HT0713-280500-013-f08 HT0713 Homo sapiens cDNA
12284	24486		1.77	3.0E-28	BE082801.1	EST_HUMAN	Homo sapiens MHC class 1 region
92	12768	26261	8.71	2.0E-28	BE082167.1	EST_HUMAN	wj86f07.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element/contains element HGR repetitive element ;
1207	13607	26320	9.63	2.0E-28	Y11107.3	NT	RC2-BT0842-210200-013-f03 BT0842 Homo sapiens cDNA
2617	15081	27854	2.47	2.0E-28	A1348634.1	EST_HUMAN	RC1-BT0284-220300-019-c05 BT0254 Homo sapiens cDNA
3407	16016	28495	0.64	2.0E-28	AL163208.2	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8449	19050	31836	1.2	2.0E-28	BF224402.1	EST_HUMAN	qc35b08.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1810483 3' similar to contains L1.b2 L1 repetitive element ;
8472	18073		5.22	2.0E-28	BF212805.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
7888	20530	33437	0.77	2.0E-28	AF003273.1	NT	hr76c03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element ;
8505	22005		11	2.0E-28	AW972305.1	EST_HUMAN	601814186F1 NIH_MGC_34 Homo sapiens cDNA clone IMAGE:4048751 5'
11481	23631	37002	1.91	2.0E-28	AF224689.1	NT	Sua scrofa domestica submaxillary apomucin mRNA, complete cds
12127	24383		1.74	2.0E-28	H06378.1	EST_HUMAN	EST384394 IMAGE resequences, MAGI Homo sapiens cDNA
1528	14118	26655	3.52	1.0E-28	D38044.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
2261	14635	27413	1.64	1.0E-28	BF333236.1	EST_HUMAN	yf76c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
2708	15265	27832	1.38	1.0E-28	AF000995.1	NT	Human gene for Ah-receptor, exon 7-9
4688	17260		0.66	1.0E-28	U08410.1	NT	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
7801	20344		7.69	1.0E-28	11428985	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
7861	20803		3.2	1.0E-28	8922793	NT	Human zinc finger protein ZNF131 mRNA, partial cds
9202	21719	34663	4.72	1.0E-28	AA308744.1	EST_HUMAN	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63097), mRNA
							Homo sapiens hypothetical protein FLJ109688 (FLJ10968), mRNA
							EST178615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9790	22288	35272	9.67	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9790	22288	35273	9.67	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
11893	24108		10.45	1.0E-28	A054182.1	EST_HUMAN	zf51cd01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
12484	24811		1.58	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12598	25034	30502	3.5	9.0E-29	AW663987.1	EST_HUMAN	h17g008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978268 3'
12245	24456		5.36	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1848	14238	26773	1.04	7.0E-29	AW968447.1	EST_HUMAN	EST378621 MAGE resequences, MAGI Homo sapiens cDNA
3607	16211		0.91	7.0E-29	BE254708.1	EST_HUMAN	601114980F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355367 5'
12844	24718		13.85	7.0E-29	AJ123252.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
621	13248	25722	7.35	6.0E-29	A836748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468885 3' similar to TR:O15475
12002	24307		9.29	6.0E-29	BE040436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
5138	17710		1.02	5.0E-29	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8686	21205		7.83	5.0E-29	AW887541.1	EST_HUMAN	RC3-OT0081-170300-011-c12 OT0081 Homo sapiens cDNA
12276	24480		1.32	5.0E-29	BE612449.1	EST_HUMAN	601451827F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3655728 5'
3289	15881		2.92	4.0E-29	A1752387.1	EST_HUMAN	en15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en15c02 random
6190	18773		6.52	4.0E-29	BE184930.1	EST_HUMAN	QV1-1T0471-280300-121-e05 HT0471 Homo sapiens cDNA
8025	20597	33469	0.92	4.0E-29	A1878101.1	EST_HUMAN	wd35g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8025	20597	33470	0.92	4.0E-29	A1878101.1	EST_HUMAN	wd35g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8690	21219	34139	6.03	4.0E-29	J04988.1	NT	Homo sapiens 90 kD heat shock protein gene, complete cds
4508	17090	28538	1.58	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
4839	17417	28870	1.28	3.0E-29	BF333236.1	EST_HUMAN	QV1-BT0821-120600-360-b03 BT0821 Homo sapiens cDNA
6098	18704	31452	0.88	3.0E-29	BE314018.1	EST_HUMAN	601152857F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3508527 5'
8668	21207	34124	2.6	3.0E-29	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
9224	21740	34683	1.93	3.0E-29	AW303317.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
9450	21978		2.01	3.0E-29	AL163248.2	NT	repetitive element; contains MER19.12 MER19 repetitive element ;
9869	22386		0.76	3.0E-29	BE350127.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
11148	23656	36698	1.88	3.0E-29	AA403053.1	EST_HUMAN	h05g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
							MER29 repetitive element ;
							z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335789
							G1335789 GAG-POL POLYPROTEIN. ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11891	24234		2.61	3.0E-29	D93882.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
12553	25044		1.95	3.0E-29	D93882.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
518	13150	25632	1.07	2.0E-29	AF084889.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
518	13150	25633	1.07	2.0E-29	AF084889.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
1580	14173	26703	7.28	2.0E-29	AI963604.1	EST_HUMAN	wr6610.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15548 HERV-E ENVELOPE GLYCOPROTEIN ;
1680	14173	26704	7.28	2.0E-29	AI963604.1	EST_HUMAN	wr6610.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15548 HERV-E ENVELOPE GLYCOPROTEIN ;
4388	16953	28393	2.01	2.0E-29	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C088
5991	18611	31346	0.88	2.0E-29	AI082459.1	EST_HUMAN	ca71e04.x1 NCL_CGAP_QC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1:12 L1 repetitive element ;
6327	18933	31708	1.45	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356880 3' similar to contains element MER8 repetitive element ;
7660	18933	31708	1.2	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356880 3' similar to contains element MER8 repetitive element ;
7917	20459	33396	1.15	2.0E-29	BE687157.1	EST_HUMAN	601442206F1 NIH_MGC 89 Homo sapiens cDNA clone IMAGE:3846948 5'
8514	21053	33975	0.55	2.0E-29	10587821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
8514	21053	33976	0.55	2.0E-29	10587821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
9427	21936	34884	3.74	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9427	21936	34885	3.74	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10138	22633	35622	3.15	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10138	22633	35623	3.15	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11350	23805		2.03	2.0E-29	11426108	NT	Homo sapiens splicing factor similar to dnlJ (SPF31), mRNA
11390	23842		2.48	2.0E-29	AW860701.1	EST_HUMAN	QV0-OT0032-080300-155-801 OT0032 Homo sapiens cDNA
11835	24075		1.83	2.0E-29	AL163227.1	NT	Homo sapiens chromosome 21 segment HS21C027
8727	21266	34186	7.44	1.0E-29	AW953880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
10503	22987	36006	0.78	1.0E-29	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein n20c07.a1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
6898	19292	32096	3.08	8.0E-30	AA781215.1	EST_HUMAN	n20c07.a1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
11773	24162		2.08	6.0E-30	11422745	NT	Homo sapiens zinc/ferritin regulated transporter-like (ZIRTL), mRNA
6481	19082		9.33	8.0E-30	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8214	20755	33669	2.85	8.0E-30	AA383873.1	EST_HUMAN	EST197317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
8617	21156	34099	4.64	8.0E-30	AI657072.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
1582	14154		0.91	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7779	20291	33190	1.28	7.0E-30	BF05327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
1810	14400	28845	1.35	6.0E-30	D28303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3224	15936	28314	2.38	6.0E-30	BE008028.1	EST_HUMAN	QVO-BN0147-280400-214-112 BN0147 Homo sapiens cDNA
4872	18838	28314	1.1	6.0E-30	BE008028.1	EST_HUMAN	QVO-BN0147-280400-214-112 BN0147 Homo sapiens cDNA
10432	22828	35932	0.72	6.0E-30	AF17727.1	NT	Homo sapiens CTCL tumor antigen s20-10 mRNA, partial cds
12615	18024		1.6	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4085	16881	29141	39.51	5.0E-30	AJ388992.1	EST_HUMAN	ig2g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
5448	24850		4.03	5.0E-30	U87831.1	NT	Human acetylase hydratase (ACO2) gene, exon 7
10787	23291		3.31	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11034	23548	36893	6.29	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11034	23548	36884	6.29	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2188	14784	27333	1.32	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-090200-080-008 DT0043 Homo sapiens cDNA
2188	14784	27334	1.32	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-090200-080-008 DT0043 Homo sapiens cDNA
8838	21375	34289	3.16	4.0E-30	AW812488.1	EST_HUMAN	GM1-ST0181-091189-035-008 ST0181 Homo sapiens cDNA
1191	13782		3.43	3.0E-30	AJ388551.1	EST_HUMAN	qq83c05.x1 Soares fetal_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER28 repetitive element
3821	16421	28883	0.87	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
7893	20435		0.47	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8423	20863		0.5	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10330	22824	35820	1.69	3.0E-30	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kir13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER28 repetitive element
10460	22954	35964	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
10460	22954	35965	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11084	23598	36632	1.78	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
703	13324	25811	1.3	2.0E-30	AW857315.1	EST_HUMAN	GM0-CT0307-310100-168-003 CT0307 Homo sapiens cDNA
1123	13726		2.35	2.0E-30	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1527	14119	28856	7.23	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-008 HT0582 Homo sapiens cDNA
2740	15295	27862	9.08	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
2944	15560	28034	6.74	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZF1) gene, complete cds
3857	16455	28919	2.18	2.0E-30	AW206581.1	EST_HUMAN	U1-H-B11-efo-c-12-4-J1.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4892	17467	29922	2.07	2.0E-30	BE268945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4892	17467	29923	2.07	2.0E-30	BE268945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
9855	19443	32259	0.82	2.0E-30	BF306337.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138883 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8412	20952	33971	0.81	2.0E-30	AA019103.1	EST_HUMAN	2858c10.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:383188 5'
8474	21014	33630	5.63	2.0E-30	C18839.1	EST_HUMAN	C18839 Human placenta cDNA (TF-ujlwara) Homo sapiens cDNA clone GEN:570C01 5'
8570	21109	34027	3.55	2.0E-30	BE070817.1	EST_HUMAN	7e37c12.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8570	21109	34028	3.55	2.0E-30	BE070817.1	EST_HUMAN	7e37c12.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8908	22405	35360	3.21	2.0E-30	AW971688.1	EST_HUMAN	EST383857 IMAGE resequences, MAGL Homo sapiens cDNA
8984	22489	35477	6.11	2.0E-30	AW470781.1	EST_HUMAN	ha33d08.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2876498 3' similar to contains THR.b3 THR repetitive element ;
308	12983	25452	12.31	1.0E-30	C18839.1	EST_HUMAN	C18839 Human placenta cDNA (TF-ujlwara) Homo sapiens cDNA clone GEN:570C01 5'
583	13194	25873	3.84	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
745	13365	25959	2.7	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2253	14827	27403	3.59	1.0E-30	AA684377.1	EST_HUMAN	ec77b08.at1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:863569 3'
2502	15068	27640	1.84	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI CGAP Brm87 Homo sapiens cDNA clone IMAGE:4157891 5'
3035	15951	28129	1.38	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; aIF-2-associated p87 (MNPEP), mRNA
3090	15705	28177	1.08	1.0E-30	AA315045.1	EST_HUMAN	EST186898 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7708	20217	33105	16.66	1.0E-30	BF183230.1	EST_HUMAN	601808932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040884 5'
12288	28029		1.48	1.0E-30	AA289211.1	EST_HUMAN	EST11898 Uterus Homo sapiens cDNA 5' end
12411	24949		6.63	1.0E-30	H55593.1	EST_HUMAN	CHR22032 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3829	18429	28890	0.72	9.0E-31	T73025.1	EST_HUMAN	yc65e08.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
3829	18429	28891	0.72	9.0E-31	T73025.1	EST_HUMAN	yc65e08.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
8268	20807	33725	1.03	9.0E-31	R18214.1	EST_HUMAN	yf9b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8268	20807	33726	1.03	9.0E-31	R18214.1	EST_HUMAN	yf9b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8559	21098		1.84	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8581	21100	34020	0.52	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
12640	24715	30667	1.89	9.0E-31	8755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1115	13719	28230	6.84	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2487	15024		4.22	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
11801	24910		2.71	8.0E-31	AF012385.1	EST_HUMAN	AF012385 Human testis (C. De Sma) Homo sapiens cDNA clone TDP3.12b

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
740	13360		2.5	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2692	15249	27818	2.37	7.0E-31	BE328517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2692	15249	27818	2.37	7.0E-31	BE328517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8240	20881	33800	0.82	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8340	20881	33801	0.82	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9190	21707		1.62	7.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12243	24455	30958	1.53	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3742	16343		2.28	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8094	20635		6.98	6.0E-31	AF056086.1	NT	Homo sapiens MHC class 1 region
8273	20814	33736	0.78	6.0E-31	BE350127.1	EST_HUMAN	hw09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
10617	23149	36181	1.69	6.0E-31	AU119105.1	EST_HUMAN	MER28 repetitive element ;
11835	24199	31038	3.26	6.0E-31	AW372868.1	EST_HUMAN	AUT119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
11894	24868		2	6.0E-31	BE694488.1	EST_HUMAN	RC5-BT0377-081299-031-D12 BT0377 Homo sapiens cDNA
208	12867	25352	3.89	6.0E-31	M60894.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3818524 5'
208	12867	25353	3.89	6.0E-31	M60894.1	NT	Homo sapiens type 1 DNA topoisomerase gene, exon 8
8382	20922		0.75	5.0E-31	BF058540.1	EST_HUMAN	Homo sapiens type 1 DNA topoisomerase gene, exon 8
622	13249		2.67	4.0E-31	AJ271735.1	NT	7x06f04.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537
1854	14442		2.42	4.0E-31	AL163280.2	NT	SIMILAR TO POGO ELEMENT ; contains L1.1 L1 repetitive element ;
2815	15397		1.02	4.0E-31	5730038	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
10427	22921	35924	0.65	4.0E-31	AF084464.1	NT	Homo sapiens chromosome 21 segment HS21C080
12008	24309		1.65	4.0E-31	AJ230125.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12399	24559		1.51	4.0E-31	AB008681.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
7377	19903	32787	7.09	3.0E-31	4828853	NT	Homo sapiens GGT1 gene, exon 1
7505	20027	32891	1.62	3.0E-31	11420328	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8102	20843		2.18	3.0E-31	AL163208.2	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
6500	22000	34857	14.68	3.0E-31	D14523.1	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
10498	22982	35990	0.64	3.0E-31	AA421242.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
10510	23048	36090	2.78	3.0E-31	P111174	SWISSPROT	Homo mRNA for ferritin L-chain, complete cds
11032	23646		6.94	3.0E-31	BF038327.1	EST_HUMAN	z006d04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731047 5'
1981	14645	27102	1.52	2.0E-31	AW838171.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
							601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
							QV2-LT0051-260300-111-603 LT0051 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2255	14829	27405	1.16	2.0E-31	AI393388.1	EST_HUMAN	ig44g05.x1 Scores_NFL_T_Q8C_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2378	14848	27522	2.08	2.0E-31	AL118245.1	EST_HUMAN	DKFZp761G1513.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2485	15050	27821	3.48	2.0E-31	AA488824.1	EST_HUMAN	aa8811.1 s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element ;
5478	18113	30522	0.81	2.0E-31	AW444488.1	EST_HUMAN	UJ-H-B3-ekb-f09-Q-U1.s1 NCL CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2733833 3'
5888	18511	31237	2.97	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element ;
8008	21543		2.32	2.0E-31	AA877764.1	EST_HUMAN	nc06R4.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8134	21669	34811	3.85	2.0E-31	7881635	NT	Homo sapiens B9 protein (B9), mRNA
9820	22318	35301	1.04	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 6'
9820	22318	35302	1.04	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
9987	22482	35467	1.73	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9987	22482	35468	1.73	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
11934	24288		3.08	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12078	25106		2.43	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
18	12697	25154	8.8	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1703	14298	26831	3.28	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1703	14298	26832	3.28	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1703	14298	26833	3.28	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4742	17323	29763	1.19	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
4742	17323	29764	1.19	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 6'
6486	18130	30538	3.47	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151288-028-ec08.1 ST0220 Homo sapiens cDNA
6282	18890	31658	1.84	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7332	19859	32722	0.84	1.0E-31	AF128145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
7772	20281	33178	0.68	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3635283 5'
10135	22630	35618	0.67	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10788	23319	36329	2.94	1.0E-31	AI086434.1	EST_HUMAN	q121103.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750708 3' similar to TR:Q18595 Q18595 FRATAXIN. ;
8749	19342	32149	2.26	9.0E-32	AV723078.1	EST_HUMAN	AV723078 HTB Homo sapiens cDNA clone HTBAAG01 6'
7591	20108		1.07	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2122	14700	27270	3.49	8.0E-32	AI068770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5873	18300	30781	0.9	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-203000-015-004 BN0048 Homo sapiens cDNA
4985	17659	30002	3.69	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P1449)
11808	24247		3.42	7.0E-32	X17283.1	NT	Human chromosome 22 Immunoglobulin V(K) gene, part with 5' breakpoint between orphan and neighbouring non-empirical region
2769	16314	27880	0.91	6.0E-32	AI478104.1	EST_HUMAN	tm34a10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2158984 3' similar to contains MER28.13
7402	19927		1.37	6.0E-32	BE888018.1	EST_HUMAN	MER28 repetitive element;
12350	25088		1.51	6.0E-32	AA894853.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1072	13677	26187	75.63	5.0E-32	AF116827.1	NT	ch37c03.s1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1458972 3' similar to contains L1.13 L1 repetitive element;
968	13977		1.55	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
7599	20112	32987	3.11	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C046
7698	20112	32988	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8300	20841		0.77	4.0E-32	BE084410.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
481	13114	25804	2.79	3.0E-32	Y17293.1	NT	RC4-BT0311-141189-011-R08 BT0311 Homo sapiens cDNA
1802	14084	26833	8.09	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens FL1-1 gene, partial
2833	15549	28025	0.73	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (trithorax) homolog; translocated to, 4 (MLLT4) mRNA
2833	15549	28026	0.73	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (trithorax) homolog; translocated to, 4 (MLLT4) mRNA
9315	21829	34760	16.81	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (trithorax) homolog; translocated to, 4 (MLLT4) mRNA
9315	21829	34761	16.81	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBHH12 5'
10805	23328	36339	7.7	3.0E-32	AA77821.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBHH12 5'
11093	23805		1.63	3.0E-32	BF035327.1	EST_HUMAN	285607.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element;
11937	24270		6.37	3.0E-32	BE278086.1	EST_HUMAN	601458953 IF1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3882088 5'
12326	15549	28025	6.26	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12325	15549	28026	6.26	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (trithorax) homolog; translocated to, 4 (MLLT4) mRNA
12491	24820		5.39	3.0E-32	BE278086.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (trithorax) homolog; translocated to, 4 (MLLT4) mRNA
5011	17584	30027	1.01	2.0E-32	BE286613.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
							601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528159 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6400	19003	31781	0.9	2.0E-32	M56418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6605	19202	32007	5.69	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6605	19202	32008	5.69	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8220	20761	33876	2.08	2.0E-32	AA114294.1	EST_HUMAN	z766c08.r1 Strategene HeLa cell s3 637218 Homo sapiens cDNA clone IMAGE:563150 5'
8220	20761	33877	2.08	2.0E-32	AA114294.1	EST_HUMAN	z766c08.r1 Strategene HeLa cell s3 637218 Homo sapiens cDNA clone IMAGE:563150 5'
12810	24694	30856	1.41	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
12810	24694	30860	1.41	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
7115	19455	32271	6.86	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8532	21071	33991	4.86	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element;
3527	16132		5.7	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6552	19150		4.1	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8723	21262	34182	2.62	9.0E-33	BF347228.1	EST_HUMAN	602021164F1 NCI CGAP_Bim07 Homo sapiens cDNA clone IMAGE:4156070 5'
10677	23209		6.39	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
66	12744	25219	2.71	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
65	12744	25220	2.71	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2206	14782	27355	1.92	7.0E-33	AI590115.1	EST_HUMAN	bt12b08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element;
2675	15233		6.6	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE08 5'
3279	15690		15.76	7.0E-33	AW971307.1	EST_HUMAN	EST383398 MAGE sequences, MAGL Homo sapiens cDNA
8876	21415		1.08	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
10708	23236	36249	4.73	7.0E-33	BF347228.1	EST_HUMAN	602021164F1 NCI CGAP_Bim07 Homo sapiens cDNA clone IMAGE:4156070 5'
11127	23635	36876	2.53	7.0E-33	AW971568.1	EST_HUMAN	EST383357 MAGE sequences, MAGL Homo sapiens cDNA
11615	24253	31008	7.43	7.0E-33	AA601416.1	EST_HUMAN	no18h01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element;
3800	18400		0.79	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6217	18827	31599	1.11	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
6217	18827	31600	1.11	6.0E-33	F30631.1	EST_HUMAN	HSPD21201-HM3 Homo sapiens cDNA clone s4000107H08
8515	21054	33977	7.9	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8636	21175	34094	4.14	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
9923	22419	35393	1.73	6.0E-33	6755608	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9923	22419	36394	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 8 (Sox8), mRNA
1814	14404		1.48	5.0E-33	BF37515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1926	14510		1.2	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (cholesterol transporter), member 7 (SLC5A7), mRNA
1943	14527	27082	1.32	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1943	14527	27083	1.32	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
4132	18724	28178	0.8	5.0E-33	AB014598.1	NT	Homo sapiens mRNA for KIAA0689 protein, partial cds
10147	22842	35632	0.76	5.0E-33	AW284679.1	EST_HUMAN	xp33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2762481 3'
10147	22842	35633	0.76	5.0E-33	AW284679.1	EST_HUMAN	xp33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2762481 3'
11720	24129		1.43	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1167	13769		1.82	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2170	14747	27316	1.67	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2484	15031		2.24	4.0E-33	AA826621.1	EST_HUMAN	ab51b11.r1 Stragelene lung carcinoma 887218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2682	15145	27713	1.82	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4581	17164	29607	1.39	4.0E-33	AW293349.1	EST_HUMAN	U1-H-B12-ah1-c-03-Q-U1.e1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5599	18229	30877	21.96	4.0E-33	AA053053.1	EST_HUMAN	z71a08.r1 Stragelene colon (#837204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671.mat HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6528	19128	31919	0.76	4.0E-33	8393984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6528	19128	31920	0.76	4.0E-33	8393984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1128	13731		5.55	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
1128	13731		3.84	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
2493	15468		1.01	3.0E-33	AV547851.1	EST_HUMAN	AV547851 GLC Homo sapiens cDNA clone GLC8CF09 3'
10338	22830	35824	1.19	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.e1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13579
19	12868		0.82	2.0E-33	AI160189.1	EST_HUMAN	Q13579 MARINER TRANSPOSASE.; contains OFR.11 OFR repetitive element ;
109	12868		2.24	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares, fetal heart, NBHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
1415	14008	28536	2.48	2.0E-33	AA010242.1	EST_HUMAN	z108e08.r1 Soares, fetal liver, spleen, INFIL_S1 Homo sapiens cDNA clone IMAGE:430214 5'
1415	14008	28537	2.48	2.0E-33	AA010242.1	EST_HUMAN	z108e08.r1 Soares, fetal liver, spleen, INFIL_S1 Homo sapiens cDNA clone IMAGE:430214 5'
4510	17084		4.41	2.0E-33	BE168039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5122	17684	30131	12.23	2.0E-33	AA626863.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to
5255	17818	30242	1.93	2.0E-33	11421332	NT	gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5255	17818	30243	1.93	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6555	19153	31949	1.5	2.0E-33	A1277492.1	EST_HUMAN	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
9028	21568		2.83	2.0E-33	A1052258.1	EST_HUMAN	q19cd01.x1 Scores_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
10497	22981	36000	0.65	2.0E-33	11421332	NT	cc21d03.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875973 3' similar to
10497	22981	36001	0.65	2.0E-33	11421332	NT	gb:M29338 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10982	23498	36526	1.8	2.0E-33	AA453847.1	EST_HUMAN	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
9	12688		1.08	1.0E-33	AF003528.1	NT	z44805.e1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:795489 3' similar to TR:G1263081
7437	19981	32827	1.21	1.0E-33	MT3976.1	NT	G1263081 MARINER TRANSPOSASE. ;
8634	25126		0.62	1.0E-33	U60822.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
11202	23707	36759	2.63	1.0E-33	AW66818.1	EST_HUMAN	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
11515	23963	37033	5.83	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12214	24437		1.8	1.0E-33	A1827191.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
12403	12688		2.81	1.0E-33	AF003528.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12434	24576	30813	2.55	1.0E-33	AV727809.1	EST_HUMAN	wo88-c06.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2482410 3'
12628	24706		4.56	8.0E-34	A1271735.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1484	14066	26626	2.3	7.0E-34	T70846.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNG12 5'
9611	14066	26626	0.68	7.0E-34	T70846.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
11869	24269		1.75	7.0E-34	H12896.1	EST_HUMAN	yd15cd5.r1 Scores_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:108320 5'
488	13128	25616	1.61	6.0E-34	U10991.1	NT	yd15cd5.r1 Scores_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:108320 5'
488	13128	25617	1.61	6.0E-34	U10991.1	NT	y14c10.r1 Scores_placenta_Nb2HP_Homo sapiens cDNA clone IMAGE:148722 5'
11787	24177	31028	1.92	6.0E-34	U03886.1	NT	Human G2 protein mRNA, partial cds
1923	14508		2.5	5.0E-34	7708500	NT	Human G2 protein mRNA, partial cds
5218	17763	30201	5.85	5.0E-34	U30883.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
8800	21338	34266	1.18	5.0E-34	AF078778.1	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
10534	23071	36084	2.28	5.0E-34	AB037856.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
11133	23841		1.9	6.0E-34	AL163208.2	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
2041	14923	27192	3.42	4.0E-34	A1804967.1	EST_HUMAN	Homo sapiens mRNA for KIAA1435 protein, partial cds
							Homo sapiens chromosome 21 segment HS21C009
							HB94-c06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248184 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2745	15300	27898	1.06	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10888 (FLJ10888), mRNA
8988	21508	34427	1.35	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6379	18983	31783	1.13	3.0E-34	M37277.1	NT	Human Ig gamma H-chain D-region genes, partial cds
11031	23545		5.04	3.0E-34	BF035327.1	EST_HUMAN	60148831F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
8881	21419	34343	1.67	2.0E-34	AI678101.1	EST_HUMAN	w335g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER28.12 MER29 repetitive element:
8881	21419	34344	1.67	2.0E-34	AI678101.1	EST_HUMAN	w335g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER28.12 MER29 repetitive element:
1552	14144	26678	7.44	1.0E-34	P12238	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ANTENIN)
3736	16337	28802	1.24	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 end flanking repeat regions
4145	16737	20190	0.82	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4145	16737	20181	0.82	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4578	17161		8.22	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0508-240400-016-H08 BT0508 Homo sapiens cDNA
8287	18895	31684	2.69	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
8287	18895	31685	2.69	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
9813	22113	35076	17.45	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563.1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11077	23589	36627	1.94	1.0E-34	11439589	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12176	25037		3.1	1.0E-34	AA607087.1	EST_HUMAN	cc31c11.a1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12423	24608		4.62	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3707	16308	28776	1.45	9.0E-35	AW863302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
243	12802		10.67	8.0E-35	6031180	NT	h77708.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988787 5'
1772	14382	26907	2.03	8.0E-35	BF589637.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1772	14392	26908	2.03	8.0E-35	BF589637.1	EST_HUMAN	nae33a08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4891	17585	30010	3.45	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA.;
10570	23106	36120	1.8	8.0E-35	BE378480.1	EST_HUMAN	nae33a08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
11907	24245		2.98	8.0E-35	BF589282.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
6610	19207	32015	2	7.0E-35	11425417	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
1458	14050	26582	1.08	6.0E-35	AA757115.1	EST_HUMAN	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300680 3'
2010	14592	27152	1.28	8.0E-35	6005976	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
						EST_HUMAN	ah53103.a1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
						NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4127	16719	28174	0.67	6.0E-35	AW207191.1	EST_HUMAN	ULP-BWO-gld-08-Q-UJ.a.1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731433 3'
7838	20380	33285	3.41	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8843	21182	34101	0.49	6.0E-35	X04232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8843	21182	34102	0.49	6.0E-35	X04232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8584	22084	35048	0.7	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0366 gene, partial cds
8817	22315	35286	2.42	6.0E-35	AB037788.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
152	12815	25303	37.87	5.0E-35	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
1747	14337	26883	1.26	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
3043	15658	28139	1.39	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4488	17083	28533	1.81	5.0E-35	AF023288.1	NT	Homo sapiens cdk2 kinase (CLK2), protein1, cat1, glucocorticoidase (G1A), and metaxdn genes, complete cds; metaxdn pseudogene and glucocorticoidase pseudogenes; and thrombospondin3 (THBS3) gene, partial cds
8125	20666		3.51	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3817229 5'
8151	20682	33806	2.29	5.0E-35	A1208755.1	EST_HUMAN	qg38c05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92338 HYPOTHETICAL PROTEIN KIAA0249. ;
8151	20682	33807	2.29	5.0E-35	A1208755.1	EST_HUMAN	qg38c05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92338 HYPOTHETICAL PROTEIN KIAA0249. ;
11056	23568		3.63	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares fetal_liver_spleen_INFILS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1481	14074	26813	13.95	4.0E-35	BE257807.1	EST_HUMAN	601109716F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3350405 5'
1855	14443	26896	4.12	4.0E-35	H91183.1	EST_HUMAN	y08a07.r1 Soares fetal liver spleen_INFILS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
4927	17502		0.58	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7260	19788		2.06	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3 MER28 repetitive element ;
8455	20865	33913	6.88	4.0E-35	AL048596.1	EST_HUMAN	DKFZp434L148_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1823	14216	26748	31.49	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345083 5'
2369	14940		2.22	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5543	18175	30589	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3686381 3' similar to TR:Q8QZH7
5543	18175	30580	22.73	3.0E-35	BF433100.1	EST_HUMAN	Q8QZH7 F-BOX PROTEIN FBL2. ;
9409	21918		1.72	3.0E-35	AF223391.1	NT	7n25a09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TR:Q8QZH7
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10078	22573	35568	0.8	3.0E-35	AW003083.1	EST_HUMAN	wr03a05.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
113	15407	25289	1.18	2.0E-35	N88065.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
1230	13828	26344	1.13	2.0E-35	T11908.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2289	14833	27411	4.88	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
3363	15961	28437	0.79	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3353	15961	28438	0.78	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3613	18218		0.85	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0885 protein, partial cds
3981	18579	28049	0.88	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBAP4328
3981	18579	28050	0.88	2.0E-35	BE247576.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBAP4328
4777	17358		2.89	2.0E-35	H48239.1	EST_HUMAN	x118a12.r1 Soares fetal liver spleen 1NF15 Homo sapiens cDNA clone IMAGE:274079 5'
5770	18396	31110	1.48	2.0E-35	BF33247.1	EST_HUMAN	QV0-BT0701-210400-189-b04 BT0701 Homo sapiens cDNA
10875	23207	36219	4.14	2.0E-35	X59417.1	NT	H. sapiens PROS-27 mRNA
11663	15961	28437	1.34	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11663	15961	28438	1.34	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12405	24563		42.69	2.0E-35	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12525	15407	25289	1.4	2.0E-35	N88065.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
50	12730	25194	5.95	1.0E-35	AA631949.1	EST_HUMAN	fmfc18 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
60	12730	25196	5.85	1.0E-35	AA631949.1	EST_HUMAN	fmfc18 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
782	13401	25903	55.23	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131089-006-d12 ST0162 Homo sapiens cDNA
782	13401	25904	55.23	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131089-006-d12 ST0162 Homo sapiens cDNA
942	13655		1.15	1.0E-35	T87947.1	EST_HUMAN	y693a01.r1 Soares fetal liver spleen 1NF15 Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN;
2578	15141	27710	1.98	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC517233), mRNA
2795	15348	27917	1.38	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28 b3 MER28 repetitive element;
2795	15348	27918	1.38	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28 b3 MER28 repetitive element;
3177	15760	28282	1.03	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3169	15811	28284	1.52	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLOCCE08 3'
3169	15811	28285	1.52	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLOCCE08 3'
4513	17097	29543	5.19	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4513	17097	29544	5.19	1.0E-35	7656908	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5701	18327	30831	1.31	1.0E-35	11528238	NT	Homo sapiens chitinase assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7069	18088	30444	0.73	1.0E-35	AW808865.1	EST_HUMAN	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA
7069	18088	30445	0.73	1.0E-35	AW808865.1	EST_HUMAN	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA
7498	20019	32883	0.8	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7637	20148	33033	0.98	1.0E-35	11418002	NT	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
9461	24794	34941	3.33	1.0E-35	AU168595.1	EST_HUMAN	AU168595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9461	24794	34942	3.33	1.0E-35	AU168595.1	EST_HUMAN	AU168595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10470	22964	35974	0.57	1.0E-35	BF589594.1	EST_HUMAN	nao06408.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
10470	22964	35975	0.57	1.0E-35	BF589594.1	EST_HUMAN	nao06408.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
11601	24044		4.48	1.0E-35	AI525119.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE ; promoter-7.D01.7 by tumor Homo sapiens cDNA 5'
11695	24998		1.3	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12287	24489		1.87	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
9156	21691	34635	0.51	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
10060	22655		2.13	8.0E-36	7708259	NT	Homo sapiens CGI-08 protein (LOC51808), mRNA
2857	15573	28050	1.15	7.0E-36	AW857579.1	EST_HUMAN	GM1-CT0315-091289-083-d07 CT0315 Homo sapiens cDNA
3152	15766		5.38	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7650	20162	33049	6.73	7.0E-36	U08872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
7650	20162	33050	6.73	7.0E-36	U08872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
12070	24350	30865	5.15	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
2048	14830	27199	2.5	6.0E-36	7708822	NT	Homo sapiens nihydrin 2 (NINJ2), mRNA
2461	15028		5.35	6.0E-36	AB035346.1	NT	Homo sapiens TGLB gene, exon 12
3701	16302	28770	0.98	6.0E-36	BF515101.1	EST_HUMAN	UIH-BW1-env-c-12-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5534	18166	30580	8.75	6.0E-36	AI435169.1	EST_HUMAN	th03b08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7163	19695	32541	3.97	6.0E-36	AW780143.1	EST_HUMAN	nao06408.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IMA2_HUMAN
8686	21125	34045	2.54	6.0E-36	AF208181.1	NT	P52282 IMPORTIN ALPHA-2 SUBUNIT ; Homo sapiens synovial precursor, mRNA, complete cds

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10125	22820		0.84	6.0E-36	C18927.1	EST_HUMAN	C18927 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-535C11 5'
11422	23873	36936	2.62	6.0E-36	A1380489.1	EST_HUMAN	195c09.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9 b2 MER9 repetitive element ;
143	12808	25288	12.3	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2779	15332	27901	15.02	5.0E-36	BE388436.1	EST_HUMAN	601285687F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3672	16273	28739	1.07	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4803	17478	28935	1.8	5.0E-36	5729729	NT	Homo sapiens API6-like 1 (API6L1), mRNA
4803	17478	28936	1.8	5.0E-36	5729729	NT	Homo sapiens API6-like 1 (API6L1), mRNA
11661	12808	25288	4.05	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11663	24285	31024	2.88	5.0E-36	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1287	13884	26381	2.14	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1491	14083	26624	1.88	4.0E-36	P10286	SWISSPROT	ENDONUCLEASE
1887	14279	28813	1.35	4.0E-36	BE382574.1	EST_HUMAN	601288674F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628388 5'
2264	14838		1.7	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3397	18005	28486	0.83	4.0E-36	BE389298.1	EST_HUMAN	601282286F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3397	16005	28487	0.83	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4868	17442	28893	0.57	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5310	17672	30294	0.58	4.0E-36	AA905381.1	EST_HUMAN	ok05b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506809 3' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
5892	18515		0.94	4.0E-36	R64023.1	EST_HUMAN	y18705.t1 Soares placent N62HP Homo sapiens cDNA clone IMAGE:139713 5'
6205	18815	31888	2.19	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7649	20161	33048	1.77	4.0E-36	M33320.1	NT	Human platelet Glycoprotein Iib (GPIIb) gene, exon 2-28
8490	21029	33947	1.15	4.0E-36	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8490	21029	33948	1.15	4.0E-36	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10867	23388	38403	2.39	4.0E-36	AA400370.1	EST_HUMAN	zu80c10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 6'
11881	24282		1.48	4.0E-36	11420518	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12026	24872		6.32	4.0E-36	AV753628.1	EST_HUMAN	AV753628 TP Homo sapiens cDNA clone TPGBH01 6'
725	13345	25837	2.82	3.0E-36	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
1545	14137	26671	1.01	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1645	14137	26672	1.01	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2338	14909	27481	0.88	3.0E-36	7662401	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4600	17184	28631	7.36	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
10985	23499	30529	2.06	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3802088 5'
3204	15816	28292	3.78	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
5094	17697	30106	9.22	2.0E-36	AW880378.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5077	18304	30786	2.55	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
6012	18632	31367	4.22	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Banto Soares Homo sapiens cDNA clone HIBBJ28 5' end
6890	19286	32089	12.01	2.0E-36	T66629.1	EST_HUMAN	yc44a07.1 Stratiogene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
8310	21824	34772	0.86	2.0E-36	BF512794.1	EST_HUMAN	UH-BW1-amu-e-11-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9488	21897	34817	0.8	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9488	21897	34817	0.8	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
818	13531	26049	2.35	1.0E-36	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2190	14766	27337	0.91	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131188-021-h07 HT0217 Homo sapiens cDNA
2190	14766	27338	0.91	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131188-021-h07 HT0217 Homo sapiens cDNA
2243	14818	27392	1.34	1.0E-36	BF673781.1	EST_HUMAN	602138493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
2538	15102		1.76	1.0E-36	AW276898.1	EST_HUMAN	xp57a06.x1 NCI_CGAP_Qv89 Homo sapiens cDNA clone IMAGE:2744434 3' similar to WP.C13F10.7 CE08148;
3398	15997		1.23	1.0E-36	AF159982.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
5904	18526	31252	0.86	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 494 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G022 5'
6059	18978	31418	0.97	1.0E-36	4827084	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6330	18936		3.97	1.0E-36	AI897714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307882 3' similar to contains Alu repetitive element
6524	18124	31916	1.13	1.0E-36	R25012.1	EST_HUMAN	yg38g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6524	18124	31917	1.13	1.0E-36	R25012.1	EST_HUMAN	yg38g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6783	19374	32190	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A228_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A228 5'
7901	20443	33347	3.18	1.0E-36	AA148034.1	EST_HUMAN	z551a12.r1 Stratiogene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
7901	20443	33348	3.18	1.0E-36	AA148034.1	EST_HUMAN	z551a12.r1 Stratiogene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
7997	20539	33441	1.22	1.0E-36	AA420487.1	EST_HUMAN	nc60a08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
7997	20539	33442	1.22	1.0E-36	AA420487.1	EST_HUMAN	nc60a08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
8120	20661	33570	0.73	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8120	20661	33571	0.73	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8959	21497	34420	2.88	1.0E-36	AW103658.1	EST_HUMAN	xe82b07.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10023	22518	35513	3.89	1.0E-36	BF364189.1	EST_HUMAN	QV3-NN1023-010800-189-h01 NN1023 Homo sapiens cDNA

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10231	22726	35717	0.71	1.0E-36	AW858688.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10231	22726	35718	0.71	1.0E-36	AW858688.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10826	23347	36363	3.55	1.0E-36	AW697636.1	EST_HUMAN	CN3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11268	23788	36844	4.94	1.0E-36	AW804143.1	EST_HUMAN	UIHF-BN0-ale-o-03-Q-UI.r1 NIH_MGC_80 Homo sapiens cDNA clone IMAGE:3079277 5'
11848	24208		6.11	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12316	24507		6.19	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
12892	24883		3.56	1.0E-36	AF202723.1	NT	Homo sapiens Sed1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7415	19940	32804	1.94	9.0E-37	AW009277.1	EST_HUMAN	ws80507.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2504245 3'
7415	19940	32805	1.94	9.0E-37	AW009277.1	EST_HUMAN	ws80507.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2504245 3'
12113	24374		1.83	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
3388	18008	28488	1.01	8.0E-37	4757978	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
5456	18091		1.58	8.0E-37	BE088077.1	EST_HUMAN	CNM-UT0003-050800-503-d08 UT0003 Homo sapiens cDNA
5994	18614	31348	4.02	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
5994	18614	31348	4.02	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
6037	18656	31398	6.7	8.0E-37	AW840840.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
7825	20367	33275	6.31	8.0E-37	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
1328	13922		2.3	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
1780	14370	26914	1.55	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1780	14370	26915	1.55	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10637	23169	36180	7.76	7.0E-37	AB17700.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
10774	23288	36303	3.74	7.0E-37	AE38702.1	EST_HUMAN	ptr5 repetitive element;
5304	17868		2.5	6.0E-37	R10039.1	EST_HUMAN	hm87g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1
8377	20917	33837	0.54	6.0E-37	AF169689.1	NT	repetitive element;
12455	24568		3.85	6.0E-37	AF202723.1	NT	Y25602.r1 Scores fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:127850 5'
6243	18852	31622	4.92	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens probocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
6243	18852	31623	4.92	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sed1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
8691	21230	34150	0.85	6.0E-37	AV750211.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10800	23323		4.94	6.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
11843	24205		5.21	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2468	15035	27602	1.7	4.0E-37	AA702784.1	EST_HUMAN	z06004.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
9278	21804	34766	0.88	4.0E-37	AA843808.1	EST_HUMAN	sk08c02.s1 Soares_parenchymal_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
10912	23431	38451	1.74	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10912	23431	38452	1.74	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2061	14841	27215	2.58	3.0E-37	AL048866.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2061	14841	27216	2.58	3.0E-37	AL048866.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2892	16808		3.5	3.0E-37	AW881160.1	EST_HUMAN	EST373222 MAGE resequencing, MAGF Homo sapiens cDNA
5128	17688		0.79	3.0E-37	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
7557	20075	32851	0.78	3.0E-37	A1748952.1	EST_HUMAN	af34c05.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2373898 3' similar to TR:Q13537
404	13078	25571	0.9	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
404	13078	25572	0.9	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1118	13722	26234	2.1	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
1119	13722	26235	2.1	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
2008	14588	27148	1.45	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3982	18580	28028	6.99	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotandinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4330	18917	29380	0.59	2.0E-37	4826885	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6765	18358	32167	3.94	2.0E-37	AA348720.1	EST_HUMAN	EST52831 Fetal heart II Homo sapiens cDNA 5' end
7938	20480	33390	0.53	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453857 5'
7938	20480	33391	0.53	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453857 5'
7991	20523	33429	2.75	2.0E-37	BF204032.1	EST_HUMAN	601869167F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
11434	23884	36951	19.39	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12633	24710		5.1	2.0E-37	11417872	NT	Homo sapiens psecidillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2135	14713	27286	2.49	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3231	15843		0.88	1.0E-37	AW862082.1	EST_HUMAN	RC3-C70347-210400-016-h03 CT0347 Homo sapiens cDNA
4243	16831	29282	0.96	1.0E-37	BE872365.1	EST_HUMAN	601448819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3852652 5'
5075	17848	30089	3.67	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6153	18768		0.8	1.0E-37	7305380	NT	Mus musculus otogelin (Otog), mRNA
8156	20697	33810	0.84	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8670	21209	34127	3.03	1.0E-37	AA171408.1	EST_HUMAN	zp21b02.1 Stratiotes neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.12 L1 repetitive element:

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23112	38126	6.61	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
12167	24408		3.8	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0098-140700-243-d07 FT0098 Homo sapiens cDNA
5950	18571	31303	1.71	8.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC58768), mRNA
1284	13861	26378	2.05	8.0E-38	11438955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2543	15107	27880	1.48	8.0E-38	BF348221.1	EST_HUMAN	802018401F1 NCL_OGAP_Bim87 Homo sapiens cDNA clone IMAGE:4153892 5'
12231	13881	26378	1.62	8.0E-38	11438955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4307	16893	26338	0.83	7.0E-38	H19092.1	EST_HUMAN	yn5107.r1 Soares adult brain N2B5HB5Y Homo sapiens cDNA clone IMAGE:171973 5'
3078	15893	28167	2.75	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3858348 5'
5778	18401	31118	1.34	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5778	18401	31117	1.34	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
11666	24110		10.47	8.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12201	24427	30952	14.11	6.0E-38	AB02058.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12614	24837	30797	1.7	6.0E-38	11418164	NT	Homo sapiens adenylsuccinate lyase (ADSL), mRNA
758	13376	25870	1.26	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2485	19559	27633	1.94	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
7098	19887	32508	2.15	5.0E-38	BE871810.1	EST_HUMAN	601450148F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3854074 5'
124	12783	25277	3.83	4.0E-38	Z26486.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
124	12783	25278	3.83	4.0E-38	Z26486.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1199	13900	26312	1.09	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2148	14726		2.39	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3759	16360		1.37	3.0E-38	7548807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-llike) (HIRP4), mRNA
3922	18520	28987	2.12	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3922	18520	28988	2.12	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4721	17302		0.69	3.0E-38	BE276301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6850	24772	32254	7.24	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7588	20103	32978	6.83	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA
8584	21123	34043	2.01	3.0E-38	H85494.1	EST_HUMAN	yy88b04.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:249775 5'
8584	21123	34044	2.01	3.0E-38	H85494.1	EST_HUMAN	yy88b04.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:249775 5'
9882	22378		1.7	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11198	23703		1.54	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12461	13900	26312	1.44	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
54	12734	25202	1.84	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1422	14016	26544	2.23	2.0E-38	5802087	NT	Homo sapiens SM13 (suppressor of mit two 3, yeast) homolog 2 (SM13H2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14280	26814	1.99	2.0E-38	AA437353.1	EST_HUMAN	z330d01.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1688	14280	26815	1.99	2.0E-38	AA437353.1	EST_HUMAN	z330d01.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
4681	17263	29714	2.88	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5263	17855	30280	0.63	2.0E-38	BE296224.1	EST_HUMAN	G01177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532590 5'
5263	17855	30281	0.63	2.0E-38	BE296224.1	EST_HUMAN	G01177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532590 5'
5327	17837	30264	0.63	2.0E-38	AA437191.1	EST_HUMAN	z330d01.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:768129 5' similar to TR:G817957
7704	20213	33102	1.57	2.0E-38	AV721103.1	EST_HUMAN	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
8420	20960		6.5	2.0E-38	BE165980.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8828	21365	34289	0.51	2.0E-38	F09450.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8895	21433	34356	1.37	2.0E-38	AF069765.1	NT	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18703
8148	21683		0.89	2.0E-38	BE222256.1	EST_HUMAN	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
10345	22838	35835	1.98	2.0E-38	D03479.2	NT	hu09g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710 GAG POLYPEPTIDE ;
11114	23824	36665	3.38	2.0E-38	AA595480.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11114	23824	36666	3.38	2.0E-38	AA595480.1	EST_HUMAN	no34g03.s1 NCL_CGAP_P723 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316
11363	23815	36876	6.15	2.0E-38	BE712790.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
11498	23945	37014	3.87	2.0E-38	AF190501.1	NT	no34g03.s1 NCL_CGAP_P723 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316
11498	23945	37015	3.87	2.0E-38	AF190501.1	NT	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
11753	24148		7.01	2.0E-38	AV726998.1	EST_HUMAN	no34g03.s1 NCL_CGAP_P723 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316
11755	24150		1.88	2.0E-38	AB012723.1	NT	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
12050	24334		3.19	2.0E-38	M55630.1	NT	QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA
12080	24343	31000	5.31	2.0E-38	H55941.1	EST_HUMAN	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12128	24384		2.87	2.0E-38	S74908.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12824	24702		1.55	2.0E-38	11418248	NT	AV726998 HTG Homo sapiens cDNA clone HTCAHX07 5'
1132	13735		2.17	1.0E-38	AA401570.1	EST_HUMAN	Homo sapiens gene for kinesin-like protein, complete cds
2042	14824	27193	1.7	1.0E-38	4886288	NT	Homo sapiens gene for kinesin-like protein, complete cds
							Human topoisomerase I pseudogene 2
							CHR220590 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
							E1 betapryruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
							Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
							z330d02.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
							MER19 repetitive element ;
							Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2066	14846	27219	1.46	1.0E-38	7661968	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2539	15103	27678	1.71	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
2645	16204	27777	14.26	1.0E-38	4758371	NT	Homo sapiens fibrinogen-like 1 (FGL1), mRNA
4235	16823	28274	1.03	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4411	16996	28439	0.81	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4416	17001	28444	1.52	1.0E-38	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4416	17001	28445	1.52	1.0E-38	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4702	17284	28728	1.18	1.0E-38	8822843	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
6289	17851		29.49	1.0E-38	N46880.1	EST_HUMAN	y58a01.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:277704 5' similar to SW:CA1H_MOUSE P39081 COLLAGEN ALPHA 1(XVII) CHAIN PRECURSOR. ;
6178	18788	31658	4.28	1.0E-38	7305350	NT	Mus musculus otogelin (Otog), mRNA
6178	18788	31657	4.28	1.0E-38	7305380	NT	Mus musculus otogelin (Otog), mRNA
7435	19959	32824	3	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
8060	21616	34551	0.97	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9331	21845	34795	8.34	1.0E-38	BE360127.1	EST_HUMAN	h08g01.x1 NCJ_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER20.b3
11465	23915	36983	1.81	1.0E-38	7682109	NT	MER29 repetitive element ;
11908	24908		2.57	1.0E-38	AL183284.2	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
58	12738	25208	8.81	8.0E-39	4502312	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1438	14031	28559	1.49	8.0E-39	4758228	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 8 (EBAG8) mRNA
1969	14455		0.88	8.0E-39	AB23404.1	EST_HUMAN	wh5310.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87880 P87880
2141	14719	27280	3.68	7.0E-39	AL183227.2	NT	POL. PROTEIN ;
10888	23218	36230	2.32	6.0E-39	BF331828.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
11639	24078	37138	1.54	6.0E-39	11528372	NT	QV1-BT0631-040900-357402 BT0631 Homo sapiens cDNA
12532	24845		2.82	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR), mRNA
1045	13853	28165	1.85	5.0E-39	AF003528.1	NT	7e34603.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.8
3014	15630	28108	7.14	5.0E-39	AF150154.1	EST_HUMAN	CE00828 ;
12219	24441		2.69	5.0E-39	11420289	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
							at06804.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
							Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.1 LTR7 repetitive element ;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
576	13208	25696	35.11	4.0E-39	AB015610.1	NT	Chlorobius aestivo mRNAs for ribosomal protein S4X, complete cds
3631	16234	28708	0.75	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5885	18815	31350	0.73	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
5886	18816	31351	0.73	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
8020	20862	33463	0.95	4.0E-39	AA682949.1	EST_HUMAN	ae82g04.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element;
9252	21778	34728	0.82	4.0E-39	DB4116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9252	21778	34728	0.82	4.0E-39	DB4116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12237	24452		4.45	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12363	24536		5.52	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-280800-278-c08 FN0063 Homo sapiens cDNA
51	12731	25186	16.82	3.0E-39	AA631949.1	EST_HUMAN	fmfc19 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
51	12731	25197	16.82	3.0E-39	AA631949.1	EST_HUMAN	fmfc19 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
51	12731	25188	16.82	3.0E-39	AA631949.1	EST_HUMAN	fmfc19 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11744	24143	36764	6.46	3.0E-39	AI084557.1	EST_HUMAN	cx33a10.s1 Soares_NHMPu S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
11744	24143	36765	6.46	3.0E-39	AI084557.1	EST_HUMAN	cx33a10.s1 Soares_NHMPu S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
11791	24174		6.83	3.0E-39	H37903.1	EST_HUMAN	yp51c08.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:180954 3'
930	13543		9.84	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
945	13558		15.07	2.0E-39	AI625119.1	EST_HUMAN	promine-7.D01.r bvtumor Homo sapiens cDNA 5'
1069	13974		3.85	2.0E-39	AF000573.1	NT	Homo sapiens homogenitatis 1,2-dioxygenase gene, complete cds
1577	14170		41.87	2.0E-39	AW372318.1	EST_HUMAN	PM0-BT0340-211289-003-d02 BT0340 Homo sapiens cDNA
2016	14568	27162	2.5	2.0E-39	AA720574.1	EST_HUMAN	rw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.L3 THR repetitive element;
2657	15216	27788	1.56	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4492	17077	26527	1.7	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
5882	18308	30804	3.89	2.0E-39	AA508880.1	EST_HUMAN	ng8603.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941683
7405	18830	32764	1.95	2.0E-39	AA080887.1	EST_HUMAN	zn06f02.r1 Stratiogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546651 5'
8252	20763	33710	0.55	2.0E-39	AF078779.1	NT	Rattus norvegicus pulvate four repeat ion channel mRNA, complete cds
9415	21924		0.56	2.0E-39	AA984531.1	EST_HUMAN	am88c11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
8544	22044		0.54	2.0E-39	AI886660.1	EST_HUMAN	bu35e03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253052 3'
11309	23802	36883	3.11	2.0E-39	DB8864.1	NT	Human mRNA for KIAA0209 gene, partial cds
1580	14152	26884	2.33	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1560	14152	26885	2.33	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1578	14171	28700	9.78	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4719	17300	29745	0.87	1.0E-39	AW298073.1	EST_HUMAN	UHH-BWO-ali-h-06-0-J1.81 NCI_CGAP_Sub0 Homo sapiens cDNA clone IMAGE:2730850 3'
4764	17345	29793	4.98	1.0E-39	AW951985.1	EST_HUMAN	EST384085 MAGE resequences, MAGB Homo sapiens cDNA
4764	17345	29794	4.98	1.0E-39	AW951985.1	EST_HUMAN	EST384085 MAGE resequences, MAGB Homo sapiens cDNA
4812	17390	29841	10.18	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5561	18192	30638	0.88	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5561	18192	30639	0.88	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5812	18436	31157	1.13	1.0E-39	T80876.1	EST_HUMAN	Alu repetitive element/contains LTR1 repetitive element
5845	18469	31184	5.75	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)
5845	18469	31195	5.75	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)
6914	19573	32780	1.87	1.0E-39	11436738	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7400	19925	32780	2.28	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8499	21038	33959	0.85	1.0E-39	O48530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
12181	24401		4.3	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
581	13211	25699	2.07	9.0E-40	5803210	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1278	13873	26392	20.54	9.0E-40	4755145	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1278	13873	26393	20.54	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1498	14090	26630	1.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3853	16451	26914	0.68	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4046	18004	28108	3.57	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3077	15892	28186	1	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HLA cDNA Library Homo sapiens cDNA clone 7H15A04
3998	16594		1.74	8.0E-40	BE398541.1	EST_HUMAN	601288958F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3619188 5'
7702	20211	33098	2.01	7.0E-40	U80325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7702	20211	33099	2.01	7.0E-40	U80325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10776	23300	36306	2.48	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2753	15308	27873	5.43	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2753	15308	27874	5.43	6.0E-40	AA381275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6094	18710		2.11	6.0E-40	BE504766.1	EST_HUMAN	h240g01.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3210480 3'
6288	18904		1.42	6.0E-40	7681999	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7016	19513	32334	4.18	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7015	19513	32335	4.18	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9887	22384	35380	8.69	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
9887	22384	35381	8.69	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
1919	14504	27061	1.42	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2155	14732		1.38	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 end flanking repeat regions
4478	17063	28513	9.28	4.0E-40	7692117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7827	20369	33277	0.59	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
7833	20475	33384	4.44	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
8985	21523	34451	3.81	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8985	21523	34452	3.81	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10595	23128	36143	3.06	4.0E-40	AW841585.1	EST_HUMAN	RG1-CN0017-120200-012-904 CN0017 Homo sapiens cDNA
4212	16801	28250	0.89	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6760	16343	32150	7.27	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8321	20862	33787	3.69	3.0E-40	5454187	NT	Homo sapiens HIV associated factor (XAP4) mRNA
8898	21437	34360	1.28	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9138	21673	34816	1.58	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10541	23078	36092	1.79	3.0E-40	D86984.1	NT	Human mRNA for KIAA0209 gene, partial cds
10903	23423	36442	2.21	3.0E-40	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11145	23653	36695	13.89	3.0E-40	6005913	NT	MER29 repetitive element ;
							Homo sapiens serine threonine protein kinase (NDR), mRNA
11445	23896	36860	1.58	3.0E-40	AW118769.1	EST_HUMAN	xd26h02.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804
347	12988		4.35	2.0E-40	A123036.1	EST_HUMAN	Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS. ;
							qq52h08.x1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
							xx24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS6_MOUSE
827	13444		22.71	2.0E-40	AW303888.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S6. ;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1866	14451		1.38	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1878	14561	27118	1.39	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit alpha type, 7 (PSMA7) mRNA, and translated products
1878	14561	27120	1.39	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit alpha type, 7 (PSMA7) mRNA, and translated products
2116	14694	27262	0.95	2.0E-40	AI088562.1	EST_HUMAN	w80a11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91829 Q91829
2214	14769	27363	1.86	2.0E-40	6453592	NT	ZINC FINGER PROTEIN. ;
2714	15271		1.25	2.0E-40	BE275832.1	EST_HUMAN	Homo sapiens adenovirus cyclase-associated protein 2 (CAP2) mRNA
3160	15774	28242	4.32	2.0E-40	5453592	NT	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
5027	17601	30046	1.84	2.0E-40	AL163280.2	NT	Homo sapiens adenovirus cyclase-associated protein 2 (CAP2) mRNA
5027	17601	30047	1.84	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5378	17938	30351	3.28	2.0E-40	4505890	NT	Homo sapiens plasminogen (PLG) mRNA
916	13529		1.06	1.0E-40	AA225898.1	EST_HUMAN	nc08a00.s1 NCI_CGAP_P41 Homo sapiens cDNA clone IMAGE:1007608
3337	15947		1.47	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4716	17267	28742	4.95	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6403	19008	31768	0.69	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6403	19008	31767	0.69	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7145	19878	32518	2.12	1.0E-40	AA573201.1	EST_HUMAN	h42704.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7145	19878	32519	2.12	1.0E-40	AA573201.1	EST_HUMAN	h42704.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7263	19811	32667	0.83	1.0E-40	P28908	SWISSPROT	POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
10797	23320	36330	4.13	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11815	24057		1.72	1.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12182	24958		7.52	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-211089-002-e10 CT0222 Homo sapiens cDNA
3878	16474	28938	0.65	8.0E-41	W01596.1	EST_HUMAN	za38a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284602 5'
7862	20404	33311	1.68	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
861	15427	25960	1.58	7.0E-41	AB94384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
861	15427	25961	1.58	7.0E-41	AB94384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5411	17688	30377	0.95	7.0E-41	11431114	NT	Homo sapiens hypothetical protein (FLJ10896), mRNA
5468	18103	30422	0.84	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6159	18772	31535	3.44	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6494	19095	31879	0.8	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7087	18086	30442	0.95	7.0E-41	U7235.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11311	23804	38884	1.88	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNQ10) mRNA
12631	24952		8.97	7.0E-41	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
302	12957	25447	1.42	6.0E-41	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
2157	14734	27307	2.33	6.0E-41	7687042	NT	Homo sapiens Down syndrome candidate region 1 (DSR1), mRNA
7812	20454	33360	1.56	6.0E-41	BF513763.1	EST_HUMAN	UIH-BW1-amp-b-03-0-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
12811	24973		1.61	6.0E-41	AW873637.1	EST_HUMAN	h04f08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains
1838	14426	26977	2.16	5.0E-41	T62628.1	EST_HUMAN	MER32.b3 MER32 repetitive element ;
4184	16774		1.01	5.0E-41	4885638	NT	y03e10.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:78928 3'
6667	19283		1.97	5.0E-41	BE067042.1	EST_HUMAN	Homo sapiens target of myb1 (chicken) homolog (TOMT), mRNA
414	13048		1.59	4.0E-41	BE156318.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
1137	13740	26249	1.12	4.0E-41	AU119344.1	EST_HUMAN	QV0-HT0367-150200-114-g08 HT0367 Homo sapiens cDNA
							AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1455	14047	26577	9.23	4.0E-41	A027117.1	EST_HUMAN	ow45e05.s1 Scores_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1455	14047	26578	9.23	4.0E-41	A027117.1	EST_HUMAN	ow45e05.s1 Scores_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1468	14061	26598	1.87	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1677	14269	26802	8.43	4.0E-41	AI500406.1	EST_HUMAN	tm96c04.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2813	15530	28001	3.73	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2913	15530	28002	3.73	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4225	16813	28260	2.27	4.0E-41	X92885.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
6632	19228		1.36	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMPBHC08 5'
9810	22110	35072	6.75	4.0E-41	BF304883.1	EST_HUMAN	601886086F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11522	23970		9.87	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CUAAC007 5'
12375	24841		2.28	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
12570	24869	30876	4.85	4.0E-41	BE887118.1	EST_HUMAN	601508319F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
983	13565	26109	1.84	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4428	17014	29456	2.7	3.0E-41	AB026898.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5273	17834		1.03	3.0E-41	AB037748.1	NT	H.sapiens mRNA for putative p64 GCP protein
5683	18310	30806	9.55	3.0E-41	X67689.1	NT	

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6518	19118	31808	1.73	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7761	20269	33187	0.7	3.0E-41	R54765.1	EST_HUMAN	X77608.r1 Soares breast 2NBTBst Homo sapiens cDNA clone IMAGE:154575 5'
11575	24021	37090	1.78	3.0E-41	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11703	24118		1.84	3.0E-41	AA609788.1	EST_HUMAN	af1710.st Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
1854	14200	28734	15.09	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2001	14583	27142	1.76	2.0E-41	AA331940.1	EST_HUMAN	EST39819 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2260	14834	27412	1.13	2.0E-41	D88982.1	NT	Human mRNA for KIAA0207 gene, complete cds
2308	14880	27458	3.79	2.0E-41	X89831.1	NT	G.gorilla DNA for ZNF90 gene homolog
2855	14200	28734	10.67	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4728	17309	28753	2.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4728	17309	28754	2.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
7688	20178	33065	0.67	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8013	20555	33458	1.36	2.0E-41	M86944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8013	20555	33459	1.38	2.0E-41	M86944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8040	20582	33489	1.59	2.0E-41	AA328255.1	EST_HUMAN	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
8905	21443	34368	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9338	21852	34800	0.74	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9338	21852	34801	0.74	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11359	23813	36873	3.76	2.0E-41	AA372837.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3240	15852	28333	1.11	1.0E-41	BE889735.1	EST_HUMAN	601445647F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3849803 5'
3240	15852	28334	1.11	1.0E-41	BE889735.1	EST_HUMAN	601445647F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3849803 5'
4686	17248	29701	11.21	1.0E-41	6878488	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9339	21853	34802	1.82	1.0E-41	AI217868.1	EST_HUMAN	q75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11039	23553	36588	2.41	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-160200-040-F09 CT0213 Homo sapiens cDNA
11842	24204		2.37	1.0E-41	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8457	20967		1.34	0.0E-42	BE178191.1	EST_HUMAN	RCO-HT0813-210300-032-g01 HT0813 Homo sapiens cDNA
9101	21637	34575	2.43	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9101	21637	34576	2.43	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
488	13121	25607	7.59	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDXA (CDXA) gene, complete cds and flanking repeat regions
11861	24959		53.38	8.0E-42	AA493896.1	EST_HUMAN	rh07c02.a1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943588 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA ;
11900	24830		2.62	8.0E-42	AW088062.1	EST_HUMAN	xc97a04.x1 NCL_CGAP_Brn38 Homo sapiens cDNA clone IMAGE:2562174 3' similar to contains OFR.12
987	13578		2.5	7.0E-42	AL163285.2	NT	OFR repetitive element ; Homo sapiens chromosome 21 segment HS21C085

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8406	20946		0.62	7.0E-42	R10983.1	EST_HUMAN	y38g04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128174 5'
9168	21745	34688	1.99	7.0E-42	A1204358.1	EST_HUMAN	qf58g12.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1744278 3'
11052	23955	36800	1.59	7.0E-42	AA569592.1	EST_HUMAN	mf23g07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914852
11052	23955	36801	1.59	7.0E-42	AA569592.1	EST_HUMAN	mf23g07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914852
1898	14481	27039	4.44	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1898	14481	27040	4.44	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2328	14899		3.36	6.0E-42	AW238958.1	EST_HUMAN	xp28f08.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741798 3' similar to contains L1.L1 L1 repetitive element
5859	18286	30764	1.48	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5853	18286	30764	1.5	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
141	12808		6.21	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
483	13087	25588	1.38	5.0E-42	BE217913.1	EST_HUMAN	h311e11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
512	13145		4.36	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
513	13148		2.72	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8768	18378	32194	1.23	5.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
8768	18378	32195	1.23	5.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
8883	18827	32484	2.58	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7283	19781	32837	1.84	5.0E-42	AF071688.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
8713	21252	34174	2.85	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
10495	22889	35987	0.6	5.0E-42	11431188	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10495	22889	35988	0.6	5.0E-42	11431188	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10877	23398	36415	1.92	5.0E-42	8923182	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
783	13402	26905	7.93	4.0E-42	AF055086.1	NT	Homo sapiens MHC class 1 region
783	13402	26908	7.93	4.0E-42	AF055086.1	NT	Homo sapiens MHC class 1 region
1104	13708	28217	2.39	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4272	16858	28307	1.48	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4355	16922	28394	5.27	4.0E-42	4506498	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4683	17265	28715	13.42	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5353	17913	30328	0.94	4.0E-42	7881635	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10378	22872	35865	0.46	4.0E-42	AW371201.1	EST_HUMAN	CMQ-BT0282-171289-127-b03 BT0282 Homo sapiens cDNA
10528	23065	36876	1.76	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23065	36077	1.78	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11290	23742	36799	3.45	4.0E-42	BF035327.1	EST_HUMAN	60145831F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662086 5'
1530	14122	26661	4.49	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2436	15003	27575	0.92	2.0E-42	AW690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCB808 6'
2466	15023		2.69	2.0E-42	AW989344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2469	15036	27603	2.41	2.0E-42	AW250059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
5931	18553	31279	13.21	2.0E-42	AW955368.1	EST_HUMAN	EST387438 MAGC resequences, MAGC Homo sapiens cDNA
5931	18553	31280	13.21	2.0E-42	AW955368.1	EST_HUMAN	EST387438 MAGC resequences, MAGC Homo sapiens cDNA
6849	19439	32253	0.84	2.0E-42	A052566.1	EST_HUMAN	cn63405.x1 Scarsas_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
8755	22253	35235	1.1	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447820 5'
9987	22462	35445	0.53	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
9987	22462	35446	0.53	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
11985	24030	37100	1.55	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
763	13381	25880	1.52	1.0E-42	X57147.1	NT	Homo endogenous retrovirus pHE.1 (ERV9)
1060	13685	26197	0.84	1.0E-42	AW265809.1	EST_HUMAN	UI-H-B1-1011-04-04-U1.s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1140	13743	26252	2.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1140	13743	26253	2.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1285	15437	28404	10.72	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homodog mRNA, nuclear gene
1286	16437	28405	10.72	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homodog mRNA, nuclear gene
1738	14328	26872	1.86	1.0E-42	11423218	NT	Homo sapiens rec (LOC51201). mRNA
2581	15144	27712	5.25	1.0E-42	5174459	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2891	15607	28037	6.58	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homodog)-like (ORC5L) mRNA, and translated products
3770	16371	28836	2.85	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255). mRNA
3862	18460	28924	0.83	1.0E-42	5031610	NT	Homo sapiens Gdgl vesicular membrane trafficking protein p18 (BET1) mRNA
3998	16597	28089	1.07	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4331	16918	28361	1.92	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4697	17279	29725	0.86	1.0E-42	AW813817.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4856	17434	28885	2.65	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31). mRNA
4856	17434	28886	2.65	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31). mRNA
4893	17468	29924	6.23	1.0E-42	4506759	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5274	17835	30260	1.48	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6274	17835	30281	1.48	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
9898	22493	35482	3.35	9.0E-43	4757989	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
10916	23435	38455	3.57	8.0E-43	AA435718.1	EST_HUMAN	z178a07.s1 Scores_NHT Homo sapiens cDNA clone IMAGE:728532 3'
680	13304	25788	22.52	8.0E-43	AV738824.1	EST_HUMAN	AV738824 CB Homo sapiens cDNA clone CBLAKH08 5'
690	13304	25787	22.52	8.0E-43	AV738824.1	EST_HUMAN	AV738824 CB Homo sapiens cDNA clone CBLAKH08 5'
728	13349	25841	7.38	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
728	13349	25842	7.38	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
728	13349	25843	7.38	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5877	18489	31225	0.82	8.0E-43	H13952.1	EST_HUMAN	y08e11.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3703	16304	28772	7.6	7.0E-43	AW248442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
5414	17971	30381	1.1	7.0E-43	AA889045.1	EST_HUMAN	cr88a07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602800 3' similar to contains LTR8.b3 LTR8 repetitive element ;
5414	17971	30382	1.1	7.0E-43	AA889045.1	EST_HUMAN	cr88a07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602800 3' similar to contains LTR8.b3 LTR8 repetitive element ;
8704	21243		3.4	7.0E-43	A1936748.1	EST_HUMAN	wp89b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466885 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
1388	13982		9.88	6.0E-43	AA491890.1	EST_HUMAN	ne72a08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:809803 similar to gb.L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2828	15190		2.44	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADGACC10 5'
6453	19054	31839	2.54	6.0E-43		NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6988	19486	32308	2.15	6.0E-43	AW488897.1	EST_HUMAN	h330b04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810891 3' similar to contains MER1.13 MER1 repetitive element ;
9785	22263	35248	2.2	8.0E-43	AA185154.1	EST_HUMAN	z36a06.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:685410 5' similar to TR:G528841 G528841 DB1, COMPLETE CDS ; contains element PTR7 repetitive element ;
10980	23494		6.53	8.0E-43	AL119186.1	EST_HUMAN	DKFZp761L1712.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
148	12812		1.7	5.0E-43	AL183213.2	NT	Homo sapiens chromosome 21 segment HS21C013
528	13160	25641	3.37	5.0E-43	AA382780.1	EST_HUMAN	EST189033 Testis I Homo sapiens cDNA 5' end
2872	15480	27861	1.18	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
6447	19481	32302	1.23	6.0E-43	A1813509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
6983	19481	32302	0.77	5.0E-43	A1813509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
8812	21351		0.49	5.0E-43	H74277.1	EST_HUMAN	y449g12.1 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:226510 5'
9286	21886	34831	3.67	5.0E-43	AA485288.1	EST_HUMAN	aa33a08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	22791	35781	2.17	5.0E-43	AF33244.1	EST_HUMAN	cc62c10.x6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1669810 3' similar to TR:P80591 P80591
10332	22826	35821	2.14	5.0E-43	AL049110.1	EST_HUMAN	PV14 GENE.:
10844	23178	36188	5.05	5.0E-43	AV983007.1	EST_HUMAN	DKFZp434D0119.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D0119
10850	23371	36380	4.1	5.0E-43	W28011.1	EST_HUMAN	MR2-SN0007-280400-004-002 SN0007 Homo sapiens cDNA
11332	23030	36039	1.71	5.0E-43	X15804.1	NT	5564 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1008	15390	26133	5.38	4.0E-43	AF003528.1	NT	Human mRNA for alpha-actinin
5484	18089	30417	0.98	4.0E-43	AI056338.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6507	19107	31882	0.82	4.0E-43	6868009	NT	oy47n03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1668013 3'
7184	18718		2.22	4.0E-43	11418783	NT	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
8118	20859	33588	4.54	4.0E-43	AI244341.1	EST_HUMAN	Homo sapiens protocadherin beta 8 (PCDH8), mRNA
8118	20859	33588	4.54	4.0E-43	AI244341.1	EST_HUMAN	q76802.x1 NCI_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
10217	22712	35704	1.33	4.0E-43	6005987	NT	MER10 repetitive element:
11184	23889	38738	1.88	4.0E-43	T77380.1	EST_HUMAN	q76802.x1 NCI_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11819	24189		4.47	4.0E-43	R20950.1	EST_HUMAN	MER10 repetitive element:
1255	13852		3.54	3.0E-43	AF223391.1	NT	q76802.x1 NCI_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
1733	14324	26868	1.8	3.0E-43	X97689.1	NT	MER10 repetitive element:
2178	14753	27323	1.15	3.0E-43	AJ276230.1	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
3630	18233	28708	1.25	3.0E-43	S88002.1	NT	yd72h10.r1 Soares fetal liver spleen 1NF15 Homo sapiens cDNA clone IMAGE:113827 5'
4378	16985	28411	0.9	3.0E-43	AA548154.1	EST_HUMAN	yd08k05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10
6498	18099	31883	2.08	3.0E-43	7305380	NT	repetitive element:
6498	18099	31884	2.08	3.0E-43	7305380	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6827	19417	32233	3.71	3.0E-43	U85487.1	NT	H. sapiens gene encoding La autoantigen
8104	20845		8.03	3.0E-43	AA458824.1	EST_HUMAN	Homo sapiens mRNA for partial phospholipase D1, splice variant PLD1a/b2
8754	21263	34213	1.59	3.0E-43	7861721	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5838 nt]
9778	22276	35281	0.77	3.0E-43	11420217	NT	nk55d06.s1 NCI_CGAP_P17 Homo sapiens cDNA clone IMAGE:1017419
11572	24019	37089	2.8	3.0E-43	5730038	NT	Mus musculus clogelin (Olog), mRNA
							Mus musculus clogelin (Olog), mRNA
							Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
							aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element:
							Homo sapiens hypothetical protein (HSA011916), mRNA
							Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC83648), mRNA
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
198	12858		9.15	2.0E-43	AI180784.1	EST_HUMAN	qd81c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains P.TR7.43
6601	19198	32003	0.96	2.0E-43	BE222778.1	EST_HUMAN	PTR7 PTR7 repetitive element ;
6601	19198	32004	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCL_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173760 3' similar to contains element
7320	19847	32707	1.12	2.0E-43	AW207390.1	EST_HUMAN	MER40 repetitive element ;
8260	20791		0.98	2.0E-43	U43701.1	EST_HUMAN	hu53a08.x1 NCL_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173760 3' similar to contains element
11079	23591		3.66	2.0E-43	T03007.1	NT	MER40 repetitive element ;
1690	14282	26817	2.54	1.0E-43	AF154836.1	NT	UI-H-B11-afi-a-09-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
1690	14282	26818	2.54	1.0E-43	AF154836.1	NT	Human ribosomal protein L23a mRNA, complete cds
1743	14333	26879	1.63	1.0E-43	AL1163284.2	NT	FB1G5 Fetal brain, STRagene Homo sapiens cDNA clone FB1G5 3' and similar to LINE.1
2750	15305	27869	4.08	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
6723	19317	32120	9.22	1.0E-43	4607168	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
6723	19317	32121	9.22	1.0E-43	4507168	NT	Homo sapiens chromosome 21 segment HS21G084
7046	18066	30468	1.8	1.0E-43	R19751.1	EST_HUMAN	602022313F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4157668 5'
7873	20415	33323	1.04	1.0E-43	AF175265.1	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8010	20552		2.79	1.0E-43	AF1188480.1	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8771	21310	34233	28.96	1.0E-43	AW983676.1	EST_HUMAN	y640e01.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
10191	22686	35678	0.85	1.0E-43	AW953229.1	EST_HUMAN	SP-ID38_MOUSE P28658 BRAIN PROTEIN DN38 ;
10843	23384	36380	8.02	1.0E-43	AI884861.1	EST_HUMAN	Homo sapiens vacuole sorting protein 35 (VPS35) mRNA, complete cds
11244	23774	36831	3.74	1.0E-43	11424378	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
11757	24152		1.95	1.0E-43	AL137984.1	EST_HUMAN	EST375749 MAGe resequences, MAGH Homo sapiens cDNA
12054	24337	30998	3.9	1.0E-43	AI875416.1	EST_HUMAN	EST3765289 MAGe resequences, MAGB Homo sapiens cDNA
12286	24488	30942	4.3	9.0E-44	11418322	NT	wr87h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
923	13536	26054	5.63	8.0E-44	AI222885.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
923	13536	26055	5.63	8.0E-44	AI222885.1	EST_HUMAN	DKFZp761D1016_1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1016 6'
			0.69	8.0E-44	AI981520.1	EST_HUMAN	wb98b04.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
6424	17681	30388	2.74	8.0E-44	X94354.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
8478	21015	33931	2.74	8.0E-44	X94354.1	NT	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
11043	23557	36593	3.86	8.0E-44	Y10498.2	NT	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
11538	23984	37058	1.86	8.0E-44	Z9139.1	NT	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
12030	24310	30992	2.76	8.0E-44	11527380	NT	ta76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092822 3' similar to TR:P63107
			0.69	8.0E-44	AI981520.1	EST_HUMAN	P63107 PF20. ;
8478	21015	33931	2.74	8.0E-44	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
11043	23557	36593	3.86	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
12030	24310	30992	2.76	8.0E-44	11527380	NT	Homo sapiens myosin mRNA, partial cds
			2.76	8.0E-44	11527380	NT	Homo sapiens polymerase (RNA) II (DNA directed) poliovirus E (POL R2E) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12419	24859	30703	2.39	8.0E-44	11418098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
687	13311		0.83	7.0E-44	R08035.1	EST_HUMAN	y88601.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124920 5'
2278	14850	27428	1.12	7.0E-44	5031898	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2893	15609	28098	2.84	7.0E-44	AF048720.1	NT	Homo sapiens minisatellite ms32 repeat region
2893	15609	28099	2.84	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3928	16527	28994	2.78	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4328	16912	29354	0.98	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4328	16912	29355	0.98	7.0E-44	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
8128	20897	33576	6.38	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000488 3'
6252	18861	31633	0.77	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU.P. Human fetal Brain Whole tissue Homo sapiens cDNA
11611	24054	37118	2.92	6.0E-44	AW654060.1	EST_HUMAN	EST366120 MAGE resequences, MAGE Homo sapiens cDNA
325	12979		3.12	5.0E-44	AJ288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
354	13003		1.75	5.0E-44	AJ288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
7828	20371	33278	3.5	5.0E-44	AI588523.1	EST_HUMAN	tr40d02.x1 NCI_CGAP_Bm28 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9308	21808		1.85	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element ;
3481	18088	28541	2.18	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5158	17727		1.18	4.0E-44	AI495226.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8215	20756	33870	0.78	4.0E-44	L21948.1	NT	tr11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8811	21360		0.54	4.0E-44	BE176618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11117	23826	36668	7.04	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
1821	14410		1.09	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3132	15748	28215	5.8	3.0E-44	AA169851.1	EST_HUMAN	tr18b05.1 Stratiens fetal retina 937202 Homo sapiens cDNA clone IMAGE:608777 5'
3959	16557	28028	2.84	3.0E-44	AA337234.1	EST_HUMAN	EST42289 Endometrial tumor Homo sapiens cDNA 5' end similar to alpha-1-antitrypsinase F
5404	17982	30373	2.57	3.0E-44	BF691080.1	EST_HUMAN	602247109F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332195 5'
9438	21984	34913	0.88	3.0E-44	AF008273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1087	13692	28201	2.13	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1087	13692	28202	2.13	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1249	13846	28363	2.89	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1249	13846	28364	2.89	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1355	13949	28475	4.41	2.0E-44	AF135585.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1412	14005	28533	1.38	2.0E-44	BE485325.1	EST_HUMAN	hw14g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2196	14772	27346	1.71	2.0E-44	AF070651.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2841	15200		2.07	2.0E-44	5901893	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3517	16122	26602	1.34	2.0E-44	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4689	17251	26703	1.86	2.0E-44	AW864379.1	EST_HUMAN	PM4-SN0016-120500-003-404 SN0018 Homo sapiens cDNA
5441	17866	30401	1.08	2.0E-44	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
6245	18854	31825	1.71	2.0E-44	11448901	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6941	18049	30471					
7444	18668	32835	1.05	2.0E-44	AF038968.1	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7444	19068	32838	4.03	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8367	20907	33825	0.86	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8367	20907	33825	0.86	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA00917), mRNA
8367	20907	33825	0.85	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA00917), mRNA
8554	21093	34013	1.47	2.0E-44	BE388058.1	EST_HUMAN	601285914F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3513585 5'
11657	24084		1.8	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2786
12608	24692		63.7	2.0E-44	11526283	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
56	12736	25205	5.03	1.0E-44	7657334	NT	Homo sapiens Mieshaen/NIK-related kinase (MINK), mRNA
56	12736	25206	5.03	1.0E-44	7657334	NT	Homo sapiens Mieshaen/NIK-related kinase (MINK), mRNA
606	13234	25708	2.28	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1239	13837		1.03	1.0E-44	AW694803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1618	14211		4.77	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2266	14840	27416					z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
2266	14840	27417	3.03	1.0E-44	AA434554.1	EST_HUMAN	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
2321	15463	27468	1.21	1.0E-44	AA398099.1	EST_HUMAN	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
2788	15341	27911	1.54	1.0E-44	AF168779.1	NT	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
3788	16398		4.07	1.0E-44	AA434554.1	EST_HUMAN	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
6208	20750	33663	1.33	1.0E-44	AW697073.1	EST_HUMAN	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
8208	20750	33664	1.33	1.0E-44	AW697073.1	EST_HUMAN	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
8380	21119	34040	0.94	1.0E-44	AL163303.2	NT	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:
8956	21494	34417	0.88	1.0E-44	AI337183.1	EST_HUMAN	z533d02.1 Scores_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element:

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10892	23413		11.29	1.0E-44	AV714808.1	EST_HUMAN	AV714808 DCB Homo sapiens cDNA clone DCBBYE03 5'
11404	23855	36921	5.07	1.0E-44	10082684	NT	Homo sapiens Supli domain (SGR repeat) containing (BK65A6.2), mRNA
11480	23910	36976	3.83	1.0E-44	AW846867.1	EST_HUMAN	RC1-CT0198-150989-011-C08 CT0198 Homo sapiens cDNA
11480	23910	36977	3.83	1.0E-44	AW846867.1	EST_HUMAN	RC1-CT0198-150989-011-C08 CT0198 Homo sapiens cDNA
4878	17260	28711	1.31	8.0E-45	89223391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4878	17260	28712	1.31	9.0E-45	89223391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6757	18350	32159	1.34	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0665 protein, partial cds
2595	15128	27698	6.45	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5241	17805	30228	7.14	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8051	20593	33501	0.84	8.0E-45	AA377985.1	EST_HUMAN	EST30863 Synovial sarcoma Homo sapiens cDNA 5' end
2884	15800		0.99	7.0E-45	AL180131.1	NT	Novel human gene mapping to chromosome 22
4050	16847		6.39	6.0E-45	AW167570.1	EST_HUMAN	aw83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to
12385	25063		2	6.0E-45	11418213	NT	SW:R13A_HUMAN P40428 60S RIBOSOMAL PROTEIN L13A ;
925	13538		1.34	5.0E-45	AL163203.2	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
2045	14827	27198	12.03	5.0E-45	BF333827.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G003
3246	15858	28341	2.25	5.0E-45	AI523766.1	EST_HUMAN	GM4-CH0044-180200-515-f01 CH0044 Homo sapiens cDNA
6703	18329	30832	8.34	5.0E-45	AA397781.1	EST_HUMAN	tp94f07.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
6170	18782	31548	1.1	5.0E-45	Y18933.1	NT	P09084 PAIRED BOX PROTEIN PAX-1 ;
6170	18782	31549	1.1	5.0E-45	Y18933.1	NT	z172d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element
6215	18825	31596	1.15	5.0E-45	AB022318.1	NT	TAR1 repetitive element ;
6215	18825	31597	1.15	5.0E-45	AB022318.1	NT	Homo sapiens MCP-1 gene and enhancer region
6336	18942	31720	1.82	5.0E-45	11496288	NT	Homo sapiens MCP-1 gene and enhancer region
6336	18942	31721	1.82	5.0E-45	11496288	NT	Homo sapiens MCP-1 gene and enhancer region
8218	20759	33873	0.51	5.0E-45	11416704	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
8971	21509	34431	1.79	5.0E-45	4759223	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
11542	23900	37082	2.52	5.0E-45	8923688	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
1183	13784	26294	11.57	4.0E-45	X95826.1	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
2330	14901	27472	21.18	4.0E-45	BE268622.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
4605	17188	26835	0.68	4.0E-45	4759249	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
8886	21424		0.86	4.0E-45	AA228220.1	EST_HUMAN	Homo sapiens golgi-like protein (GLP), mRNA
							H. sapiens ART4 gene
							601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
							Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
							nc28s07.s1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:1008284 similar to contains element L1
							repetitive element ;

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11828	24071		2.17	4.0E-45	BE044076.1	EST_HUMAN	h038h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039611 3' similar to contains MER28.b3
11873	26008	30813	1.86	4.0E-45	11435947	NT	MER29 repetitive element;
12278	24482		2.14	4.0E-45	BF676077.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
4161	15882		1.32	3.0E-45	171480.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
6383	18987	31767	1.29	3.0E-45		NT	y035f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6383	18987	31768	1.29	3.0E-45	6753851	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahe11), mRNA
8398	20928		1.29	3.0E-45	6753851	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahe11), mRNA
8728	21285	34185	3.78	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
10209	22704	35688	11.34	3.0E-45	AL163227.2	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10209	22704	35687	11.34	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
2547	15111		4.13	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3067	16882	28154	0.88	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6844	19240	32043	5.48	2.0E-45	L01685.1	NT	Homo eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7605	20118	32694	1.35	2.0E-45	BE762184.1	EST_HUMAN	601487789F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870838 5'
8354	20894	33815	0.75	2.0E-45	AW834834.1	EST_HUMAN	RC0-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
10882	24798	38225	28.88	2.0E-45	BE934380.1	EST_HUMAN	MRO-HT0923-180800-201-e02 HT0923 Homo sapiens cDNA
11055	23567	36803	5.39	2.0E-45	AA458770.1	EST_HUMAN	aa87f12.r1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11378	23830	36892	2.33	2.0E-45	AW270280.1	EST_HUMAN	TR:G1144569 G1144569 R-SLY1.;
11378	23830	36893	2.33	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2748868 3'
12648	24953		2.42	2.0E-45	11418157	NT	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2748868 3'
128	13067		2.71	1.0E-45	BE388855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
434	13067		3.24	1.0E-45	BE388855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
488	13130	25619	1.81	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1216	13816	26331	1.54	1.0E-45	7657260	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3137	15751	28219	10.2	1.0E-45	U32168.1	NT	Homo sapiens Langerhans cell specific alpha-type lectin (LANGERIN), mRNA
3539	16144	28827	0.88	1.0E-45	8659558	NT	Human pro-alpha2 chain of collagen type XI (COL11A2) gene, complete cds
3632	18235	28710	0.68	1.0E-45	AB046811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4575	17158	29602	5.67	1.0E-45	BE388833.1	EST_HUMAN	Homo sapiens mRNA for KIAA1561 protein, partial cds
5335	17898	30311	11.79	1.0E-45	7706128	NT	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3616803 5'
7874	20516	33422	0.71	1.0E-45	11422238	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
7874	20516	33423	0.71	1.0E-45	11422238	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
7874	20516	33423	0.71	1.0E-45	11422238	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8543	21082	34003	0.89	1.0E-45	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9049	21688	34517	4.07	1.0E-45	BE887843.1	EST_HUMAN	601511220F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912635 5'
9441	21967	34916	0.86	1.0E-45	AB002207.1	NT	Human mRNA for KIAA2089 gene, partial cds
11875	24225	31045	4.89	1.0E-45	11418098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12083	24348		9.84	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12088	24349		10.38	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12513	24632	30895	3.48	1.0E-45	11418167	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8170	20711	33628	1.87	9.0E-48	8910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
8569	21108		6.51	9.0E-48	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10374	22868	35861	10.22	9.0E-48	AW246884.1	EST_HUMAN	2822449.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2486	16051	27622	9.69	8.0E-48	AI433261.1	EST_HUMAN	83208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_m2
2486	16051	27623	9.69	8.0E-48	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
7988	20540		6.07	8.0E-48	BE187244.1	EST_HUMAN	83208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_m2
11513	23961		2.67	8.0E-48	11418728	NT	TUBULIN BETA-1 CHAIN (HUMAN);
2280	14854	27432	1.07	7.0E-48	U48007.1	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
4880	17282		6.38	7.0E-48	BE388185.1	EST_HUMAN	Rattus norvegicus espin mRNA, complete cds
4928	17504		0.88	7.0E-48	BE084386.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818119 5'
6193	18803	31572	3.72	7.0E-48	8922708	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6620	19217	32022	1.29	7.0E-48	BF105845.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
12203	24428		1.6	7.0E-48	AL163246.2	NT	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042738 5'
2783	15336	27806	3.13	6.0E-48	AI864381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
2783	15336	27807	3.13	6.0E-48	AI864381.1	EST_HUMAN	wm3108.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
6278	18886	31655	9.32	6.0E-48	AI835448.1	EST_HUMAN	MER19 repetitive element;
7289	19797	32653	0.83	6.0E-48	AW513244.1	EST_HUMAN	MER19 repetitive element;
11288	23008		2.81	6.0E-48	BE784971.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
218	12879		5.85	5.0E-48	AL163210.2	NT	SA GENE.;
3581	16185	28687	1.37	5.0E-48	BE677194.1	EST_HUMAN	xx42e04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2708664 3' similar to gb:LO8089 DNAJ
3581	16185	28688	1.37	5.0E-48	BE677194.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
							601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
							Homo sapiens chromosome 21 segment HS21C010
							7881901.x1 Lupaoki_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7881901.x1 Lupaoki_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6833	19423	32239	1.83	5.0E-48	BF590442.1	EST_HUMAN	ncs3807.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3268767 3' similar to TR:O76202
7021	19555	32380	3.81	5.0E-48	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
7152	18884	32528	0.74	5.0E-48	AW582253.1	EST_HUMAN	802021164F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4156670 5'
9533	22033	34992	0.48	5.0E-48	AA398381.1	EST_HUMAN	QV4-ST0212-120700-076-008 ST0212 Homo sapiens cDNA
689	13283		1.73	4.0E-48	AA601143.1	EST_HUMAN	z62c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726928 3'
							ncs4e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1741	14331	28876	3.98	4.0E-48	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
							LYSOZYME C PRECURSOR (HUMAN);contains element MIER37 repetitive element ;
1741	14331	28876	3.98	4.0E-48	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
2767	15321	27887	3.11	4.0E-48	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN);contains element MIER37 repetitive element ;
5828	18257	30727	2.09	4.0E-48	M36852.1	NT	Human endogenous retrovirus RTVL-H2
5828	18257	30728	2.09	4.0E-48	M36852.1	NT	Human lg germline gamma-3 heavy-chain gene V region, partial cds
12332	24516	30921	1.88	4.0E-48	AB002056.1	NT	Human lg germline gamma-3 heavy-chain gene V region, partial cds
4482	17087	29517	0.81	3.0E-48	4506376	NT	Homo sapiens DNA for Human P20X, complete cds
							Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4889	17484	28918	0.98	3.0E-48	Z73660.1	NT	H. sapiens lg lambda light chain variable region gene (7c.11.2) germline; lg-Light-Lambda; VLambda
4889	17484	28919	0.98	3.0E-48	Z73660.1	NT	H. sapiens lg lambda light chain variable region gene (7c.11.2) germline; lg-Light-Lambda; VLambda
8684	21223	34143	7.65	3.0E-48	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2
8935	21473	34392	0.56	3.0E-48	L08850.1	NT	THR repetitive element ;
8935	21473	34393	0.56	3.0E-48	L08850.1	NT	Human AD amyloid mRNA, complete cds
11448	23898	36981	3.14	3.0E-48	D31786.1	NT	Human AD amyloid mRNA, complete cds
870	13485	26000	8.24	2.0E-48	AA468848.1	EST_HUMAN	Human mRNA for KIAA0081 gene, partial cds
1608	14201		1.41	2.0E-48	AA678248.1	EST_HUMAN	nc08e09.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
1683	14275	26808	2.17	2.0E-48	U78027.1	NT	repetitive element ;
							z127a11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431896 3'
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
							(L44L) and FTP3 (FTP3) genes, complete cds
5110	17682	30119	1.2	2.0E-48	AA398286.1	EST_HUMAN	z159e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW:RSP1_MOUSE
							Q01730 RSP-1 PROTEIN ;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7497	20020	32884	6.85	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8014	20556		1.81	2.0E-46	BE669151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849287 5'
11125	23633		1.56	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
11802	24983		1.74	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997328 5'
12094	24361		1.43	2.0E-46	AA001788.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428016 6'
12408	24846	30800	5.26	2.0E-46	AW277214.1	EST_HUMAN	xq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2769789 3'
1278	13871	26391	5.79	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2320	14892	27487	4.56	1.0E-46	AW978518.1	EST_HUMAN	EST390826 MAGe resequences, MAGP Homo sapiens cDNA
2443	15010	27582	2.81	1.0E-46	H97330.1	EST_HUMAN	EST480895 WATM1 Homo sapiens cDNA clone 480895
3286	15897	28376	22.33	1.0E-46	AA631912.1	EST_HUMAN	np78b02.x1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H. sapiens MT-11 mRNA. (HUMAN);
4989	17672		3.21	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0080 protein, partial cds
5878	18500	31226	11.77	1.0E-46	BF194707.1	EST_HUMAN	7c82b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
6131	24757	31500	4.79	1.0E-46	8923782	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6131	24757	31501	4.79	1.0E-46	8923782	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6725	19319	32124	0.72	1.0E-46	BF198247.1	EST_HUMAN	7n48e07.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567652 3' similar to contains element
10742	18500	31226	4.43	1.0E-46	BF194707.1	EST_HUMAN	MER22 repetitive element ;
11831	24198	31035	1.87	1.0E-46	BF531102.1	EST_HUMAN	7c82b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
11831	24198	31036	1.97	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215398 5'
12626	24704		1.39	1.0E-46	AV715377	EST_HUMAN	602072284F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215398 5'
798	13415		3.52	9.0E-47	AJ271735.1	NT	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
9085	17638	30081	2.39	9.0E-47	AW770928.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
6514	19114	31603	0.78	8.0E-47	11425439	NT	h93e04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008534 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN. ;
12355	24951	30827	3.64	9.0E-47	11417898	NT	Homo sapiens zinc finger protein ZNF288 (ZNF288), mRNA
1844	14432	26986	18.42	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1844	14432	26996	18.42	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2742	15297	27864	1.1	8.0E-47		NT	Homo sapiens HLA-C gene, exon 6, individual 18323
3058	15874	28150	2.05	8.0E-47	AJ228043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B58), epsilon isoform (PPP2R5E) mRNA
3686	16287	28756	0.8	8.0E-47	AB041926.1	NT	Homo sapiens 650 kb contig between AYL1 and CBR1 on chromosome 21q22, segment 3/3
3686	16287	28757	0.8	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
12436	24846		1.55	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9200	21717	34691	6.33	6.0E-47	AI695189.1	EST_HUMAN	zb98k02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296859 3'
9828	22128	35091	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9828	22128	35092	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6691	19287	32080	6.97	6.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10874	23208		4.92	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Striatogene (cat#38206) Homo sapiens cDNA clone HFBCF07
1445	14037	26567	3.92	4.0E-47	4657556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6920	19579	32408	0.94	4.0E-47	BE938898.1	EST_HUMAN	MR4-TN0108-280800-201-404 TN0108 Homo sapiens cDNA
8417	20957	33874	2.47	4.0E-47	BE619483.1	EST_HUMAN	601280486F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3822437 5'
8417	20957	33875	2.47	4.0E-47	BE619483.1	EST_HUMAN	601280486F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3822437 5'
8553	21092	34012	0.57	4.0E-47	AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-105 BN0034 Homo sapiens cDNA
11494	23943		6.19	4.0E-47	AW615609.1	EST_HUMAN	xx68607.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
570	13201	25692	3.11	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-8, [1];
570	13201	25693	3.11	3.0E-47	BE907634.1	EST_HUMAN	601487639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
851	13467	25976	5.09	3.0E-47	N57483.1	EST_HUMAN	601487639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
981	13593	26108	9.88	3.0E-47	AL163284.2	NT	Y64604.s1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:277327 3'
3343	15953	28429	0.77	3.0E-47	4504118	NT	Homo sapiens chromosome 21 segment HS21C084
4038	16636		5.04	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
6163	18776	31538	4.81	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SDF1) mRNA, partial cds
6163	18776	31539	4.81	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-Q-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6690	19278		1.71	3.0E-47	AI222413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-Q-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7416	19941	32806	0.75	3.0E-47	A1819755.1	EST_HUMAN	q104607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843718 3'
7416	19941	32807	0.75	3.0E-47	A1819755.1	EST_HUMAN	w11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8767	21306	34228	0.56	3.0E-47	AW963798.1	EST_HUMAN	w11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8767	21306	34229	0.56	3.0E-47	AW963798.1	EST_HUMAN	EST375869 MAGe resequences, MAGH Homo sapiens cDNA
159	12822	25310	1.38	2.0E-47	4505318	NT	EST375869 MAGe resequences, MAGH Homo sapiens cDNA
1003	13614	26127	2.14	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1003	13614	26128	2.14	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1613	14206		1.1	2.0E-47	A1969279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1637	14228	26762	1.07	2.0E-47	7682108	NT	wq88602.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2478851 3'
1717	14309	26848	3.75	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
4439	17025	26465	1.88	2.0E-47	4504868	NT	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4473	17056	26506	1.81	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4473	17059	26507	1.91	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4604	17187	28634	2.84	2.0E-47	5174948	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4636	17510	28957	1.29	2.0E-47	AW965168.1	EST_HUMAN	EST377239 MAGE resequences, MAGI Homo sapiens cDNA
5898	18578	31312	0.93	2.0E-47	AF079921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGSG) mRNA, complete cds
6130	18745	31408	1.46	2.0E-47	BE778475.1	EST_HUMAN	601483932F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3867487 5'
6130	18745	31499	1.48	2.0E-47	BE778475.1	EST_HUMAN	601483932F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3867487 5'
7888	24788		1.25	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7895	20447	33353	1.74	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7895	20447	33354	1.74	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8652	21191	34109	1.77	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9410	21918	34867	1.33	2.0E-47	11526139	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11863	24994	30608	2.82	2.0E-47	R42423.1	EST_HUMAN	yf82608.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28898 3' similar to contains OFR repetitive element
1431	14043	28571	6.05	1.0E-47	A133429.1	EST_HUMAN	q880h03.x1 Soares fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1931189 3'
3894	16483	28963	0.83	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3894	16483	28984	0.83	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5235	17789	30218	2.44	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7109	19449	32285	5.59	1.0E-47	A1880888.1	EST_HUMAN	at119e08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355588 3' similar to gb:M22886
8802	21341						RAS-RELATED PROTEIN RAP-1A (HUMAN);
10258	22753	35741	7.08	1.0E-47	AW684648.1	EST_HUMAN	h184a11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878972 3' similar to gb:M26328
1894	14248	28779	2.38	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3612	18215	28695	0.78	8.0E-48	BF359947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5980	18482	31205	0.83	9.0E-48	BE888198.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5980	18482	31206	0.83	9.0E-48	BE888198.1	EST_HUMAN	CM2-MT0100-310700-280-705 MT0100 Homo sapiens cDNA
6373	18977	31755	0.69	9.0E-48	AU123240.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913108 5'
10895	23509	38542	3.37	9.0E-48	BE383813.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913108 5'
1293	13888		2.34	8.0E-48	4501800	NT	AUT23240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1294	13888		1.78	8.0E-48	4501800	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
3189	15783	28254	3.3	8.0E-48	AW788477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3189	15783	28255	3.3	8.0E-48	AW788477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
							h181b03.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
							h181b03.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4005	16903	28077	0.6	8.0E-48	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
518	13149		2.03	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
617	13149		20.88	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1644	14138	26970	1.08	7.0E-48	6912719	NT	Homo sapiens toubled-like kinase 1 (TLK1) mRNA
1678	14271	26804	3.48	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6672	19268	32072	21.95	7.0E-48	11418331	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
3658	16261	28733	1.19	6.0E-48	AF761111.1	EST_HUMAN	wf68h03.x1 NCL CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2398613 3'
6208	18818	31589	0.98	6.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE-75, complete cds
6881	19815	32450	0.87	6.0E-48	11420995	NT	Homo sapiens BLM non-receptor tyrosine kinase (BLM), mRNA
6051	21858	34520	2.17	6.0E-48	AF026818.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
6460	21856	34940	1.72	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
9608	22106	35089	3.5	8.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Striatum hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
2263	14867	27442	1.43	5.0E-48	4827059	NT	Homo sapiens xylulokinase (H. Influenzae) homolog (XYLB) mRNA
2300	14873	27449	1.15	5.0E-48	4827059	NT	Homo sapiens xylulokinase (H. Influenzae) homolog (XYLB) mRNA
3350	18002	28436	1.84	5.0E-48	4828891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
5418	17979	30383	1.13	5.0E-48	AF218936.1	NT	Homo sapiens diacylglycerol kinase loba (DGKl) gene, exon 32
8511	21050	33972	6.64	5.0E-48	BE064410.1	EST_HUMAN	RCA-BT0311-141169-011-h08 BT0311 Homo sapiens cDNA
10836	23367	36373	4.24	4.0E-48	AI620420.1	EST_HUMAN	tu47a02.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2254154 3'
1428	14021	28549	1.75	3.0E-48	AF580984.1	EST_HUMAN	AV680984 GKC Homo sapiens cDNA clone GKORE12 5'
2019	14601	27165	9.63	3.0E-48	4895170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2019	14601	27166	9.63	3.0E-48	4895170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3465	16072	28545	0.98	3.0E-48	AF172463.1	NT	Homo sapiens opid growth factor receptor mRNA, complete cds
3693	16294	28764	0.76	3.0E-48	AW664531.1	EST_HUMAN	hi14b12.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
4332	16918		0.67	3.0E-48	AA009541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
6053	18671	31410	2.98	3.0E-48	BE084571.1	EST_HUMAN	z04g03.r1 Soares fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:428844 5'
7087	19858	32497	1.01	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-147D
8330	20871		3.02	3.0E-48	AA859930.1	EST_HUMAN	nv03f05.s1 NCL CGAP_P722 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
10763	23277	36290	6.32	3.0E-48	BF514170.1	EST_HUMAN	PTRE5 repetitive element ;
5	12685	26142	2.18	2.0E-48	AA485007.1	EST_HUMAN	UI-H-BW1-ant-e-10-Q-JL.a1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
49	12729	25163	2.12	2.0E-48	AA631840.1	EST_HUMAN	z68c03.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:810052 5'
							hmf07 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-28

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4828	17212	28883	0.93	2.0E-48	BE240065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia BayCor-HGSC project TCBA Homo sapiens cDNA clone TCBAP3842
5095	17688	30107	1.8	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain; Strategene Homo sapiens cDNA clone FB2E2 3' end
5095	17688	30108	1.8	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain; Strategene Homo sapiens cDNA clone FB2E2 3' end
7528	20048	32919	4.15	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7528	20048	32920	4.15	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7539	20059	32933	3.51	2.0E-48	11498238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p85)) (RELA), mRNA
8298	20837	33758	1.53	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCGG10 8'
11828	12885	25142	4.4	2.0E-48	AA468007.1	EST_HUMAN	z80c03.f1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
60	12739	25210	3.22	1.0E-48	7706534	NT	Homo sapiens c14p11 resistance-associated overexpressed protein (LOC61747), mRNA
908	13520	26038	5.3	1.0E-48	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1114	13718	26228	2.68	1.0E-48	7857430	NT	Homo sapiens EBNA-2 co-activator (100kd) (p100), mRNA
1114	13718	26228	2.58	1.0E-48	7857430	NT	Homo sapiens EBNA-2 co-activator (100kd) (p100), mRNA
1339	13934	26455	4.33	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6), mRNA
1982	14548	27103	19.18	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3535	16140	28622	0.81	1.0E-48	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C946
5312	17874	30296	1.37	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6431	18034	31818	1.14	1.0E-48	AI889077.1	EST_HUMAN	Id17c01.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2075804 3' similar to TR:O14588 O14588 SIMILARITY TO U73941
6431	18034	31819	1.14	1.0E-48	AI889077.1	EST_HUMAN	Id17c01.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2075804 3' similar to TR:O14588 O14588 SIMILARITY TO U73941
6626	19222		0.94	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
7303	19831	32890	2.58	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
8785	21304	34225	0.52	1.0E-48	4758696	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8786	21304	34228	0.52	1.0E-48	4758696	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8140	21875	34618	0.84	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9192	21708	34653	6	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9495	21942	34889	0.73	1.0E-48	BE168410.1	EST_HUMAN	QV34-H10513-080400-147-401 HT0513 Homo sapiens cDNA
9502	22002	34959	3.86	1.0E-48	BF304693.1	EST_HUMAN	601889088F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10272	22787	35754	3.54	1.0E-48	11428808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10272	22787	35755	3.54	1.0E-48	11428808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
11789	24937		1.62	1.0E-48	W28786.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2052	14633	27204	0.96	8.0E-49	AB026497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
6204	18814	31584	3.44	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6204	18814	31585	3.44	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8236	20777	33698	3.22	8.0E-49	U23860.1	NT	Human trophoblast 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
9900	22397	35372	1.23	8.0E-49	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
10736	23261	36276	1.8	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element
145	13052	25542	2.62	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
145	13052	25543	2.62	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
417	13052	25542	2.38	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
417	13052	25543	2.38	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
418	13052	25542	2.59	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
418	13052	25543	2.59	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
1263	13960	26377	3.49	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5851	18278	30765	1.97	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
5861	18288	30768	1.11	7.0E-49	AL120937.1	EST_HUMAN	DKFZp782C033_s1 762 (synonym: hnd2) Homo sapiens cDNA clone DKFZp782C033 3'
5973	18278	30766	1.14	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
211	12872	25358	57.13	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2000504 3' similar to gb:U17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4183	16782	29231	0.59	6.0E-49	AL162091.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
6571	19169	31898	0.69	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'
11159	23888	30711	3.66	6.0E-49	AW452218.1	EST_HUMAN	UI-H-B13-ab-05-0-J1.x1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11514	23982	37031	3.9	6.0E-49	AA369556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
11514	23982	37032	3.9	6.0E-49	AA369556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
12166	24825		7.5	6.0E-49	AA707587.1	EST_HUMAN	z23c08.s1 Soares_fetal_liver_aplees_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461694 3'
741	13361	25854	8.81	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
741	13361	25855	8.81	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1830	14419	26988	3.16	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stratiopsis neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233228 RTVL-H PROTEIN, contains LTR7.3 LTR7 LTR7 repetitive element;
2778	15331	27800	4.85	5.0E-49	U11714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3311	16022	28398	6.09	5.0E-49	11438355	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinase 1) (H. sapiens) (LOC633602), mRNA
551	13182	25659	28.48	4.0E-49	AW189533.1	EST_HUMAN	X08001.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2875593 3' similar to WP:B0350.2B CE08703 ;
7316	19843	32704	0.79	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7316	19843	32705	0.79	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
8798	21337	34263	0.46	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
8798	21337	34264	0.46	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
12021	25055		4.9	4.0E-49	AA210798.1	EST_HUMAN	z79055.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:982977 5'
12110	24371		3.14	4.0E-49	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
586	13216	25693	1.09	3.0E-49	XB9898.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase z831cd05.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
2874	16232		1.43	3.0E-49	AA016131.1	EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
5120	17692	30130	2.33	3.0E-49	U46989.1	NT	EST25e12 WATM1 Homo sapiens cDNA clone 26e12
7448	19872	32839	9.89	3.0E-49	H39479.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
11181	23887	36734	1.98	3.0E-49	AA337581.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
688	13313		1.57	2.0E-49	BE165980.1	EST_HUMAN	y23cd06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:282571 5'
3259	15871	28351	1.3	2.0E-49	N28446.1	EST_HUMAN	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
3827	16230	28708	0.87	2.0E-49	AF026584.1	NT	alpha8d02.x1 Soares, senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1882403 3' similar to gb:IM31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element ;
4918	17493	28945	0.87	2.0E-49	AI167357.1	EST_HUMAN	UI-H-B14-eps-D-02-O-UI.s1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3088538 3'
4832	17507	28954	0.81	2.0E-49	BF511848.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBABL01 5'
6934	19424	32240	1.13	2.0E-49	AV717938.1	EST_HUMAN	EST02558 Fetal brain, Striatagene (cat9839206) Homo sapiens cDNA clone HFB CY50
8043	20585		1.71	2.0E-49	M86033.1	EST_HUMAN	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12121	24928		1.81	2.0E-49	AF169884.1	NT	60145831F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
932	13545		9.12	1.0E-49	BF035327.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
1600	14192	26723	14.28	1.0E-49	4357897	NT	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3359273 5'
1837	14426	26976	4.07	1.0E-49	BE255218.1	EST_HUMAN	601820653F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
5582	18193	30640	8.31	1.0E-49	BF131007.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6228	18837	31610	0.85	1.0E-49	H18291.1	EST_HUMAN	Y44H04.1 Soares adult brain N2b5-1855Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6234	18843	31615	0.94	1.0E-49	AW064640.1	EST_HUMAN	EST1376713 MAGE ressequences, MAGH Homo sapiens cDNA
7275	18803	32681	3.31	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7275	18803	32682	3.31	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7342	18888	32733	2.3	1.0E-49	N25884.1	EST_HUMAN	Y478g12.61 Soares placenta 8b6weeks 2NbHP8t69W Homo sapiens cDNA clone IMAGE:258408 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7342	18888	32734	2.3	1.0E-49	N25884.1	EST_HUMAN	Y478g12.61 Soares placenta 8b6weeks 2NbHP8t69W Homo sapiens cDNA clone IMAGE:258408 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8023	20585	33487	1.23	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8023	20585	33488	1.23	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8609	21148		0.93	1.0E-49	8984184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
8923	21481	34378	1.28	1.0E-49	BE409340.1	EST_HUMAN	601300982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10033	22528	35523	1.28	1.0E-49	AL043126.2	EST_HUMAN	DKFZp434D2423.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
10927	23445	36466	2.28	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
11190	23695	36744	3.48	1.0E-49	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11853	24081		1.39	1.0E-49	BE159343.1	EST_HUMAN	MRQ-HT0407-010200-006-02 HT0407 Homo sapiens cDNA
12015	24314		2.46	1.0E-49	11418323	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (GELSR1), mRNA
8538	25117		0.88	9.0E-50	BE285759.1	EST_HUMAN	601178250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
181	12843	25327	2.91	8.0E-50	AL183202.2	NT	Homo sapiens chromosome 21 segment HS21C002
748	13368	25862	1.7	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
748	13368	25863	1.7	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1070	13675		6.61	8.0E-60	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
1800	14390	26835	2.81	8.0E-50	4501860	NT	Homo sapiens actinin, alpha 1 (ACTN1), mRNA
2522	15086	27658	1	8.0E-60	7708394	NT	Homo sapiens p47 (LOC51874), mRNA
2522	15086	27659	1	8.0E-60	7708394	NT	Homo sapiens p47 (LOC51874), mRNA
2723	15278	27845	0.98	8.0E-50	4826858	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
4182	18772	28221	0.99	8.0E-50	AL183281.2	NT	Homo sapiens chromosome 21 segment HS21C081
847	13270	25748	0.97	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
8880	18814	32448	0.94	7.0E-50	BF081922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
8880	18814	32449	0.94	7.0E-50	BF081922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7348	19872	32738	1.25	7.0E-50	AA827822.1	EST_HUMAN	nc58a12.61 NCI CGAP C69 Homo sapiens cDNA clone IMAGE:1148208 3' similar to gb:X68381 60S
10636	23188	36179	22.7	7.0E-50	AI872137.1	EST_HUMAN	RIBOSOMAL PROTEIN L8 (HUMAN);
							wm55g11.1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439808 3'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4435	17021		0.62	6.0E-50	BE784381.1	EST_HUMAN	801689665F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943677 5'
8155	20698		6.9	6.0E-50	BE044076.1	EST_HUMAN	h03h04.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28.b3 MER28 repetitive element:
10694	23224	36237	5.53	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
10694	23224	36238	5.53	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1829	14418	26988	0.98	5.0E-50	BF332638.1	EST_HUMAN	CMO-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1829	14418	26987	0.98	5.0E-50	BF332638.1	EST_HUMAN	CMO-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9022	21559		4.65	5.0E-50	AA557683.1	EST_HUMAN	nl45h10.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element:
11619	24081	37125	1.57	5.0E-50	AA403093.1	EST_HUMAN	z82b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
950	13582		1.74	4.0E-50	AA601143.1	EST_HUMAN	nc54409.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_mn1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN):
7285	19813	32668	1.04	4.0E-50	BE087536.1	EST_HUMAN	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
1882	14565		2.4	3.0E-50	JA18048.1	NT	Human endogenous retrovirus RTVL-H2
3338	15948	28424	0.78	3.0E-50	AA748142.1	EST_HUMAN	0003008.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
3815	16415	28879	0.83	3.0E-50	AW765254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5 Cardiomyopathy associated gene 5
6882	18596	32427	1.45	3.0E-50	11421514	NT	Homo sapiens similar to serpin domain, Immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83232), mRNA
7840	20182	33036	4.41	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7840	20182	33037	4.41	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8518	21057	33980	0.73	3.0E-50	0601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9732	22230	35207	1.32	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1588 protein, partial cds
9741	22239	35220	0.98	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine tcn homolog) (TCP10), mRNA
10412	22806	35903	0.67	3.0E-50	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
10981	23495	38524	1.78	3.0E-50	11438855	NT	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
11339	23037	38046	5.96	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
810	13427		9.29	2.0E-50	AF059066.1	NT	Homo sapiens MHC class 1 region
1118	13721	28233	4.82	2.0E-50	4557782	NT	Homo sapiens midline 1 (Optic/BBB syndrome) (MID1) mRNA
1482	14084	28825	3.66	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
3326	15936	28412	0.91	2.0E-50	AF111189.2	NT	Homo sapiens acine palmitoyl transferase, subunit II gene, complete cds; and unknown genes

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4347	16834	29375	0.6	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
8258	20798	33716	1.24	2.0E-50	AB038182.1	NT	Homo sapiens TFF gene cluster for trypsin factor, complete cds
8268	20799	33717	1.24	2.0E-50	AB038182.1	NT	Homo sapiens TFF gene cluster for trypsin factor, complete cds
8393	20933	33854	0.32	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8393	20933	33855	0.32	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9796	22297	35281	2.89	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9796	22297	35282	2.89	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11512	23860		2.09	2.0E-50	AF023861.1	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
487	13120	25606	1.58	1.0E-50	AL163209.2	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
2403	14971		0.87	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region; segment 1/2
10095	22580	35583	0.77	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6196	18750	31507	0.89	9.0E-51	AW511225.1	EST_HUMAN	h444402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812378 3' similar to TR:Q95638
6372	18976	31754	0.69	9.0E-51	AA744837.1	EST_HUMAN	Q95638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
8606	21145	34060	0.7	9.0E-51	A1791154.1	EST_HUMAN	ny67h03.x1 NCI_CGAP_Q061 Homo sapiens cDNA clone IMAGE:1283381 3'
9248	21774	34726	1.16	9.0E-51	AA043738.1	EST_HUMAN	ab23g04.x5 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9420	21928	34876	0.52	9.0E-51	A1791154.1	EST_HUMAN	z51c09.r1 Source_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:486352 5'
9420	21928	34876	0.52	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4532	17116	29581	2.81	8.0E-51	4503832	NT	ab23g04.x5 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4532	17116	29582	2.81	8.0E-51	4503832	NT	ab23g04.x5 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4867	17249	29702	13.1	8.0E-51	AA610842.1	EST_HUMAN	ab23g04.x5 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
5319	17881	30300	1.68	8.0E-51	AF092132.1	NT	ab23g04.x5 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
7648	20160	33047	2.08	8.0E-51	11439587	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
9385	21808		0.99	8.0E-51	AU138560.1	EST_HUMAN	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
3051	15867	28145	0.72	7.0E-51	AW274720.1	EST_HUMAN	np88409.x1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:U12871_maf
3321	15931	28408	1.51	7.0E-51	AW889219.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
3408	16017	28466	0.76	7.0E-51	AW274720.1	EST_HUMAN	Homo sapiens PAK2 mRNA, complete cds
4247	16835	29286	2.14	7.0E-51	AL079828.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
							Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
							AU138560 PLACE1 Homo sapiens cDNA clone IMAGE:1008887 5'
							np34403.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895564 3' similar to TR:Q92340
							Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							QV4-NT0028-200400-180-405 NT0028 Homo sapiens cDNA
							np34403.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895564 3' similar to TR:Q92340
							Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							DKFZp434B2228_1 434 (synonym: hhes3) Homo sapiens cDNA clone IMAGE:2895564 3' similar to TR:Q92340
							DKFZp434B2228_1 434 (synonym: hhes3) Homo sapiens cDNA clone IMAGE:2895564 3' similar to TR:Q92340

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4247	16835	28287	2.14	7.0E-51	AL078628.1	EST_HUMAN	DKFZp434B2229_r1_434 (synonym: hta33) Homo sapiens cDNA clone DKFZp434B2229 5'
4443	17028	28469	1.69	7.0E-51	AW285603.1	EST_HUMAN	U1H-BW0-4ip-b-05-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728817 3'
11634	23882	37063	1.65	7.0E-51	AF181449.1	NT	Homo sapiens HSPC331 mRNA, partial cds
1575	14168	26699	17.84	6.0E-51	6878763	NT	Homo sapiens putative DNA binding protein (M68), mRNA
2022	14804	27169	5.19	6.0E-51	7657268	NT	Homo sapiens KIAA0929 protein Max2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3520	16125	28605	17.1	6.0E-51	7657268	NT	Homo sapiens KIAA0929 protein Max2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4397	16982	29426	1.09	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4397	16982	29427	1.09	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6142	18756	31514	57.08	6.0E-51	X01788.1	NT	Human haptoglobin related (Hpr) gene exon 3
6152	18765	31527	11.76	6.0E-51	AF070063.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6152	18766	31528	11.76	6.0E-51	AF070063.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6858	18592	32424	1.05	6.0E-51	4506798	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6972	18549	32373	0.71	6.0E-51	11416781	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
7044	18064	30454	2.22	6.0E-51	11426665	NT	Homo sapiens cerebral cell adhesion molecule (LOC31148), mRNA
9084	21601	34530	0.88	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9084	21601	34531	0.88	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9601	22101	35084	1.79	6.0E-51	7681935	NT	Homo sapiens B9 protein (B9), mRNA
9877	22178	35151	1.35	6.0E-51	U50083.1	NT	Human ankyrin (ANK1) gene, exon 2
11138	23844	36684	1.83	6.0E-51	11526289	NT	Homo sapiens Interleukin 17 receptor (IL17R), mRNA
11403	23854	36919	1.58	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
11403	23854	36920	1.58	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
824	13441	25948	8.74	6.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
836	13492	25992	1.38	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1028	15431	26153	1.01	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1851	14243	26777	0.99	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated p601 homolog (POH1) mRNA
2628	15191	27759	9.09	5.0E-51	AJ007556.1	NT	Homo sapiens mRNA for nucleoporin 155
4017	16815	29088	1.21	5.0E-51	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4017	16816	29089	1.21	5.0E-51	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5231	17795	30214	1.86	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11089	23581	36821	2.02	5.0E-51	BE601320.1	EST_HUMAN	7e41e02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3221258 3'

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11160	23687	38712	4.76	6.0E-61	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
140	12805	25294	15.49	3.0E-51	AI597348.1	EST_HUMAN	h81c08.x1 NCL CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1218	13818	26333	34.32	3.0E-51	AI597348.1	EST_HUMAN	h81c08.x1 NCL CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4420	17005	29448	2.04	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
7579	20095	32872	1.18	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cde4 RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
8773	21312		6.15	3.0E-51	M20083.1	NT	Human hnRNP C2 protein mRNA
8998	25124		0.8	3.0E-51	AW593777.1	EST_HUMAN	la04d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
12348	24529		2.15	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
369	13035	25524	2.03	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
717	13338	25824	0.94	2.0E-51	BE391083.1	EST_HUMAN	801285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607483 5'
717	13338	25825	0.94	2.0E-51	BE391083.1	EST_HUMAN	801285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607483 5'
1726	14317	28860	5.61	2.0E-51	AA233352.1	EST_HUMAN	z30a05.r1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:684880 5' similar to TR:G233228 G233228 RTVL-H PROTEIN, contains LTR7.13 LTR7 repetitive element;
3795	16305	28860	2.71	2.0E-51	AI492415.1	EST_HUMAN	h27g03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4592	17175	29821	1.73	2.0E-51	AW137826.1	EST_HUMAN	UHH-B11-adj-4-02-0-UI.at NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5630	18259	30730	0.76	2.0E-51	AI732851.1	EST_HUMAN	d334f08.x5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5630	18259	30731	0.76	2.0E-51	AI732851.1	EST_HUMAN	d334f08.x5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
6168	18778	31542	3.29	2.0E-51	BE782015.1	EST_HUMAN	801470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873963 5'
7360	19876		0.77	2.0E-51	AF210927.1	NT	Homo sapiens diacylglycerol kinase iota (DGKI) gene, exon 23
7480	20002	32867	1	2.0E-51	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0888), mRNA
8632	21171	34088	2.08	2.0E-51	BE901994.1	EST_HUMAN	801676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8632	21171	34089	2.06	2.0E-51	BE901994.1	EST_HUMAN	801676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8984	21502	34424	0.95	2.0E-51	11037084	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9431	21657	34905	1.48	2.0E-51	AI917078.1	EST_HUMAN	h74407.x1 NCL CGAP_QC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;
9521	22021	34878	5.22	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9337	22037	34897	0.61	2.0E-51	AB007826.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10326	22823	35819	1.73	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
10368	22862	35856	1.03	2.0E-51	AA378559.1	EST_HUMAN	EST01206 Synovial sarcoma Homo sapiens cDNA 5' end
11207	18259	30730	11.47	2.0E-51	AI732851.1	EST_HUMAN	cb34f09.x8 NCI_CGAP_K15 Homo sapiens cDNA clone IMAGE:132609 3' similar to SW:NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11207	18259	30731	11.47	2.0E-51	AI732851.1	EST_HUMAN	cb34f09.x8 NCI_CGAP_K15 Homo sapiens cDNA clone IMAGE:132609 3' similar to SW:NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12343	24824	30824	2.8	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) homologue; translocated to, 4 (MLLT4), mRNA
119	12780	25272	27.93	1.0E-51	4503828	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1541	14133	28631	28.47	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCG12 5'
4498	17082	28631	1	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4498	17082	28632	1	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5588	18219	30669	2.88	1.0E-51	T18962.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b120561
7646	20167	33044	0.85	1.0E-51	AI572532.1	EST_HUMAN	bc9g02.x1 Scores_NHMPU_ST Homo sapiens cDNA clone IMAGE:2089108 3'
7844	20386	33289	7	1.0E-51	BF434386.1	EST_HUMAN	7c8b602.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3844091 3' similar to TR:P87892 P87892 PROTEASE ;
11813	25129		3.01	1.0E-51	AV760580.1	EST_HUMAN	AV760580 MDS Homo sapiens cDNA clone MDSCB802 5'
10668	23104	36118	1.71	9.0E-52	R91638.1	EST_HUMAN	yq10h04.r1 Scores fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:198587 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
10568	23104	36118	1.71	9.0E-52	R91638.1	EST_HUMAN	yq10h04.r1 Scores fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:198587 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
12105	24367		6.53	9.0E-52	AA777821.1	EST_HUMAN	z05g07.s1 Scores_fetal_liver_spleen TNFSL_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element ;
163	12828	25313	8	8.0E-52	AA720574.1	EST_HUMAN	mw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element ;
1543	14135	26669	1.32	8.0E-52	X94900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain
1694	14286	26821	2.12	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1894	14286	26822	2.12	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4086	14286	26821	6.96	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4086	14286	26822	6.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7526	20046	32815	1.8	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7526	20046	32816	1.8	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8943	21481	34403	1.39	7.0E-52	W58471.1	EST_HUMAN	z559a06.t1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1228	13828		0.85	6.0E-52	BE072408.1	EST_HUMAN	QV3-BT0337-271299-049-407 BT0337 Homo sapiens cDNA
1732	14323	26865	2.63	6.0E-52	AF108607.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5902	18524	31249	2.12	6.0E-52	AJ208794.1	EST_HUMAN	qg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11098	23598	36635	1.83	6.0E-52	BE048172.1	EST_HUMAN	tz48h04.y1 NCI_CGAP_Bm92 Homo sapiens cDNA clone IMAGE:2281871 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
4535	17119	28566	1.77	5.0E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA18H7
1702	14295	26830	1.27	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1823	14412	26957	1.35	4.0E-52	4758943	NT	Homo sapiens nucleoprotein 155kD (NUP155) mRNA
4000	18588	28070	0.82	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4849	17427	26879	0.77	4.0E-52	A1766814.1	EST_HUMAN	w189b02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5490	18124	30531	1.2	4.0E-52	4508132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5490	18124	30532	1.2	4.0E-52	4508132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7882	20524	33430	1.63	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
8471	21011	33928	5.51	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
11933	24267		6.12	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12456	24589		13.66	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
12601	24687		1.57	4.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4198	16757		12.28	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
588	13218	25694	4.18	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
588	13218	25695	4.18	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1793	14383	26928	2.64	2.0E-52	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
2544	15108	27681	1.1	2.0E-52	BE207575.1	EST_HUMAN	b566b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE);
2764	15318		6.55	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5113	17695	30121	3.51	2.0E-52	AL131768.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5881	18503	31229	3.32	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231288-053-E12 CT0214 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	19105	31890	1.85	2.0E-52	11141863	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
6814	19405	32221	0.89	2.0E-52	AB026004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7022	19556	32381	0.88	2.0E-52	AF072148.1	EST_HUMAN	ce46d12.y5 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1608311 5'
8567	21126		10.89	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
8868	21405	34326	0.82	2.0E-52	AA778785.1	EST_HUMAN	z45g05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9400	21823		1.25	2.0E-52	4768769	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10024	22519	35514	5.62	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10024	22518	35515	5.62	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11083	23595	36630	6.08	2.0E-52	AB31482.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2 THR repetitive element;
11083	23595	36631	6.08	2.0E-52	AB31482.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2 THR repetitive element;
11094	23606	36646	3.85	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DOBAIE03 5'
11231	23762		1.87	2.0E-52	W70260.1	EST_HUMAN	z449g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11484	23933		3.4	2.0E-52	11417660	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
11741	25099	30500	14.03	2.0E-52	AW236287.1	EST_HUMAN	zn72e07.x1 NCI_CGAP_OML1 Homo sapiens cDNA clone IMAGE:2700038 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
12154	24398		3.83	2.0E-52	AB08885.1	EST_HUMAN	wf87d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE;
558	13189	25698	1.59	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1414	14007	26536	11.81	1.0E-52	4504026	NT	Homo sapiens glutamate-aminonia ligase (glutamine synthase) (GLUL) mRNA
2573	15136		1.75	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3086	16710	28181	1.65	1.0E-52	S61070.1	NT	pd=reverse transcriptase homolog (retroviral element) (human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt)
5536	18168	30582	4.64	1.0E-52	M28428.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6527	19127	31921	2.18	1.0E-52	U36904.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
7458	19881	32846	2.21	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8401	20941		1.24	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9116	21652	34593	0.61	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10469	22863		1.13	1.0E-52	AW020370.1	EST_HUMAN	df05g05.y1 Morton_Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10479	22873		0.78	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10846	23178	36181	10.04	1.0E-52	U48298.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
10716	23244		2.37	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3859	16487	28920	1.13	9.0E-53	4508084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
6188	17751	30182	0.91	9.0E-53	7661713	NT	Homo sapiens predicted osteoblast protein (OS3788), mRNA
11087	24267		3.79	7.0E-53	BF238485.1	EST_HUMAN	601804771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132783 5'
12432	24968		5.2	7.0E-53	A1421782.1	EST_HUMAN	84407.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2066077 3' similar to contains THR.11
4174	16765	29213	4.45	5.0E-53	4758643	NT	THR repetitive element;
5384	17924	30338	1	5.0E-53	AL163282.2	NT	Homo sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
12035	24324		1.58	5.0E-53	AW813563.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
53	12733	25200	1.15	4.0E-53	AL163285.2	NT	RC9-ST0197-151098-011-g10 ST0197 Homo sapiens cDNA
53	12733	25201	1.15	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4947	17522	26884	0.89	4.0E-53	7705414	NT	Homo sapiens chromosome 21 segment HS21C085
9337	21851		0.88	4.0E-53	A181037.1	EST_HUMAN	Homo sapiens hock1 protein (HOOK1), mRNA
9871	22170		0.71	4.0E-53	F13080.1	EST_HUMAN	508h04.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2278327 3'
11091	23803	36842	3.98	4.0E-53	BF128701.1	EST_HUMAN	HS31D041 normalized infant brain cDNA Homo sapiens cDNA clone c-31d04
11091	23803	36843	3.98	4.0E-53	BF128701.1	EST_HUMAN	601810889F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
							601810889F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (OLEC1, ORCTL3, ORCTL4 genes, complete cds)
2884	15242	27810	2.08	3.0E-53	AB028888.1	NT	
3794	16394	28859	1.19	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2568798 3'
4691	17273	29721	0.85	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
5818	18247	30888	0.89	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5908	18433	31154	0.91	3.0E-53	11526297	NT	Homo sapiens MLL1 protein (MLL1), mRNA
6341	18947	31724	0.89	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7155	19687	32530	0.82	3.0E-53	Y10388.3	NT	H. sapiens graf gene
7155	19687	32531	0.82	3.0E-53	Y10388.3	NT	H. sapiens graf gene
8248	20787	33708	10.03	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
8793	21332	34259	0.51	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8987	21525		7.06	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
11887	24221		1.27	3.0E-53	11428423	NT	Homo sapiens acyl-Coenzyme A carboxylase alpha (ACACA), mRNA
483	13116		32.98	2.0E-53	AA368558.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2385	14936	27508	5.15	2.0E-53	U78027.1	NT	Homo sapiens Brn-1 tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2574	15137		12.23	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA

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2752	15307	27871	0.9	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2752	15307	27872	0.9	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3255	15887	28347	0.85	2.0E-53	7705887	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3282	15893	28372	0.87	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4133	18725	28178	2.15	2.0E-53	M81873.1	NT	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
5819	18248	30889	3.27	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
6819	18248	30700	3.27	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
7812	20355	33263	0.84	2.0E-53	AW875596.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
7949	20491		0.83	2.0E-53	AA095632.1	EST_HUMAN	IS428.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 6'
8328	21843		17.91	2.0E-53	AW245678.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1495	14087	26827	1.88	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3458	18083	28538	1.4	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4220	18908	28256	0.67	1.0E-53	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWFO9 5'
5059	17671	30110	1.08	1.0E-53	BE286386.1	EST_HUMAN	601176726F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3331919 5'
6764	19385	32201	1.34	1.0E-53	BF334201.1	EST_HUMAN	GM4-NN1028-150800-543-e02 NN1028 Homo sapiens cDNA
7295	19823	32682	0.93	1.0E-53	BE012071.1	EST_HUMAN	RCS-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
7878	20418	33326	0.5	1.0E-53	AA248072.1	EST_HUMAN	19571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8018	21555	34483	15.04	1.0E-53	X78538.1	NT	H. sapiens mRNA for hnRNP core protein A1
3290	15901	28391	0.57	9.0E-54	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5505	24743	30549	5.34	9.0E-54	4506788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
221	12882	25387	3.54	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814031 5'
1876	14481	27018	1.82	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4841	17419	28871	0.6	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4841	17419	28872	0.6	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
6082	18708	31456	20.41	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
407	13082	25574	1.55	7.0E-54	AA812537.1	EST_HUMAN	af76c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377048 3' similar to contains MER30.13 MER30 repetitive element ;
1870	14458	27013	2.37	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2248	14820	27395	5.06	7.0E-54	N27177.1	EST_HUMAN	yw68412.s1 Soares_placenta_86weeks_2NBHP684W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element ;
4694	17276		23.4	7.0E-54	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10034	22529	35524	2.32	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA qb87g03.x1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.H1 OFR repetitive element:
11171	23678		7.41	7.0E-54	AI160189.1	EST_HUMAN	
28	12705	25163	2.31	6.0E-54	AB003818.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
408	13083	25575	1.14	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
408	13083	25576	1.14	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
1917	14502	27058	1.44	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
1917	14502	27059	1.44	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3322	15832	28409	1.08	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4078	16872	28133	35.08	6.0E-54	4502872	NT	Homo sapiens chloride channel 8 (CLCN8) mRNA
4561	17144	28591	0.88	6.0E-54	AV754748.1	EST_HUMAN	AV754748 TP Homo sapiens cDNA clone TPGAAC10 5'
4889	17543	28985	1.07	6.0E-54	4505808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5001	17574		1.81	6.0E-54	Y09846.1	NT	H. sapiens aho pseudogene, p88 isoform
6140	17574		2.28	6.0E-54	Y09846.1	NT	H. sapiens aho pseudogene, p88 isoform
11329	23027	38036	3.33	6.0E-54	AW813667.1	EST_HUMAN	RC3-ST0197-151099-011-108 ST0197 Homo sapiens cDNA
2195	14771	27345	2.41	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
195	12855		111.77	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
							EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
991	13803	28117	69.58	4.0E-54	AA308784.1	EST_HUMAN	Human mRNA for KIAA0077 gene, partial cds
1841	14429	28981	2.97	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1841	14429	28982	2.97	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
							w228411.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:002711 O02711 PRO-POL-DUTPASE POLYPROTEIN:
3238	15850		1.45	4.0E-54	AI935086.1	EST_HUMAN	
97	12773	25255	9.57	3.0E-54	AA313487.1	EST_HUMAN	EST165371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2804	15168	27733	0.97	3.0E-54	AL110383.1	EST_HUMAN	DKFZp434E0731_r1_434 (synonym: hhas3) Homo sapiens cDNA clone DKFZp434E0731 5'
6063	18890	31422	1.44	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7422	18848	32811	1.54	3.0E-54	AA844081.1	EST_HUMAN	AI92c08.s1 Scores_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7422	18848	32812	1.54	3.0E-54	AA844081.1	EST_HUMAN	AI92c08.s1 Scores_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
10884	23478	36504	4.52	3.0E-54	BF345660.1	EST_HUMAN	602019408F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4155121 5'
							z70112.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G181315 G181315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.:
11247	23777	36834	4.44	3.0E-54	AA363382.1	EST_HUMAN	EST166628 MAGC resequences, MAGC Homo sapiens cDNA
11844	24208	31040	2.75	3.0E-54	AW954559.1	EST_HUMAN	
11885	25059		4.05	3.0E-54	AW748965.1	EST_HUMAN	RC1-BT0313-131188-011-509 BT0313 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
670	13294	25774	29.57	2.0E-54	5031800	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1409	14002	28530	1.59	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
1595	14188	28719	1.03	2.0E-54	AA655008.1	EST_HUMAN	nt78609.at NCL_CGAP_P3 Homo sapiens cDNA clone IMAGE:1204800 similar to contains element L1 repetitive element:
2577	15139	27709	0.88	2.0E-54	AW163175.1	EST_HUMAN	au2203.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW_CUL1_HUMAN Q13816 CULLIN HOMOLOG 1:
2835	15195	27768	1.29	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2920	15537	28012	1.28	2.0E-54	AW067524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING:
3602	16208		5.09	2.0E-54	AA532825.1	EST_HUMAN	nt45009.at NCL_CGAP_P8 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X63777.60S RIBOSOMAL PROTEIN L23 (HUMAN):
3915	16513	28975	0.82	2.0E-54	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
3915	16513	28976	0.82	2.0E-54	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4283	16969		2.42	2.0E-54	4502842	NT	Homo sapiens chaperonin containing T-complex subunit 8 (CT8), mRNA
4536	17120		1.11	2.0E-54	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4541	17125		3.09	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5698	18293	30773	2.15	2.0E-54	4769089	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5788	18413	31130	0.98	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281348 5'
5935	18556	31284	3.88	2.0E-54	11426857	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6022	18841	31381	11.85	2.0E-54	AB048811.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
6022	18841	31382	11.65	2.0E-54	AB048811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6763	19356	32165	0.88	2.0E-54	AF008916.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
7177	19709	32557	8.13	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9547	22047	35008	3.27	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain natriuretic receptor, complete cds
9922	22418	35392	1.45	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10028	22523	35519	0.88	2.0E-54	11416782	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10028	22523	35520	0.88	2.0E-54	11416782	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
11573	24020		3.33	2.0E-54	7657454	NT	Homo sapiens pescadillo (zabrafish) homolog 1, containing BRCT domain (PEST), mRNA
12368	24539	30903	2.87	2.0E-54	8967387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4584	17147		1.23	1.0E-54	BF315418.1	EST_HUMAN	601899230.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8684	21203	34121	0.64	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (Nf-kappaB), mRNA
10162	22847	35640	0.56	1.0E-54	AA412409.1	EST_HUMAN	zu10a09.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731484 5'

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10152	22647	35641	0.50	1.0E-54	AA412408.1	EST_HUMAN	zu10608.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
12547	24652		3.58	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 and
10262	22757	35744	0.81	8.0E-55	BE081489.1	EST_HUMAN	QV2-BT0836-160400-143-h12 BT0836 Homo sapiens cDNA
1359	13953		0.91	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1362	13956		2.21	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11075	23587		2.49	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660907 5'
1120	13723	26236	1.55	7.0E-55	R09346.1	EST_HUMAN	yf26a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127898 5' similar to SP:C581_BOVIN P10897 CYTOCHROME:
8738	21278		1.75	7.0E-55	AW103839.1	EST_HUMAN	xd76a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603522 3' similar to TR:O60365
9709	21645	34585	1.34	7.0E-55	AA89591.1	EST_HUMAN	O60365 FOS38554_1:
9142	21677	34620	1.88	7.0E-55	AU139909.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
11087	23599	36636	14.07	7.0E-55	AI561056.1	EST_HUMAN	AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 6'
11087	23599	36637	14.07	7.0E-55	AI561058.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12516	24985		9.8	7.0E-55	H261396.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11389	23841	36906	2.37	6.0E-55	AB040934.1	NT	ym67g07.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
1808	14396	26940	1.13	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
1808	14396	26941	1.13	6.0E-55	AA704971.1	EST_HUMAN	zif5b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6661	19257	32060	1.98	5.0E-55	4502240	NT	zif5b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6661	19257	32061	1.88	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6772	24769	32174	2.24	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
8772	24769	32175	2.24	5.0E-55	4505952	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7337	19864	32728	0.79	5.0E-55	11434422	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7938	20478	33388	0.65	5.0E-55	11526491	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
8974	21512	34435	2.35	5.0E-55	4506302	NT	Homo sapiens BCL2-associated athanogene (BAG1), mRNA
9243	21769		1.89	5.0E-55	BE084386.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
8960	22445	35426	1.55	5.0E-55	AB014511.1	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
8950	22446	35428	1.55	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10122	22617	35608	0.93	5.0E-55	5463765	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
11926	24260		2.15	5.0E-55	11417972	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
59	15408	25209	1.87	4.0E-55	AW957994.1	EST_HUMAN	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
700	13322	25809	41.63	4.0E-55	4826973	NT	EST370064 MAGE reassortances, MAGE Homo sapiens cDNA
1489	14082	26821	1.12	4.0E-55		NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
						NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14082	26822	1.12	4.0E-55	7891713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1681	14153		1.02	4.0E-55	BF081411.1	EST_HUMAN	7152b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element:
2071	14651	27222	1.47	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2071	14651	27223	1.47	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2132	14710	27281	8.27	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2132	14710	27282	8.27	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2349	14920	27485	1.84	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
3318	16928	28405	1.01	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8285	20828		7.61	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11108	23618		4.93	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11845	24207		1.88	4.0E-55	BF303941.1	EST_HUMAN	60188575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6710	18304	32108	0.83	3.0E-55	AA077156.1	EST_HUMAN	7809A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7809A09
10224	22719	35709	0.48	3.0E-55	AF005273.1	NT	Sus scrofa domestica submediary apomucin mRNA, complete cds
11760	24167		6.76	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
12563	24663		1.93	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
400	13044	25535	2.16	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
577	13207		2.15	2.0E-55	M10878.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
677	13301	25783	3.11	2.0E-55	4507288	NT	Homo sapiens syntactin-binding protein 1 (STXBP1) mRNA, and translated products
2986	15802	28082	0.93	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4888	17483	28917	2.37	2.0E-55	BE19988.1	EST_HUMAN	CM1-HT0878-150800-357-g03 HT0878 Homo sapiens cDNA
7515	24785	32802	0.67	2.0E-55	AW501988.1	EST_HUMAN	U1-HF-BN0-ake-f-06-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
8995	21533	34462	0.46	2.0E-55	BF224492.1	EST_HUMAN	hr78h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
8995	21533	34463	0.46	2.0E-55	BF224492.1	EST_HUMAN	hr78h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9037	21623		3.77	2.0E-55	A1002838.1	EST_HUMAN	am88h06.g1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to cortals
9185	21700		0.7	2.0E-55	BE007959.1	EST_HUMAN	THR.b2 THR repetitive element
10144	22639	35626	0.47	2.0E-55	AI439401.1	EST_HUMAN	QV0-BN0147-280400-213-g08 BN0147 Homo sapiens cDNA
10828	23349	36365	2.22	2.0E-55	AU110344.1	EST_HUMAN	q03h08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140479 3'
100	12778	25258	1.25	1.0E-55	4505080	NT	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
203	12884	25348	84.41	1.0E-55	U09823.1	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
600	13228	25702	0.86	1.0E-55	A1026718.1	EST_HUMAN	Oryzobolus curvicaulis New Zealand white elongation factor 1 alpha (Rabefia2) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1189	13780	28301	6.18	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1983	14575	27134	1.21	1.0E-58	BE277881.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
1993	14576	27135	1.21	1.0E-55	BE277881.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
2363	14834		2.58	1.0E-56	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2378	15389	27519	1.04	1.0E-56	AF000880.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2558	15122	27681	10.31	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2690	15152	27718	4.82	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2690	15152	27719	4.82	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2642	15201	27774	1.88	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
4061	16658	29120	4.09	1.0E-55	AL183267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4382	16668	29417	1.24	1.0E-55	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4837	17415		1.17	1.0E-55	N77261.1	EST_HUMAN	yy44g03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245820 5'
4954	17528	28970	1.81	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4954	17628	28971	1.81	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5311	17673	30285	1.03	1.0E-55	8923125	NT	Homo sapiens hypochloral protein FLJ20128 (FLJ20128), mRNA
5889	18315	30814	8.13	1.0E-55	AF118858.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6417	19020	31804	7.22	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6417	19020	31805	7.22	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7830	20472	33381	2.11	1.0E-55	11432884	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chaplyn-110) (DLG2), mRNA
7930	20472	33382	2.11	1.0E-55	11432884	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chaplyn-110) (DLG2), mRNA
8028	20568	33471	0.97	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8028	20568	33472	0.97	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
10791	23314	36322	4.95	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
10791	23314	36323	4.95	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11322	23020	36028	2.23	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11342	23040	36049	1.88	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA CofB-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F181 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
11448	23898	36984	1.81	1.0E-55	10587821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
7401	19828	32791	1.97	9.0E-58	BE379074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809552 5'
2761	15316	27882	3.95	7.0E-58	H18934.1	EST_HUMAN	yn82g03.r1 Soares adult brain N2b5bB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;
7636	20148	33031	2.11	7.0E-58	AW361213.1	EST_HUMAN	RC1-CT0252-231098-013-b07 CT0252 Homo sapiens cDNA
7636	20148	33032	2.11	7.0E-58	AW361213.1	EST_HUMAN	RC1-CT0252-231098-013-b07 CT0252 Homo sapiens cDNA
1730	14321	26863	1.59	5.0E-58	AW69712.1	EST_HUMAN	RC3-BN0053-170200-011-p01 BN0053 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9088	21624	34559	0.8	5.0E-56	AW015507.1	EST_HUMAN	U1H-B10p-eau-e-05-0-U1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10289	22784		1.35	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12020	25048	30509	3.74	6.0E-56	H59089.1	EST_HUMAN	CHR220308 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
30	12709	25168	22.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	12709	25167	22.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2733	15288	27855	7.6	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2733	15288	27856	7.6	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2838	13183	25681	3.4	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8405	19008	31789	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
8408	19008	31760	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10400	22894	35889	1.2	4.0E-56	AF043348.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
10803	23326	36335	8.31	4.0E-56	AI98086.1	EST_HUMAN	hm5g12.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2163048 3'
10803	23326	36336	8.31	4.0E-56	AI98086.1	EST_HUMAN	hm5g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
1366	13980	26507	2.12	3.0E-56	8924028	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1801	14391	26938	4.33	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3159	16773	28240	1.89	3.0E-56	AA325826.1	EST_HUMAN	EST128889 Cerabellum II Homo sapiens cDNA 5' end
3159	16773	28241	1.89	3.0E-56	AA325826.1	EST_HUMAN	EST128889 Cerabellum II Homo sapiens cDNA 5' end
3903	16502		2.38	3.0E-56	AF055086.1	NT	Homo sapiens MHC class 1 region
3981	16889	28081	0.9	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4477	17082	29512	0.82	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4515	17089	29546	5.15	3.0E-56	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4673	17255	29707	2.57	3.0E-56	5902085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
4925	17600		1.14	3.0E-56	BE863572.1	EST_HUMAN	601438154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'
5280	17842	30269	0.6	3.0E-56	6912583	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5346	17842	30269	0.59	3.0E-56	6912583	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5863	18485	31208	1.4	3.0E-56	4759183	NT	Homo sapiens sparc/osteonectin, cwev and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5863	18485	31209	1.4	3.0E-56	4759183	NT	Homo sapiens sparc/osteonectin, cwev and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6956	19533	32358	6.22	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
8750	21289	34209	5.2	3.0E-56	11416704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9727	22226	35202	0.86	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10375	22869	35862	1.63	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11194	23689	36749	6.31	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11194	23689	36750	6.31	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11883	24230	31002	1.3	3.0E-56	11434878	NT	Homo sapiens caveolin 3 (CAV3), mRNA
11883	24230	31003	1.3	3.0E-56	11434878	NT	Homo sapiens caveolin 3 (CAV3), mRNA
550	13161		2.35	2.0E-56	AA196816.1	EST_HUMAN	z652a08.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645208 3'
762	15424	25878	1.37	2.0E-56	BE084396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
762	15424	25879	1.37	2.0E-56	BE084396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2426	14994	27567	1.32	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPRA) mRNA, complete cds
2426	14994	27568	1.32	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPRA) mRNA, complete cds
3017	15633	28110	1.33	2.0E-56	AB037836.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3368	15968		1.2	2.0E-56	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3368	16190	28674	1.34	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
7147	19680	32621	1.9	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1016	13628		12.77	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3737	16338	28603	1.67	1.0E-56	AW598933.1	EST_HUMAN	hg23c11.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946452 3'
3737	16338	28604	1.67	1.0E-56	AW598933.1	EST_HUMAN	hg23c11.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946452 3'
9866	22363		0.71	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9861	22456	35439	1.57	1.0E-56	AW846987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
853	13278		1.74	9.0E-57	AW880885.1	EST_HUMAN	QV6-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
11099	23609	36849	1.92	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11099	23609	36850	1.92	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11397	23849	36915	2.01	8.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
15	12694	25150	0.98	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
319	12973	25462	2.71	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-161199-037-05 ST0234 Homo sapiens cDNA
917	13530	26048	8.64	8.0E-57	AW264599.1	EST_HUMAN	xt05d10.x1 NCL_CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05676
1832	14440	26997	1.52	8.0E-57	AA409109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3428	16036	28516	1	8.0E-57	4756279	NT	z51512.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
3428	16036	28517	1	8.0E-57	4756279	NT	Homo sapiens EphA4 (EPHA4) mRNA
5187	17752	30183	0.8	8.0E-57	BE269916.1	EST_HUMAN	Homo sapiens EphA4 (EPHA4) mRNA
5450	24958	30631	3.17	8.0E-57	11416185	NT	800944440F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960864 5'
8500	19187	31089	12.5	8.0E-57	AB023177.1	NT	Homo sapiens acetylase 2, mitochondrial (AC02), mRNA
8590	19187	31980	12.6	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7726	20237	33128	2.72	8.0E-57	AB026644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds

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7728	20237	33128	2.72	8.0E-67	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11351	12684	25150	3.59	8.0E-67	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12271	24477	30936	1.41	8.0E-67	11845732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1261	13858	26375	1.16	7.0E-67	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
3287	15898	28376	1.08	7.0E-67	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3287	15898	28377	1.08	7.0E-67	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3308	15920	28397	1	7.0E-67	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3948	16544	29011	2.3	7.0E-67	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3948	16544	29012	2.3	7.0E-67	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
4524	17108		1.06	7.0E-67	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 6
12634	24982		5.12	5.0E-67	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
3817	16417	28880	1.68	4.0E-67	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
837	13453	25983	1.03	3.0E-67	4607768	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1378	13689		39.52	3.0E-67	AA230279.1	EST_HUMAN	nc1367.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2434	16001	27573	1.01	3.0E-67	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10 ;
2727	15282	27849	0.93	3.0E-67	BE676822.1	EST_HUMAN	EST64770 Hippocampus II Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H8C.2
2727	15282	27850	0.93	3.0E-67	BE676822.1	EST_HUMAN	733b10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H8C.2
3618	16221	28898	0.93	3.0E-67	AF232705.1	NT	CE20263 ;
3760	16381		60.31	3.0E-67	AW853864.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein [(Ch) gene, complete cds
6180	18790	31559	1.34	3.0E-67	11226608	NT	RG3-CT0254-110300-027-410 CT0254 Homo sapiens cDNA
6272	18880	31648	3.17	3.0E-67	BE786537.1	EST_HUMAN	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
8087	20828	33542	3.09	3.0E-67	W28130.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8111	20682	33580	2.27	3.0E-67	11645798	NT	4268 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8111	20682	33581	2.27	3.0E-67	11645798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8223	20764	33681	0.61	3.0E-67	11427757	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8368	20808	33827	1.18	3.0E-67	J05282.1	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
8792	21331	34255	4.05	3.0E-67	AU117659.1	EST_HUMAN	Human farnesyl pyrophosphate synthetase mRNA, complete cds
9174	21751	34688	0.63	3.0E-67	11545798	NT	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
							Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9174	21751	34697	0.63	3.0E-57	11845788	NT	Homo sapiens hypothetical protein FLJ11858 (FLJ11858), mRNA
10787	23311	36318	3.02	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
11800	25068	30513	7.99	3.0E-57	W23871.1	EST_HUMAN	zb45d11.1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12272	24892		1.69	3.0E-57	AW178576.1	EST_HUMAN	RCO-HT0112-080989-001-C08 HT0112 Homo sapiens cDNA hm25c10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157618 3' similar to contains Alu repetitive element;
1480	14073	26612	0.88	2.0E-57	AJ478904.1	EST_HUMAN	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1548	14140	26873	0.88	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1548	14140	26874	0.88	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2444	15011	27583	1.15	2.0E-57	BE172528.1	EST_HUMAN	MRQ-HT0559-010400-008-h10 HT0559 Homo sapiens cDNA
2766	15311	27877	4.79	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.e1 Scores_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3486	16091		2.28	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3605	16209	28688	0.71	2.0E-57	R07702.1	EST_HUMAN	y68h01.1 Scores_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3605	16209	28689	0.71	2.0E-57	R07702.1	EST_HUMAN	y68h01.1 Scores_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4004	16602	28076	0.62	2.0E-57	BE073284.1	EST_HUMAN	MRQ-BT0351-060300-103-b03 BT0351 Homo sapiens cDNA
4608	17191	28637	8.02	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5849	18473		1.57	2.0E-57	AA018131.1	EST_HUMAN	zs31c05.1 Scores_retina_N2b-4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
6184	18794		29.73	2.0E-57	BF115268.1	EST_HUMAN	7n80f04.x1 NCL_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3570968 3' similar to contains TAR1.1f1 MER22 repetitive element;
6307	18914	31688	0.73	2.0E-57	11431281	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
8586	21105	34024	1.22	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p84 mRNA, complete cds
9760	22268	35241	2.66	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11150	23658	36701	2.05	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11150	23658	36702	2.05	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11192	23697	36746	1.84	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
11192	23697	36747	1.84	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
8826	21165		3.5	1.0E-57	BE043031.1	EST_HUMAN	hc32a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3038062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN;
12049	24333		6.35	1.0E-57	AW470791.1	EST_HUMAN	h333408.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
5857	18480	31203	1.02	9.0E-58	AA287847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12395	24518	30822	2.62	9.0E-58	BE396081.1	EST_HUMAN	601309465f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
615	13242		3.87	8.0E-58	BE688715.1	EST_HUMAN	601445948f1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'

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682	13308	26789	3.77	8.0E-58	AF798378.1	EST_HUMAN	t34b07.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O16475 O16476 UNNAMED HERV-H PROTEIN;
682	13308	26790	3.77	8.0E-58	AF798378.1	EST_HUMAN	t34b07.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O16475 O16476 UNNAMED HERV-H PROTEIN;
1897	14482	27041	2.82	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1897	14482	27042	2.82	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
3003	15619		2.94	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC61304), mRNA
10735	23260		6.42	7.0E-58	5174642	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
10809	23332	36344	3.77	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-ail-g-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078887 5'
10809	23332	36345	3.77	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-ail-g-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078887 5'
2414	14982	27668	3.39	6.0E-58	AF130889.1	EST_HUMAN	AU130889 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2928	15542	28017	1.26	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylar-HGSC project-TCAA Homo sapiens cDNA clone TCAAP1219
2928	15542	28018	1.26	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylar-HGSC project-TCAA Homo sapiens cDNA clone TCAAP1219
6318	18925	31702	1.15	6.0E-58	AF108911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10211	22708	36700	0.99	6.0E-58	11434748	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12150	24393		1.87	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
322	12978	25484	3.26	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
739	13359	25853	5.81	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160900-016-605 NT0057 Homo sapiens cDNA
1236	13835	26350	3.59	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-407 UM0043 Homo sapiens cDNA
1236	13835	26351	3.59	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-407 UM0043 Homo sapiens cDNA
1237	13836	26350	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-407 UM0043 Homo sapiens cDNA
1237	13835	26351	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-407 UM0043 Homo sapiens cDNA
3365	15973	28490	4.17	5.0E-58	AA988183.1	EST_HUMAN	cr89e07.x1 NCI CGAP_LU5 Homo sapiens cDNA clone IMAGE:1603908 3'
4345	16932	29373	0.78	5.0E-58	AF636745.1	EST_HUMAN	ts89e07.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2238488 3' similar to SW:PRO2_ACACA
5105	17677		1.12	5.0E-58	AW848834.1	EST_HUMAN	P18884 PROFILIN II;
5811	18435		2.08	5.0E-58	11466282	NT	IL3-CT0214-090300-081-F08 CT0214 Homo sapiens cDNA
6326	18931	31707	5.73	5.0E-58	H23072.1	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6326	18128	31922	0.87	5.0E-58	AL163285.2	NT	ym51h07.r1 Scars Infant brain INIB Homo sapiens cDNA clone IMAGE:52071 5'
8597	19194	31999	1.24	5.0E-58	11421330	NT	Homo sapiens chromosome 21 segment HS21C085
7181	18693	32639	0.72	5.0E-58	4885400	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
							Homo sapiens haemoglobin c synthase (cytochrome c heme-lyase) (HCCS) mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7810	20452	33359	9.87	5.0E-58	8922893	NT	Homo sapiens hypothetical protein FLJ10828 (FLJ10828), mRNA
8294	20835	33787	0.74	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1817 protein, partial cds
9263	21789	34739	0.72	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
9263	21789	34740	0.72	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
9771	22268	35253	0.74	5.0E-58	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10030	22825	35521	1.39	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10300	22794	35784	0.59	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10300	22794	35785	0.59	6.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
11859	24887		6.17	5.0E-58	11528283	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12331	25016		1.81	5.0E-58	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
12577	24873		1.34	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12653	24726	30853	1.37	5.0E-58	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12653	24726	30854	1.37	5.0E-58	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
396	13042	25532	5.55	4.0E-58	4602302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA
828	13448	25953	1.76	4.0E-58	4504834	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
1517	14109	26845	1.88	4.0E-58	4503848	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9), mRNA
2811	15173	27741	1.13	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2690	15219	27790	1.75	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3387	15975	28452	1.62	4.0E-58	D16470.1	NT	Human mRNA, Xa terminal portion
3803	16403	28887	1.26	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11221	23724	36779	9.32	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
357	13008		1.77	3.0E-58	R17879.1	EST_HUMAN	hg10cd2.1 Sources Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
1433	14026	26554	2.23	3.0E-58	4756881	NT	Homo sapiens peptide YY (PYY) mRNA
3059	15675		0.73	3.0E-58	R17879.1	EST_HUMAN	hg10cd2.1 Sources Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
3212	15824	28300	3.1	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
3212	15824	28301	3.1	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
6407	19010	31782	0.72	3.0E-58	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-f08 BT0702 Homo sapiens cDNA
6572	19170	31667	0.98	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-1tg08
6751	19344	32151	1.25	3.0E-58	AV172977.1	EST_HUMAN	AV172977 DCA Homo sapiens cDNA clone DCAZG04 5'
978	13588	26103	8.92	2.0E-58	AF069824.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1333	13927		30.8	2.0E-58	BE208532.1	EST_HUMAN	ba0807.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X68391.60S RIBOSOMAL PROTEIN L8 (HUMAN); gb:X81987.M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5539	18171	30588	0.75	2.0E-58	AW074831.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2587704 3'
5560	24746	30607	4.01	2.0E-58	BE907186.1	EST_HUMAN	601499881F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5560	24745	30637	4.01	2.0E-58	BE907186.1	EST_HUMAN	601499881F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6207	18817	31588	1.26	2.0E-58	BF513488.1	EST_HUMAN	U1H-BW1-ema-g-11-q-U1.g1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
							am57a02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639874 3' similar to WP:ZK328.1 CE05085 UBIQUITIN CONJUGATING ENZYME\ RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN ;
6270	18878	31646	2.1	2.0E-58	A124874.1	EST_HUMAN	YQ08h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186378 5'
6302	18909	31681	0.88	2.0E-58	R02587.1	EST_HUMAN	gm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7008	18504	32323	1	2.0E-58	A1261407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7210	19741	32594	2.91	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7210	19741	32595	2.91	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10620	23152	36164	19.73	2.0E-58	BF307745.1	EST_HUMAN	601880812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131881 5'
10844	23365	36361	2.67	2.0E-58	AW872841.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
751	13371	25865	4.83	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1106	13710	26219	5.81	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22KD, 822) (NDUFB9), mRNA
1372	13986	26492	1.24	1.0E-58	AW957182.1	EST_HUMAN	EST368252 MAGe resequences, MAGD Homo sapiens cDNA
1372	13986	26493	1.24	1.0E-58	AW957182.1	EST_HUMAN	EST368252 MAGe resequences, MAGD Homo sapiens cDNA
1440	14033	26561	2.04	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1704	14297	26834	0.9	1.0E-58	BE468132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3168805 3'
2828	15380	27950	1.17	1.0E-58	4759189	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
3590	16194	28879	0.62	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3590	16194	28880	0.62	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3783	16383	28848	0.57	1.0E-58	4507628	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
5109	17878	30117	6.64	1.0E-58	A1141083.1	EST_HUMAN	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
6007	18827	31382	1.2	1.0E-58	BE081880.1	EST_HUMAN	aa43h01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678128 3'
6846	18523	32345	0.73	1.0E-58	11422031	NT	RC1-BT0254-290100-076-e01 BT0254 Homo sapiens cDNA
8803	21342	34268	0.7	1.0E-58	4606314	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8912	21450	34371	0.83	1.0E-58	AV751001.1	EST_HUMAN	Homo sapiens myosin (M-protein) 2 (165KD) (MYOM2), mRNA
8910	21547	34475	0.65	1.0E-58	AA412397.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09.6
9010	21547	34476	0.65	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
			0.85	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10089	22584	35577	0.55	1.0E-58	11432884	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chaparrin-110) (DLG2), mRNA
11610	24053		5.43	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2273	14947	27423	16.05	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
8121	20652	33572	2.08	8.0E-59	A1761963.1	EST_HUMAN	wh50d08.x1 NCJ CGAP_K1411 Homo sapiens cDNA clone IMAGE:2384171 3'
190	15409		2.18	6.0E-59	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3682088 5'
8188	20728	33641	0.59	6.0E-59	A1750970.1	EST_HUMAN	cn08h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn08h02 random
1790	14380	26924	1.32	5.0E-59	AW157281.1	EST_HUMAN	au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:075788 075788 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1780	14380	26925	1.32	5.0E-59	AW157281.1	EST_HUMAN	au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:075788 075788 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3181	15775	28243	7.81	5.0E-59	A1807484.1	EST_HUMAN	wt48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4782	17343	28781	4.42	5.0E-59	X83497.1	NT	H. sapiens DNA for ZNF60-linked ERV9 long terminal repeat
5888	18508	31235	0.81	5.0E-59	6005698	NT	Homo sapiens etaxin 2 related protein (A2LP), mRNA
7084	18083	30440	8.32	5.0E-59	AW162304.1	EST_HUMAN	au88c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
8741	21280	34203	1.35	5.0E-59	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
9821	22121	35085	1.85	5.0E-59	AV782869.1	EST_HUMAN	AV782869 MDS Homo sapiens cDNA clone MDSEIC12 5'
10788	23310	36317	3.47	5.0E-59	11434008	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
826	13443	25851	2.85	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
5728	18354	31058	1.22	4.0E-59	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12004	24917		5.54	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	12889		4.75	3.0E-59	AW985524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
245	12804	26385	3.86	3.0E-59	7682247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1748	14338	26884	8.2	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1748	14338	26885	8.2	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2174	14751	27320	7.15	3.0E-59	AB029035.1	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2174	14751	27321	7.16	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2788	15477	27920	1.29	3.0E-59	AF232289.1	NT	Homo sapiens NF1-2 pseudogene, exon 17
3074	15688	28181	0.77	3.0E-59	T18895.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3074	15688	28182	0.77	3.0E-59	T18895.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3183	15777	28247	4.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	15777	28248	4.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3897	16498	28958	1.12	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2), mRNA
4798	17374	29828	0.98	3.0E-59	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4987	17541	29884	1.33	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
6369	18973	31751	2.1	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7395	19920	32785	1.87	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
7872	20414	33321	1.28	3.0E-59	X12956.1	NT	Human mRNA for dbl proto-oncogene
7872	20414	33322	1.26	3.0E-59	X12956.1	NT	Human mRNA for dbl proto-oncogene
9957	22452	35433	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
9957	22452	35434	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
11880	24291		1.26	3.0E-59	11417898	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12130	24388		9.09	3.0E-59	11417898	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6044	18663	31402	0.98	2.0E-59	BF508383.1	EST_HUMAN	UI-H-B14-acy-b-02-O-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
6044	18663	31403	0.98	2.0E-59	BF508383.1	EST_HUMAN	UI-H-B14-acy-b-02-O-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
9555	22055		5.27	2.0E-59	A3309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10419	22913		1.34	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT0038-100700-032-s07 NT0038 Homo sapiens cDNA
10710	23238	36252	2.49	2.0E-59	AW410698.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981654 5'
10710	23238	36253	2.49	2.0E-59	AW410698.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981654 5'
11879	24228	31046	5.78	2.0E-59	A1831809.1	EST_HUMAN	w838c12.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12437	24943	30821	2.86	2.0E-59	L11845.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ;
174	12837		18.31	1.0E-59	BE280411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2516	15080	27652	1.02	1.0E-59	A138341.1	EST_HUMAN	601178757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2516	15080	27653	1.02	1.0E-59	A138341.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:1710254 3'
2849	16208		1.45	1.0E-59	AA749468.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:1710254 3'
7563	20080	32856	1.98	1.0E-59	AJ130894.1	NT	oe56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309028 3' similar to TR:Q13537
7703	20212	33100	0.93	1.0E-59	BE256814.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7703	20212	33101	0.93	1.0E-59	BE256814.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
8307	21907	34855	1.2	1.0E-59	11419880	NT	Homo sapiens mRNA for transcription factor
8522	22022	34978	0.82	1.0E-59	11428848	NT	601111951F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352892 5'
9522	22022	34980	0.82	1.0E-59	11428849	NT	601111951F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3352892 5'
10734	20080	32956	9.52	1.0E-59	AJ130894.1	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
795	13413	25917	1.28	8.0E-60	AW977845.1	EST_HUMAN	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1520	14112	28648	3.21	8.0E-60	4759169	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2218	14791	27384	1.95	8.0E-60	5174856	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2218	14791	27385	1.95	8.0E-60	5174856	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6135	18749	31508	1.01	8.0E-60	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6828	19224	32029	1.85	8.0E-60	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
7684	20195	33083	0.78	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
7806	20448	33353	2.66	8.0E-60	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
8689	21408	34332	4.03	8.0E-60	11428949	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
8392	21815	34784	0.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8392	21815	34785	0.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10465	22959	35989	0.68	8.0E-60	645397	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10712	23240	36255	5.93	8.0E-60	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10712	23240	36256	5.93	8.0E-60	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
784	13403	25907	12.12	7.0E-60	AF050066.1	NT	Homo sapiens MHC class 1 region
785	13403	25907	52.6	7.0E-60	AF050066.1	NT	Homo sapiens MHC class 1 region
848	13484	25972	1.28	7.0E-60	4504834	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2173	14750	27319	1.95	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4258	18844	28283	2.74	7.0E-60	4505480	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
9328	21842	34794	3.6	7.0E-60	H59041.1	EST_HUMAN	y1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
11243	23773	36830	1.87	7.0E-60	H59041.1	EST_HUMAN	y1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
8378	20916		7.58	8.0E-60	H52458.1	EST_HUMAN	y178h09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201853 5' similar to contains OFR repetitive element ;
87	12763	25245	1.13	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
87	12763	25246	1.13	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
3000	15619		1.47	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7390	18915	32779	0.7	4.0E-60	BF196088.1	EST_HUMAN	tr8105.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
8034	21591		0.62	4.0E-60	AL163278.2	NT	Q81085 GTP-RHO BINDING PROTEIN 1 ;
1898	14484	27044	5.28	3.0E-60	BE862811.1	EST_HUMAN	Q81085 GTP-RHO BINDING PROTEIN 1 ;
1898	14484	27045	5.28	3.0E-60	BE862811.1	EST_HUMAN	Q81085 GTP-RHO BINDING PROTEIN 1 ;
1910	14495		2.4	3.0E-60	6031190	NT	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680395 5'
							601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680395 5'
							Homo sapiens prohibitin (PHB) mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4558	17139	28587	1.88	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8022	18448	31168	2.04	3.0E-60	AW836186.1	EST_HUMAN	RC3-L T0023-200100-012-401 LT0023 Homo sapiens cDNA
7034	18064	30477	1	3.0E-60	A1792814.1	EST_HUMAN	cl00111.y5 NCJ CGAP_K143 Homo sapiens cDNA clone IMAGE:1634053 5' similar to SW:UDP_MOUSE
8341	20882	33802	5.3	3.0E-60	5174844	NT	P52824 URIDINE PHOSPHORYLASE;
8341	20882	33803	5.3	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8519	21058	33881	0.51	3.0E-60	A1040235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8077	21218	34136	4.75	3.0E-60	5174844	NT	ox58d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q08860 FORMIN;
12620	24880		1.71	3.0E-60	AA485288.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
33	12712	25171	2.84	2.0E-60	AY008285.1	NT	ab07h04.r1 Sitragene lung (#837210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element;
1470	14082	26697	2.86	2.0E-60	Z11694.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1759	14348	26693	1.24	2.0E-60	M24803.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
3838	18241	28717	0.72	2.0E-60	4757867	NT	Human bcr protein mRNA, 5' end
3887	18585	28056	0.78	2.0E-60	AF231918.1	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4203	18782		0.95	2.0E-60	BF513458.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
8443	19045	31833	0.94	2.0E-60	A1761952.1	EST_HUMAN	UI-H-BW1-arms-s-05-Q-J1.s1 NCJ CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
8618	19215	32020	1.95	2.0E-60	AF004877.1	NT	nm01112.y5 NCJ CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.H THR repetitive element;
8818	19407	32224	0.88	2.0E-60	AF157478.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
8934	18042	30486	2.08	2.0E-60	4503044	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
8934	18042	30487	2.08	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7164	19898	32542	8.14	2.0E-60	AA311159.1	EST_HUMAN	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7628	20140	33389	1.05	2.0E-60	BF512808.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7947	20489	33389	1.05	2.0E-60	X85597.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
8801	21340	34287	3.38	2.0E-60	L36033.1	NT	UI-H-BW1-arms-s-02-Q-J1.s1 NCJ CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
9888	22385	35362	2.87	2.0E-60	11981859	NT	HS159EST human adult testis Homo sapiens cDNA clone CAM_EST15
9888	22385	35363	2.87	2.0E-60	11981859	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
12168	24407		3.88	2.0E-60	11418192	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
							Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
							Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12309	24908		1.71	2.0E-60	AF08757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12311	24903		1.88	2.0E-60	11418088	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC83504), mRNA
12329	24515		1.95	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
548	13179	25637	0.92	1.0E-60	BE178395.1	EST_HUMAN	PM3-HT0905-270200-001-e08 HT0905 Homo sapiens cDNA
3970	16968	28037	0.95	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
5091	17664	30104	1.32	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7869	20431	33340	0.73	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
8890	21229		2.63	1.0E-60	AA244041.1	EST_HUMAN	nc04612.1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007162 similar to contains L1.1 L1 repetitive element
8717	21266	34178	1.51	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1138	13741	28250	2.37	8.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2894	15251	27821	1.11	8.0E-61	AW008478.1	EST_HUMAN	W05b10.x1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2508555 3'
2894	15251	27822	1.11	8.0E-61	AW008478.1	EST_HUMAN	W05b10.x1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2508555 3'
2878	15594		2.53	8.0E-61	X97147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
7836	20378	33284	0.78	8.0E-61	AA583958.1	EST_HUMAN	nc58008.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
133	12798	25286	0.89	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
133	12798	25287	0.99	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
287	12943	25428	3.39	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
844	13480	25959	2.13	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1366	13960	26485	13.81	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1872	14284	26798	0.91	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1689	14281	26816	2.23	6.0E-61	AA598033.1	EST_HUMAN	nc68409.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2172	14749	27318	0.93	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3347	15957	28433	11.8	6.0E-61	AU130889.1	EST_HUMAN	AU130889 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5'
6182	18792	31581	3.08	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7380	19806	32771	1.71	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7814	20127	33004	1.95	6.0E-61	AF03737.1	NT	Homo sapiens general transcription factor 24 (GTF2I) mRNA, complete cds
12085	13480	25959	1.38	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
236	12898	25379	2.08	5.0E-61	8922890	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
236	12898	25380	2.08	5.0E-61	8922890	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
382	13028	25517	0.61	6.0E-61	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1718	14310	26849	2.36	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3071	15998	28158	1.9	5.0E-61	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4053	16650		1.91	5.0E-61	AJ226041.1	NT	Homo sapiens 656 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5144	13028	25517	0.69	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11858	24215		4.95	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801 5'
4292	16878	29325	0.98	3.0E-61	BE368279.1	EST_HUMAN	601309785F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3631220 5'
8360	20900	33821	0.63	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAQB04
8829	21188	34083	0.51	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
8629	21188	34084	0.61	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
524	13158	25638	1.29	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1254	13851	26368	1.98	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-001 HT0513 Homo sapiens cDNA
1254	13851	26369	1.98	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-001 HT0513 Homo sapiens cDNA
1705	14298	26835	1.22	2.0E-61	N53039.1	EST_HUMAN	w63d11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246453 3' similar to
2687	16225		1.54	2.0E-61	N39397.1	EST_HUMAN	gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
							w03f11.r1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:270189 5'
							Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein
6557	19155	31951	0.85	2.0E-61	11426168	NT	1A (110/118KD) (ATP6V1A), mRNA
8045	21483	34406	1.01	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG08 5'
9481	21890		1.55	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0638 protein, partial cds
9836	22334	35316	1.59	2.0E-61	AW500266.1	EST_HUMAN	UI-HF-BN0-ekd-r-12-0-U1.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076774 5'
10149	22844	35638	1.99	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC38), mRNA
10764	23288		0.83	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
480	13094		0.91	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
805	13422	25928	1.25	1.0E-61	5453828	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homologue) (ORC2L) mRNA
1443	14036	26565	0.98	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1896	14483	27043	3.87	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2238	14813	27385	1.55	1.0E-61	AW827281.1	EST_HUMAN	xn11b09.y1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element
3422	16030	28511	0.88	1.0E-61	7692319	NT	MSR1 repetitive element:
4534	17118	29584	1.48	1.0E-61	4759249	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4534	17118	29585	1.48	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4982	17568	29998	10.61	1.0E-61	AW298181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4982	17568	29999	10.61	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-qlb-b-08-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
5886	18490	31216	0.89	1.0E-61	7692303	NT	UI-H-BW0-qlb-b-08-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
6043	18682	31401	1.17	1.0E-61	11416891	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6981	19479	32300	8.17	1.0E-61	M30135.1	NT	Homo sapiens survival of motor neuron 1, isoformic (SMN1), mRNA
							Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7148	19681	32522	0.73	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRP128), mRNA
7242	19771	32627	1.54	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7242	19771	32628	1.54	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8075	20817	33531	6.29	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8255	20798	33713	3.19	1.0E-61	AF224693.1	NT	Homo sapiens mimosinase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8206	21723		2.29	1.0E-61	AW989728.1	EST_HUMAN	MRO-BN0070-040400-010-H01 BN0070 Homo sapiens cDNA
9279	21805	34756	1.1	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
9842	22437	35414	5.78	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10514	23092	36063	2.82	1.0E-61	11426578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11751	24066		1.58	1.0E-61	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
11793	24955	30629	3.23	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11793	24955	30630	3.23	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12173	24412	30845	1.61	1.0E-61	M20806.1	NT	Homo sapiens kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
12494	24622	30891	17.77	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10259	22754	35742	1.82	8.0E-62	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
4849	17231	29898	1.03	8.0E-62	AA830420.1	EST_HUMAN	cc68h11.a1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:1364725 3' similar to SW:POL_MLVRK
12652	24724		1.59	8.0E-62	AA788991.1	EST_HUMAN	P31795 POL POLYPROTEIN ;
1148	13749	26256	1.31	7.0E-62	AV714334.1	EST_HUMAN	nz75601.a1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:1301328 3'
3554	16166	28841	0.7	7.0E-62	P17480	SW/ISSPROT	AV714334 DGB Homo sapiens cDNA clone DCBAMA08 5'
6075	18992	31438	0.96	7.0E-62	11427965	NT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
11228	23760	36816	5.72	7.0E-62	AI208691.1	EST_HUMAN	(AUTOANTIGEN NOR-90)
3029	15945		1.8	6.0E-62	U09410.1	NT	Homo sapiens hypothetical protein (FLJ20281), mRNA
7821	20134	33011	3.43	6.0E-62	AI782801.1	EST_HUMAN	qg56a04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103
7821	20134	33012	3.43	6.0E-62	AI782801.1	EST_HUMAN	O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
8030	20572		0.78	6.0E-62	AW501124.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
8200	20741	33654	1.35	6.0E-62	11431139	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
8276	21802	34752	3.92	6.0E-62	AW814983.1	EST_HUMAN	w04402.x1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:2389251 3'
441	13074	25569	1.99	6.0E-62	AI850528.1	EST_HUMAN	w04402.x1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:2389251 3'
							U1-HF-BP0p-at-d-09-0-UI-1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
							Homo sapiens CGI-18 protein (LOC51008), mRNA
							MR3-ST0203-130100-025-409 ST0203 Homo sapiens cDNA
							wx51e07.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-95 ; contains element MER22 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2451	15018	27568	3	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2451	15018	27569	3	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2626	15188	27755	0.87	5.0E-62	U93487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
2626	15188	27756	0.87	5.0E-62	U93487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3488	16073	28546	2.52	5.0E-62	4508758	NT	Homo sapiens ryanodine receptor 3 (RYS3) mRNA
4421	17006	28449	2.23	5.0E-62	AA431093.1	EST_HUMAN	2478409 x1 Soerea_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4657	17239		0.95	5.0E-62	AW005887.1	EST_HUMAN	P47245 NARDILYSIN ;
8485	21024	33941	0.64	5.0E-62	4508758	NT	RCA-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
9436	21962	34911	5.85	5.0E-62	AW410887.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYS3) mRNA
11144	23652	36803	2.54	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
11144	23652	36894	2.54	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
873	13488	26003	4.05	4.0E-62	AW161479.1	EST_HUMAN	eu71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
873	13488	26004	4.05	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
874	13488	26003	3.94	4.0E-62	AW161479.1	EST_HUMAN	eu71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
874	13488	26004	3.94	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1511	14103		1.01	4.0E-62	AA311281.1	EST_HUMAN	eu71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2498	15082	27636	1.7	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2498	15082	27637	1.7	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3446	16054		7.95	4.0E-62	4557887	NT	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end
8081	18898	31445	1.79	4.0E-62	4508978	NT	wf12b08.x1 Soerea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
8439	19041	31829	2.58	4.0E-62	11420654	NT	wf12b08.x1 Soerea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
7223	19754	32609	1.86	4.0E-62	11421041	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
7530	20142	33021	2.6	4.0E-62	7657057	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7630	20142	33022	2.5	4.0E-62	7657057	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
8112	20653	33582	0.95	4.0E-62	11429873	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens 26S proteasome-associated peb1 homolog (POH1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8780	21319	34243	5.44	4.0E-82	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
10890	23411	36428	2.16	4.0E-82	Z78786.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA18D3
10890	23411	36430	2.16	4.0E-82	Z78786.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA18D3
11148	23654	36898	2.05	4.0E-82	AW023559.1	EST_HUMAN	df5g04.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487751 5'
12003	24912		1.89	4.0E-82	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12420	24908	30887	1.78	4.0E-82	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12475	24600	30884	15	4.0E-82	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12475	24600	30885	15	4.0E-82	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12528	24642	30898	2.66	4.0E-82	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
78	12765	28238	0.85	3.0E-82	4557784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2), mRNA
3082	15997	28169	0.93	3.0E-82	AB040509.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3082	15997	28170	0.93	3.0E-82	AB040509.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3761	16382	28830	5.68	3.0E-82	X62858.1	NT	Human cyclophilin-related processed pseudogene
8477	21018	33932	3.98	3.0E-82	AI632733.1	EST_HUMAN	wa33f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299803 3' similar to contains THR.L2
1274	13870	26390	2.31	2.0E-82	AL163284.2	NT	THR repetitive element;
8709	21248	34170	4.31	2.0E-82	BF326811.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8709	21248	34171	4.31	2.0E-82	BF326811.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
							RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10076	22571		3.84	2.0E-82	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11537	23985		18.68	2.0E-82	BF330678.1	EST_HUMAN	QV4-BT0257-Q81199-017-e03 BT0257 Homo sapiens cDNA
1082	13687	26199	1.74	1.0E-82	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1592	14185	26717	9.15	1.0E-82	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
							af70a11.1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
1834	14422	26972	1.05	1.0E-82	AA825207.1	EST_HUMAN	CE03453;
2839	15555	28031	1.22	1.0E-82	AL039044.1	EST_HUMAN	DKFZp568F104_r1 568 (synonym: hfk22) Homo sapiens cDNA clone DKFZp568F104 5'
4625	17208	29658	1.46	1.0E-82	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6305	17867	30260	0.74	1.0E-82	AA148822.1	EST_HUMAN	Z08b08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491511 5' similar to
7188	19720	32567	1.01	1.0E-82	AA490050.1	EST_HUMAN	SW:C581_BOVIN_P10897 CYTOCHROME B581;
7189	18730	32581	3	1.0E-82	AA722878.1	EST_HUMAN	ab05c02.s1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:836908 3'
7189	18730	32582	3	1.0E-82	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8892	21231	34151	0.71	1.0E-82	AA280050.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8988	21528	34455	1.64	1.0E-82	7682289	NT	za93c07.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:705060 5'
							Homo sapiens KIAA0763 gene product (KIAA0763), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8988	21526	34458	1.64	1.0E-62	7682289	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9030	21567	34495	2.39	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9030	21567	34486	2.39	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9476	21876	34822	2.95	1.0E-62	AA465170.1	EST_HUMAN	es33d08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11245	23775	36832	2.49	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA14D8
12289	24490		6.66	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12508	24830	30894	2.04	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
360	13009	25492	1.88	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-105 ST0234 Homo sapiens cDNA
2383	14952		2.15	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TF1jlvare) Homo sapiens cDNA clone GEN-558C10 5'
4114	16708	28162	9.09	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4114	16708	29163	9.09	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5453	18022	37142	3.93	9.0E-63	11418185	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
5657	18284	30762	1.55	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7234	19784	32620	3.96	9.0E-63	11426986	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8288	20809	33729	1.12	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
2382	14951	27624	1.5	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2412	14980	27555	2.47	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3508	16113	28590	4.92	8.0E-63	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3508	16113	28591	4.92	8.0E-63	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4352	18539	29381	3.64	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C0068
964	13575		2.31	7.0E-63	A1872137.1	EST_HUMAN	wri55g11.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439808 3'
5542	18174		34.98	6.0E-63	AA420803.1	EST_HUMAN	nc83f02.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745847 similar to gb:Y00381 80S
8807	21348	34270	0.5	5.0E-63	11528484	NT	RIBOSOMAL PROTEIN (HUMAN);
3363	15971	28449	0.81	4.0E-63	AL163278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3881	16479	28940	0.98	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C0078
3881	16479	28941	0.98	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6573	18171	31968	5.49	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6573	18171	31969	5.46	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-180100-072-609 BT0595 Homo sapiens cDNA
11012	23528	36561	2.3	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-180100-072-609 BT0595 Homo sapiens cDNA
11012	23528	36562	2.3	4.0E-63	AW134709.1	EST_HUMAN	UIH-B11-abq-e-02-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1979	14582	27121	1.75	3.0E-63	AB018260.1	NT	UIH-B11-abq-e-02-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2807	16359	27928	1.56	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
							Human Met-tRNA-I gene 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2848	13877	26399	11.17	3.0E-63	6005683	NT	Homo sapiens zinc finger protein 144 (Maf-18) (ZNF144), mRNA
6900	19197	32002	29.68	3.0E-63	11546910	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
8822	22122	35086	0.77	3.0E-63	BE878158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888263 5'
8822	22122	35087	0.77	3.0E-63	BE878158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888263 5'
206	12866	26361	3.47	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
212	12873	26359	1.4	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
523	13155		5.21	2.0E-63	4557824	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
859	13475	25988	8.8	2.0E-63	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1612	14205	26739	3.37	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1612	14205	26740	3.37	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1803	14393	26938	1.06	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838103 5'
2128	14706	27277	1.33	2.0E-63	AI863961.1	EST_HUMAN	wj54502.x1 NCI_OGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406803 3' similar to gb:M57609 GLI3 PROTEIN (HUMAN);
3192	15804	28277	1	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3324	15934	28411	1.7	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3976	16574	28044	2.08	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4980	17584	30009	1.18	2.0E-63	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5467	24742	30420	1.95	2.0E-63	11419428	NT	Homo sapiens similar to ecdystrolide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
6045	18684	31404	2.51	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6045	18684	31405	2.51	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6333	18839	31715	1.04	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6333	18839	31716	1.04	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T,
6803	18394	32210	1.62	2.0E-63	U80069.1	NT	TCRBV13S9/13S>
6844	19434	32248	0.87	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6844	19434	32250	0.87	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7135	19474	32285	1.43	2.0E-63	6910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56834), mRNA
7135	19474	32286	1.43	2.0E-63	6910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56834), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7755	20263	33158	0.89	2.0E-63	AB048844.1	NT	Homo sapiens mRNA for KIAA1824 protein, partial cds
8470	21010	33927	2.81	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8984	21522	34449	1.12	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8984	21522	34450	1.12	2.0E-63	11420948	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9852	22350	35331	0.8	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10825	23157	36170	22.7	2.0E-63	N78945.1	EST_HUMAN	zb18b05.61 Scores_fetal_lung_NhlL18W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
10852	23184	36198	2.83	2.0E-63	AF09810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
10852	23184	36198	2.83	2.0E-63	AF09810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
11898	24851	30702	6.92	2.0E-63	11418186	NT	Homo sapiens acetylase 2, mitochondrial (ACG2), mRNA
12823	24701	30884	1.4	2.0E-63	AB011398.1	NT	Homo sapiens gene for AF-4, complete cds
4434	17020	28460	3.52	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4434	17020	28461	3.52	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5555	18187	30602	1.32	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
5943	18583	31283	1.38	1.0E-63	AW582268.1	EST_HUMAN	QV0-S10215-080100-083-b09 ST0215 Homo sapiens cDNA
8408	20948		2.21	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12581	24870		17.03	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6122	18737	31489	1.08	9.0E-64	AW401433.1	EST_HUMAN	UHF-BK0-eed-b-09-0-UL1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:3063153 5'
7808	20351	33259	4.35	9.0E-64	A1478186.1	EST_HUMAN	hm50507.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1084	13689		13.09	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6289	18897	31688	3.17	8.0E-64	BE885755.1	EST_HUMAN	60150898F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
11694	24109		1.48	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
11752	24148		3.58	8.0E-64	T60851.1	EST_HUMAN	y688b02.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:76179 5'
3582	16168		0.84	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4838	17418	29898	2.85	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4838	17418	29899	2.85	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7768	20274	33172	0.68	7.0E-64	4508788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
9846	22441	35418	4.54	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rp22 and bam22 genes
1760	14350	26894	2.4	6.0E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1760	14350	26895	2.4	6.0E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3166	15770	28238	4.48	6.0E-64	AW026445.1	EST_HUMAN	wt13e03.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3166	16770	28237	4.48	6.0E-64	AW026445.1	EST_HUMAN	wt13e03.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2529436 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	18430	31149	3.71	6.0E-04	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5805	18430	31150	3.71	6.0E-04	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5923	18447	31169	5.6	6.0E-04	M1976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7288	19814	32870	2.45	6.0E-04	11528878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7288	19814	32871	2.45	6.0E-04	11528879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9250	21778	34727	8.24	6.0E-04	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9425	21834	34883	2	6.0E-04	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9634	22134	35089	2.23	6.0E-04	S76476.1	NT	tRAC (human, brain), mRNA, 2715 nt
10849	23181	36184	7.87	6.0E-04	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10849	23181	36195	7.87	6.0E-04	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10898	15770	28238	1.64	6.0E-04	AW028445.1	EST_HUMAN	wt13a03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528438 3'
10898	15770	28237	1.64	6.0E-04	AW028446.1	EST_HUMAN	wt13a03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528438 3'
11803	24242	31008	2.45	6.0E-04	11528198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
853	13469	25979	3.09	5.0E-04	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
853	13469	25980	3.09	5.0E-04	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1383	13977	26504	0.95	5.0E-04	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1487	14059	28593	2.55	5.0E-04	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1487	14059	28594	2.55	5.0E-04	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1749	14339	26886	1.52	5.0E-04	U89358.1	NT	Human [(3)mbt protein homolog mRNA, complete cds
2853	14120	26657	3.5	6.0E-04	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2853	14120	26658	3.5	5.0E-04	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4032	16830	29089	7.78	5.0E-04	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
4181	16771	29220	0.68	5.0E-04	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
10692	23222	36235	3.91	4.0E-04	AW813783.1	EST_HUMAN	RC3-STO197-120200-015-403 ST0197 Homo sapiens cDNA
10692	23222	36236	3.91	4.0E-04	AW813783.1	EST_HUMAN	RC3-STO197-120200-015-403 ST0197 Homo sapiens cDNA
2239	14814	27388	3.14	3.0E-04	C18898.1	EST_HUMAN	G18895 Human placenta cDNA (TFujihara) Homo sapiens cDNA clone GEN-568E02 5'
3283	15904	28384	0.76	3.0E-04	BE794381.1	EST_HUMAN	601589595F1 NIH_JMGC_7 Homo sapiens cDNA clone IMAGE:3843577 5'
3491	18098	28570	2.67	3.0E-04	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3491	18098	28571	2.67	3.0E-04	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6232	18841	31613	1.53	3.0E-04	Z26273.1	NT	Hi.sapiens isoform 1 gene for L-type calcium channel, exon 28
6619	19218	32021	3.11	3.0E-04	BF370000.1	EST_HUMAN	RC6-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8402	20942	33864	1.83	3.0E-04	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8402	20942	33865	1.83	3.0E-04	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8432	20972	33885	4.49	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:L08068 DNABJ PROTEIN_HOMOLOG 2 (HUMAN);
8432	20972	33886	4.49	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:L08068 DNABJ PROTEIN_HOMOLOG 2 (HUMAN);
9348	21862	34810	1.23	3.0E-64	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9348	21862	34811	1.23	3.0E-64	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9433	21859	34807	0.72	3.0E-64	AW977384.1	EST_HUMAN	EST388493 MAGe resequences, MAGO Homo sapiens cDNA
9433	21859	34808	0.72	3.0E-64	AW977384.1	EST_HUMAN	EST388493 MAGe resequences, MAGO Homo sapiens cDNA
11118	23827	36609	1.83	3.0E-64	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11118	23827	36670	1.83	3.0E-64	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11539	23987	37058	4.89	3.0E-64	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1127	13730	28241	1.26	2.0E-64	AA608940.1	EST_HUMAN	af08d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1441	14034	28582	8.3	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA w087b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2568	15130		1.88	2.0E-64	A1927030.1	EST_HUMAN	L1 repetitive element;
2570	15133	27702	1.25	2.0E-64	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2570	15133	27703	1.25	2.0E-64	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
3174	15787	28259	1.17	2.0E-64	4504088	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3856	16453	28916	0.83	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGO Homo sapiens cDNA
3856	16453	28917	0.83	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGO Homo sapiens cDNA
6157	18770	31534	2.28	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6389	18892	31772	1.52	2.0E-64	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6811	19208	32016	4.45	2.0E-64	BF688537.1	EST_HUMAN	602123474F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4280385 5'
6706	19301	32105	1.38	2.0E-64	A1078387.1	EST_HUMAN	0229b03.x1 Soares_testis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6802	19393	32209	53.03	2.0E-64	M77185.1	NT	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
8603	21142	34055	1.98	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
8603	21142	34058	1.98	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9157	21682	34638	1.14	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
9889	22386	35384	0.48	2.0E-64	T08397.1	EST_HUMAN	EST04286 Fetal brain, Stragelens (cat#838206) Homo sapiens cDNA clone HF8DS88
9889	22386	35385	0.48	2.0E-64	T08397.1	EST_HUMAN	EST04286 Fetal brain, Stragelens (cat#838206) Homo sapiens cDNA clone HF8DS88
10643	23175	38187	2.38	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4180556 5'
10829	23447	38488	5.36	2.0E-64	A1922011.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
10829	23447	38489	5.36	2.0E-64	A1922011.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11112	23822	36663	1.78	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
11826	24194	31034	1.5	2.0E-64	8587987	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12285	24487		2.44	2.0E-64	H55162.1	EST_HUMAN	GHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
278	12836	25421	1.64	1.0E-64	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
1816	14405	28949	8.83	1.0E-64	AI928418.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519138 3' similar to gb:L21688 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
3045	15861	28142	0.62	1.0E-64	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
3591	16166	28648	5.94	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3844	15247	28722	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3844	16247	28723	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3988	16568	29036	0.87	1.0E-64	8922828	NT	Homo sapiens TRIAD3 mRNA, partial cds
8976	22471	35454	0.84	1.0E-64	AA042876.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
11798	24178		1.37	1.0E-64	AL163240.2	NT	ZK53108.s1 Soares pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:486567 3'
2315	14887	27462	1.02	9.0E-65	X89211.1	NT	Homo sapiens chromosome 21 segment HS21C048
2315	14887	27463	1.02	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
11410	23861		35.61	9.0E-65	BF330676.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
11383	23835	36897	14.63	8.0E-65	AI929244.1	EST_HUMAN	QV4-BT0257-081198-017-e03 BT0257 Homo sapiens cDNA
10038	22564	35550	2.06	7.0E-65	BE081663.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P 48778 60S RIBOSOMAL PROTEIN L21.;
1094	13699	26209	1.68	8.0E-65	AV721888.1	EST_HUMAN	QV2-BT0635-240400-162-e02 BT0635 Homo sapiens cDNA
1866	14550		5.21	6.0E-65	AA650929.1	EST_HUMAN	AV721888 HTB Homo sapiens cDNA clone HTBBZC08 5'
8681	21220	34140	2.24	6.0E-65	AW083282.1	EST_HUMAN	ri88d10.s1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:988379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
8941	21479	34400	4.18	6.0E-65	AA427878.1	EST_HUMAN	xc07b08.x1 NCL CGAP_C021 Homo sapiens cDNA clone IMAGE:2683645 3' similar to TR:Q63308 Q63308 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S ; contains L1.b2 L1 repetitive element ;
8941	21479	34401	4.18	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9004	21541	34471	1.04	6.0E-65	A1085314.1	EST_HUMAN	zw53b06.s1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9004	21541	34472	1.04	6.0E-65	A1085314.1	EST_HUMAN	qf18h05.x1 NCL CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1750425 3'
10752	23276	36289	12.35	6.0E-65	BE587816.1	EST_HUMAN	qf18h05.x1 NCL CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1750425 3'
11135	23643	36883	1.73	6.0E-65	AW208762.1	EST_HUMAN	60134048F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682877 5'
11369	23821	36883	4.4	6.0E-65	AL163210.2	NT	UJ-H-B1-e1q-d-10-Q-UJ.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722628 3'
						NT	Homo sapiens chromosome 21 segment HS21C010

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
959	13282	26762	0.75	5.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1397	13991	26518	1.8	5.0E-66	7861961	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1397	13991	26519	1.8	5.0E-65	7861951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2200	14776	27349	0.87	5.0E-65	AB033768.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3294	15905	28385	2.39	5.0E-65	4507948	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3294	15905	28388	2.39	5.0E-65	4507948	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10364	22658	35850	0.99	5.0E-65	AF008668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
207	12668	26354	2.15	4.0E-65	AL120419.1	EST_HUMAN	DKFZ761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108.5
775	13394	26894	1.3	4.0E-65	AI268468.1	EST_HUMAN	qim48e01.x1 Soares_placenta_816weeks_2N1bHP816c9W Homo sapiens cDNA clone IMAGE:1891800.3
775	13394	26895	1.3	4.0E-65	AI268468.1	EST_HUMAN	qim48e01.x1 Soares_placenta_816weeks_2N1bHP816c9W Homo sapiens cDNA clone IMAGE:1891800.3
1117	13720	26232	1.52	4.0E-65	4829735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1593	14126	26682	17.23	4.0E-65	4508638	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2374	14944	27516	1.14	4.0E-65	BE221468.1	EST_HUMAN	hu25e04.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102.3
2374	14944	27517	1.14	4.0E-65	BE221468.1	EST_HUMAN	hu25e04.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102.3
6303	18910	31682	4.44	4.0E-65	AB033083.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
6303	18910	31683	4.44	4.0E-65	AB033083.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
7171	19703	32550	0.85	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7271	19798	32666	2.39	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7763	20326	33230	0.81	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
7763	20326	33231	0.81	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
6072	21609	34539	0.8	4.0E-65	11426127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10473	22867		2.65	4.0E-65	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
10833	23354	36369	1.83	4.0E-65	AV738764.1	EST_HUMAN	AV738764 CB Homo sapiens cDNA clone CBCC8E05.5
10977	23482	36522	3.39	4.0E-65	AF118848.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12124	13720	26232	1.41	4.0E-65	4826736	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
101	12778	25261	2.51	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
102	12778	25261	2.35	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1275	15393		11.57	3.0E-65	X76932.1	NT	H. sapiens HZF8 mRNA for zinc finger protein
1805	14197	26729	0.98	3.0E-65	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1861	14449	27007	1	3.0E-65	AI008682.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173.3 similar to contains element MSR1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3019	15635	28111	0.8	3.0E-65	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3315	15923	28403	0.93	3.0E-65	4504850	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3784	16384	28849	1.19	3.0E-65	A1000692.1	EST_HUMAN	ov23f03.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
4764	17335	28779	1.38	3.0E-65	6812385	NT	Homo sapiens rab8 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
5081	22478	35458	1.44	3.0E-65	BE787388.1	EST_HUMAN	601479888F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
11287	23005	38013	13.23	3.0E-65	AA430009.1	EST_HUMAN	zw65a08.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3451	16036	28534	5.71	2.0E-65	BF680294.1	EST_HUMAN	602155022F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285968 5'
6857	19253	BE78373.1	5.63	2.0E-65	BE78373.1	EST_HUMAN	601190833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7186	19718	32565	25.57	2.0E-65	BF76922.1	EST_HUMAN	602134358F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289285 5'
8778	21318	34241	1.21	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ000358 protein, partial cds
8779	21318	34242	1.21	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ000358 protein, partial cds
11750	24147		6.58	2.0E-65	AA307604.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
12241	24832		2.26	2.0E-65	BF746086.1	EST_HUMAN	601854033F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4073769 5'
94	12770		0.78	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028501 5'
584	13193	25674	1.4	1.0E-65	7857495	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX5), mRNA
2084	14885	27236	0.95	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3419	16027	28508	0.94	1.0E-65	BE466881.1	EST_HUMAN	h224a09.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:3208886 3'
4070	16696	29127	1.85	1.0E-65	4504082	NT	Homo sapiens glycine 4 (GPC4) mRNA
4070	16696	29128	1.85	1.0E-65	4504082	NT	Homo sapiens glycine 4 (GPC4) mRNA
4285	16871	29317	2.39	1.0E-65	AW029340.1	EST_HUMAN	wx08c08.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4285	16871	29318	2.39	1.0E-65	AW029340.1	EST_HUMAN	wx08c08.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5688	18295	30775	0.74	1.0E-65	A1243738.1	EST_HUMAN	qh88p07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1654109 3' similar to TR:Q07823
8198	20737	33648	4.11	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0288-140200-042-112 ST0288 Homo sapiens cDNA
8198	20737	33649	4.11	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0288-140200-042-112 ST0288 Homo sapiens cDNA
8222	20763	33670	0.98	1.0E-65	BE732118.1	EST_HUMAN	601586124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8222	20763	33680	0.58	1.0E-65	BE732118.1	EST_HUMAN	601586124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8281	20802	33719	2.05	1.0E-65	AU141285.1	EST_HUMAN	AU141285 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
8281	20802	33720	2.05	1.0E-65	AU141285.1	EST_HUMAN	AU141285 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
8774	21313	34235	2.42	1.0E-65	BF688707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
8850	21489	34410	2.86	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8950	21488	34411	2.88	1.0E-06	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
8981	21498		2.54	1.0E-06	11431884	NT	Homo sapiens Inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
9098	21821	34770	5.09	1.0E-06	AI191716.1	EST_HUMAN	qds6a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M28581 ZINC FINGER PROTEIN 8 (HUMAN); contains MER19.11 MER19 repetitive element;
9800	22298	35283	1.39	1.0E-05	AU153783.1	EST_HUMAN	AU153783 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
10203	22698	35692	0.85	1.0E-06	AA088559.1	EST_HUMAN	z7f5a04.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
10483	22957	35968	1.12	1.0E-06	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10529	23088	36078	3.58	1.0E-05	M28167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
10958	23188	36204	22.3	1.0E-05	4508680	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11010	23524	36558	2.79	1.0E-06	BF688707.1	EST_HUMAN	602128239F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4283313 5'
11088	23600	36638	2.25	1.0E-05	AI021017.1	EST_HUMAN	ts78a08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:223170 3' similar to gb:L15533_mna1
11788	24179		2.28	1.0E-06	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
11898	24238	31006	6.17	1.0E-06	11418322	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
75	12753	25232	4.57	9.0E-06	AL160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (GELSR1), mRNA
75	12753	25233	4.57	9.0E-06	AL160311.1	NT	Novel human gene mapping to chromosome 22
1398	13992	28520	1.84	9.0E-06	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1388	13992	28521	1.54	9.0E-06	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1531	14123		4.45	9.0E-06	M87289.1	NT	Human transposon-like element, partial
4802	17380	29830	0.57	9.0E-06	AL137183.1	NT	Novel human gene mapping to chromosome X
4801	17379	29829	0.98	9.0E-06	AA424304.1	EST_HUMAN	zv60c05.t1 Soares_Nhi-MRtu_S1 Homo sapiens cDNA clone IMAGE:767048 5'
11225	23766		1.78	7.0E-06	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-H08 BT0311 Homo sapiens cDNA
4455	17041	29483	1.11	6.0E-06	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448597 3' similar to WP:F16G8.4A CE18595;
4455	17041	29484	1.11	6.0E-06	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448597 3' similar to WP:F16G8.4A CE18595;
4455	17041	29485	1.11	6.0E-06	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448597 3' similar to WP:F16G8.4A CE18595;
8373	20813		0.48	6.0E-06	BE178563.1	EST_HUMAN	PM2-HT0604-030300-001-508 HT0604 Homo sapiens cDNA
11038	23552	36587	7.01	6.0E-06	X69181.1	NT	H. sapiens mRNA for ribosomal protein L31
1411	14004	26532	1.25	5.0E-06	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-H08 BT0311 Homo sapiens cDNA
5278	17840	30268	0.57	5.0E-06	BE888944.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
5278	17840	30287	0.67	5.0E-06	BE888944.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
9218	21735	34877	14.1	5.0E-06	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
823	13440	25947	1.13	4.0E-68	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1771	14361	26908	0.87	4.0E-68	AW807798.1	EST_HUMAN	RC1-NN0063-100500-022-02 NN0063 Homo sapiens cDNA
2319	14891	27468	1.64	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2613	15077		2.35	4.0E-68	AJ223384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4898	17473		6.78	4.0E-68	9635487	NT	Human endogenous retrovirus, complete genome
5739	18365	31072	3.33	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5918	18540	31266	0.8	4.0E-68	AW938118.1	EST_HUMAN	QV1-DT0069-110200-087-g10 DT0069 Homo sapiens cDNA
6940	18048	30470	4.62	4.0E-68	AW965473.1	EST_HUMAN	EST137548 IMAGE resequences, MAGI Homo sapiens cDNA
7185	18717	32584	7.41	4.0E-68	U78188.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
7625	18365	31072	1.06	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8022	20564	33466	6.44	4.0E-68	11421638	NT	Homo sapiens hypothetical protein FLJ20118 (FLJ20118), mRNA
8076	20616	33532	0.96	4.0E-68	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
1473	14065	26601	11.5	3.0E-68	4502088	NT	Homo sapiens solute carrier family 26 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1473	14065	26602	11.5	3.0E-68	4502088	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2026	14608	27173	1	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Scores_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2. [2] PIR:B56812;
2026	14608	27174	1	3.0E-68	N55323.1	EST_HUMAN	yz27g12.r1 Scores_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2. [2] PIR:B56812;
2026	14608	27175	1	3.0E-68	N55323.1	EST_HUMAN	yz27g12.r1 Scores_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2. [2] PIR:B56812;
2732	16287	27854	3.43	3.0E-68	11141880	NT	Homo sapiens TGF-beta-induced transcription factor 2 (TGIF2), mRNA
3151	15765	28232	6.88	3.0E-68	7682223	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
5658	18285	30763	0.9	3.0E-68	AB020696.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5946	18568	31266	2.07	3.0E-68	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5946	18568	31267	2.07	3.0E-68	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
9444	21970	34918	0.39	3.0E-68	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9835	22135	35100	0.88	3.0E-68	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9885	22480	35464	0.8	3.0E-68	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10415	22908	35808	0.92	3.0E-68	AF155858.1	NT	Homo sapiens myoblast fusion cofactor blosynthesis protein E (MCBPE) mRNA, complete cds

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11384	23836	36898	9.34	3.0E-68	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
55	12735	25203	1.34	2.0E-68	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
55	12735	25204	1.34	2.0E-68	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
447	12878	25132	1.21	2.0E-68	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
447	12878	25133	1.21	2.0E-68	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1868	14432	27011	1.73	2.0E-68	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3002	15918	28096	1.55	2.0E-68	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3572	16178	28658	0.87	2.0E-68	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3828	16428	28889	0.72	2.0E-68	AL117233.1	NT	Novel human gene mapping to chromosome 1
4139	16731	29184	0.57	2.0E-68	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4760	17341	29788	16.35	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4760	17341	29788	16.35	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4760	17341	29788	16.35	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5982	18602	31337	0.8	2.0E-68	AW98884.1	EST_HUMAN	EST380930 MAGE resequences, MAG1 Homo sapiens cDNA
5982	18602	31337	0.8	2.0E-68	AW98884.1	EST_HUMAN	EST380930 MAGE resequences, MAG1 Homo sapiens cDNA
8781	21320	34244	2.24	2.0E-68	N45480.1	EST_HUMAN	Y59-02.1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:277828 5'
12132	26057		1.8	2.0E-68	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2819	15536	28010	1.65	1.0E-68	AV171817.1	EST_HUMAN	AV171817 DCB Homo sapiens cDNA clone DCBADC07 5'
2819	15536	28011	1.65	1.0E-68	AV171817.1	EST_HUMAN	AV171817 DCB Homo sapiens cDNA clone DCBADC07 5'
4474	16538	28010	3.57	1.0E-68	AV171817.1	EST_HUMAN	AV171817 DCB Homo sapiens cDNA clone DCBADC07 5'
4474	16538	28011	3.57	1.0E-68	AV171817.1	EST_HUMAN	AV171817 DCB Homo sapiens cDNA clone DCBADC07 5'
5583	18214	30663	5.49	1.0E-68	BF073088.1	EST_HUMAN	602152886F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
5952	18574	31307	0.68	1.0E-68	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
5952	18574	31308	0.68	1.0E-68	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
7018	19519	32338	0.95	1.0E-68	BF328623.1	EST_HUMAN	RC5-BN0183-010900-034-G08 BN0183 Homo sapiens cDNA
8395	20935	33857	1.6	1.0E-68	AA688558.1	EST_HUMAN	aa6804.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827292 3'
8347	21861	34809	0.74	1.0E-68	AA016828.1	EST_HUMAN	ze57612.1 Soares retina NZB44R Homo sapiens cDNA clone IMAGE:363118 5'
10273	22768	35756	0.75	1.0E-68	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10273	22768	35756	0.75	1.0E-68	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10509	23003	36011	0.61	1.0E-68	BE044595.1	EST_HUMAN	h047802.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040583 3'
10821	23342	36357	1.98	1.0E-68	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11901	24240		3	6.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
403	13078	25570	3.59	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1425	14018	26547	1.75	7.0E-67	AA383416.1	EST_HUMAN	ZK353
1601	14193	26724	1.25	7.0E-67	W85947.1	EST_HUMAN	zh58b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1601	14193	26726	1.25	7.0E-67	W86947.1	EST_HUMAN	zh58b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2838	13078	25570	3.15	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6231	18840	31812	0.98	7.0E-67	10100805	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6416	18019	31802	1.79	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6416	18019	31803	1.79	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6823	19413	32230	1.03	7.0E-67	4865084	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
7627	20139	33018	0.89	7.0E-67	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
7627	20139	33019	0.99	7.0E-67	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8012	20554	33457	0.49	7.0E-67	4826885	NT	Homo sapiens phosphodiesterase 11 nucleotide pyrophosphatase 3 (PDNP3) mRNA
8265	20806	33724	0.8	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8862	21401	34326	0.78	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11626	23973	37043	2.92	7.0E-67	UB2488.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
11675	24094	37147	2.95	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11675	24094	37148	2.95	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12159	24399	30876	1.44	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
585	13215	25892	1.84	6.0E-67	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
828	13445	25952	1.84	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1316	13610	26430	1.2	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3485	16080	26562	1.47	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3485	16080	26563	1.47	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4205	16794	26240	0.74	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4205	16794	26241	0.74	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4815	17363	26845	3.86	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4815	17363	26846	3.86	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3258	15870	28350	2.65	5.0E-67	AF008680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10863	23384		1.9	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1373	13667	28494	1.16	4.0E-67	R0818.1	EST_HUMAN	yn02d11.1 Scores adult brain N2b4HB557 Homo sapiens cDNA clone IMAGE:167253 5'
7864	20506	33413	0.88	4.0E-67	AF73032.1	EST_HUMAN	q28c05.x1 NCI_CGAP_K103 Homo sapiens cDNA clone IMAGE:1493288 3' similar to SW:Z33A_HUMAN
8322	20863		1.3	4.0E-67	BF387321.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ;
10942	23458		1.92	4.0E-67	AA714294.1	EST_HUMAN	RC0-HT0834-150900-028-c03 HT0834 Homo sapiens cDNA
2839	13284	26766	6.7	3.0E-67	AA333788.1	EST_HUMAN	hw08a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
4804	17382	29832	3.38	3.0E-67	AW989159.1	EST_HUMAN	PRO-POL-OUTPASE POLYPROTEIN ;
4831	17408		0.93	3.0E-67	AL183278.2	NT	EST137903 Embryo, 9 week Homo sapiens cDNA 5' end
							MIR3-SN0068-040500-008-101 SN0068 Homo sapiens cDNA
8122	20863	33573	1.17	3.0E-67	BF196088.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
11139	23647		22.61	3.0E-67	AA827874.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_K101 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
201	12862	25346	1.74	2.0E-67	BE348354.1	EST_HUMAN	Q81085 GTP-RHO BINDING PROTEIN 1 ;
878	13492	26010	4.89	2.0E-67	AW816403.1	EST_HUMAN	am18007.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1144	13747		1.84	2.0E-67	AF167480.1	NT	hw18g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1928	14512	27069	1.5	2.0E-67	BE303037.1	EST_HUMAN	CE08817 ;
							QV4-ST0234-181189-037-105 ST0234 Homo sapiens cDNA
1928	14512	27070	1.5	2.0E-67	BE303037.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
2428	14965	27570	2.84	2.0E-67	AF308581.1	NT	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805978 5' similar to TR:O94882 O94882
2475	15042	27610	0.95	2.0E-67	4758785	NT	KIAA0798 PROTEIN ;
3514	16118	28599	4.48	2.0E-67	AA826785.1	EST_HUMAN	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
4074	16870	29131	2.78	2.0E-67	AL183300.2	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
6222	18831	31805	0.83	2.0E-67	AL049784.1	NT	zu01g01.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
6273	18881	31849	5.18	2.0E-67	BF240758.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
8438	18040	31827	2.25	2.0E-67	AB051763.1	NT	Novel human gene mapping to chromosome 13
8438	18040	31828	2.25	2.0E-67	AB051763.1	NT	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
8493	21032	33953	0.98	2.0E-67	AA334606.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8927	21465	34381	1.09	2.0E-67	AW602635.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8927	21465	34382	1.09	2.0E-67	AW602635.1	EST_HUMAN	EST138850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
9488	21043	34890	1.24	2.0E-67	AV731333.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
9825	22125	35089	1.19	2.0E-67	AW283824.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
							AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
							UI-H-B12-shm-e-10-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10781	23305	35313	1.57	2.0E-07	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301706 5'
10834	26127		3.62	2.0E-07	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11107	23617	36859	1.85	2.0E-07	BE285714.1	EST_HUMAN	601175782F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11330	23028	36037	2.01	2.0E-07	BF377169.1	EST_HUMAN	PM2-TN0103-040800-001-c02 TN0103 Homo sapiens cDNA
12034	24911	30714	2.53	2.0E-07	11418180	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12347	24526	30925	2.28	2.0E-07	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
274	12831	25418	3.31	1.0E-07	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
737	13357	25651	1.2	1.0E-07	AA702784.1	EST_HUMAN	z190504.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2220	14785	27368	1.73	8.0E-08	BE870732.1	EST_HUMAN	601448588F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3837	16535	28001	6.37	8.0E-08	AA209456.1	EST_HUMAN	z182110.r1 Striatogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848183 5' similar to SW:SAV_SULAC Q07690 SAV PROTEIN. ;
3837	16535	28002	6.37	8.0E-08	AA209456.1	EST_HUMAN	z182110.r1 Striatogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848183 5' similar to SW:SAV_SULAC Q07690 SAV PROTEIN. ;
8045	20587	33403	0.53	7.0E-08	A1810505.1	EST_HUMAN	wb39e03.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2312860 3'
10346	22840	35838	2.63	8.0E-08	11422088	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12349	24530		3.32	6.0E-08	BE612554.1	EST_HUMAN	601462087F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761 5'
835	13389	25960	0.67	5.0E-08	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
835	13389	25961	0.67	5.0E-08	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
852	13468	25977	4.54	5.0E-08	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
852	13468	25978	4.54	5.0E-08	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2808	15360	27927	72.53	6.0E-08	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3181	15794	28288	3.22	5.0E-08	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4260	18846		0.63	5.0E-08	4826867	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4590	17173	28818	1.21	5.0E-08	AL157645.1	EST_HUMAN	DKFZp547D207_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D207 5'
5111	17683		8.82	4.0E-08	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6118	18734	31487	0.76	4.0E-08	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6870	19604	32437	6.01	4.0E-08	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6870	19604	32438	6.01	4.0E-08	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7674	20185	33073	0.92	4.0E-08	7861083	NT	Homo sapiens DKFZP588L0724 protein (DKFZP588L0724), mRNA
8870	21508	34429	5.04	4.0E-08	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8870	21508	34430	5.04	4.0E-08	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9108	21642	34582	2.9	4.0E-08	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
10882	23403	38420	5.14	4.0E-08	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10882	23403	38421	5.14	4.0E-68	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
12225	24448	30853	2.91	4.0E-68	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3722	18323	28790	2.56	3.0E-68	AF23082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9378	20317		6.16	3.0E-68	A1342323.1	EST_HUMAN	q38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1850281 3' similar to cortalins
10386	22860	35884	1.77	3.0E-68	F28784.1	EST_HUMAN	THR12 THR repetitive element ;
12571	24829		2.05	3.0E-68	AW939485.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
2887	18011		27.71	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4097	18592	29149	0.78	2.0E-68	BE675786.1	EST_HUMAN	QV1-DT0072-010200-036-h08 DT0072 Homo sapiens cDNA
4789	17369	29821	1.58	2.0E-68	AB003681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN ;
6957	18534		8.88	2.0E-68	R45098.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
7123	19463	32280	4.61	2.0E-68	BF035316.1	EST_HUMAN	y339p04.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34898 3'
8879	21417	34341	0.64	2.0E-68	Q05859	SWISSPROT	601458514F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882034 5'
10494	22898	35998	0.46	2.0E-68	N78493.1	EST_HUMAN	FORMIN 4 (LIMB DEFORMITY PROTEIN)
11792	25077		2.11	2.0E-68	BE589376.1	EST_HUMAN	y27807.1 Soares_multiple_sclerolact_2N8HMS Homo sapiens cDNA clone IMAGE:289185 5'
12639	24714		1.84	2.0E-68	AW016803.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
83	12759	25242	0.78	1.0E-68	4508222	NT	UI-H-B10-aam-b-05-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
318	12972	25461	12.22	1.0E-68	AW818405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2294	14888	27443	0.89	1.0E-68	AB011149.1	NT	QV4-ST0234-181199-037-R05 ST0234 Homo sapiens cDNA
2294	14888	27444	0.89	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2785	15338	27809	1.12	1.0E-68	AW451832.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
6178	17745	30174	0.66	1.0E-68	AA897943.1	EST_HUMAN	UI-H-B13-alk-t-01-0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
5233	17797	30215	0.88	1.0E-68	BE298032.1	EST_HUMAN	el47g12.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5626	18157	30572	1.51	1.0E-68	7682348	NT	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3932344 5'
10085	22580	35573	0.49	1.0E-68	11419429	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
10732	23258	36274	2.83	1.0E-68	11418869	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
10732	23258	36275	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10783	23307	36314	3.41	1.0E-68	L76416.1	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11072	23584	36625	1.72	1.0E-68	11433277	NT	Homo sapiens MIF2 suppressor (HSM1T3) mRNA, complete cds
11179	23685	36731	2.23	1.0E-68	U50318.1	NT	Homo sapiens myosin IC (MYO1C), mRNA
11179	23685	36732	2.23	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11517	23985	37038	2.1	1.0E-68	11418431	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11517	23065	37037	2.1	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51832), mRNA
12330	12769	25242	2.37	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNI), mRNA
12618	24697		1.62	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
23	12702	26158	13.45	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
23	12702	26159	13.45	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1065	13670	26180	1.44	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1065	13670	26181	1.44	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4208	16797	29245	0.69	9.0E-69	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
5384	17943	30356	0.9	9.0E-69	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
10769	23263		11.7	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000988 5'
3433	16041		1.59	8.0E-69	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
6493	19094	31878	5.18	7.0E-69	9986912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
7804	20347	33254	22.34	6.0E-69	A182764.1	EST_HUMAN	qcd2h01.x1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L111688 60S RIBOSOMAL PROTEIN L18 (HUMAN);
7804	20347	33255	22.34	6.0E-69	A182764.1	EST_HUMAN	qcd2h01.x1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L111688 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8904	21442	34385	0.88	5.0E-69	AA828039.1	EST_HUMAN	cd60a03.e1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1972300 3'
548	13177		1.07	4.0E-69	A187330.1	EST_HUMAN	wrm26h11.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3'
5934	24751	31283	1.56	4.0E-69	BE561083.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877641 5'
6009	18629	31364	4.7	4.0E-69	A1764973.1	EST_HUMAN	wh57b06.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2394819 3' similar to TR:O55137
6739	16333	32139	2.45	4.0E-69	4557792	NT	O55137 ACYL-COA THIOESTERASE ;
6739	19333	32140	2.45	4.0E-69	4557792	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8945	21364	34309	0.59	4.0E-69	AU119634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
12663	24733		2.98	4.0E-69	A187952.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1008283 5'
408	13084	25577	4.82	3.0E-69	BE268012.1	EST_HUMAN	qcd3h05.x1 Soares_besite_NHT Homo sapiens cDNA clone IMAGE:1738881 3'
840	13263	25739	2.24	3.0E-69	AF221712.1	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
1802	14194		1.13	3.0E-69	T60514.1	EST_HUMAN	y408a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48836
2415	14983		1.34	3.0E-69	5729810	NT	A48836 SPEGF III=EGF REPEAT-CONTAINING FIBROPEL-LIKE PROTEIN - SEA URCHIN ;
4688	17270		0.77	3.0E-69	T68234.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5407	17270		0.81	3.0E-69	T68234.1	EST_HUMAN	y448h04.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:121015 5'
5482	18021	37141	1.37	3.0E-69	11418185	NT	y448h04.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:121015 5'
							Homo sapiens acylase 2, mitochondrial (ACO2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6884	19828		0.89	3.0E-69	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3)-deoxyribonucleosidase (dNT-2 gene), exons 1-5
7407	19932	32708	0.87	3.0E-69	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7449	19973	32840	1.42	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurexulin (CTNND2) mRNA, partial cds
7594	20073	32849	7.75	3.0E-69	AF288075.1	NT	Homo sapiens TRAF8-binding protein T6BP mRNA, complete cds
8313	20854	33780	0.87	3.0E-69	AW138848.1	EST_HUMAN	UI-HB1-act-g-01-Q-UI.s1 NCI_CGAP Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8703	21242		1.8	3.0E-69	AA378399.1	EST_HUMAN	EST88807 HSC172 cells I Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
8907	21445	34387	0.5	3.0E-69	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9334	21848	34797	1.77	3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
9452	21978	34930	8.82	3.0E-69	X08233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
9743	22241	35222	0.55	3.0E-69	5730036	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10520	23058	36068	3.93	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10721	23249		12.34	3.0E-69	AA378399.1	EST_HUMAN	EST88807 HSC172 cells I Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
11813	24185		3.88	3.0E-69	11419157	NT	Homo sapiens HGC8.2 protein (HGC8.2), mRNA
134	13082	25556	1.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
134	13082	25567	1.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
429	13082	25556	5.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
429	13082	25557	5.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1928	14513	27071	1.46	2.0E-69	BE257857.1	EST_HUMAN	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
2889	15487		2.88	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:3350074 5'
8489	21028	33948	0.82	2.0E-69	AA114270.1	EST_HUMAN	zm28g01.r1 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:527088 5'
1740	14330	26874	1.89	1.0E-69	AF053788.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP80 mRNA, partial cds
5173	17740		0.58	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3835781 5'
8201	18811	31580	0.78	1.0E-69	BE902601.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
8201	18811	31581	0.78	1.0E-69	BE902601.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6717	18311	32114	4.38	1.0E-69	AW393969.1	EST_HUMAN	QVO-TT0010-031189-045-c07 TT0010 Homo sapiens cDNA
6808	19842	32478	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0718 gene product (KIAA0718), mRNA
6908	19842	32479	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0718 gene product (KIAA0718), mRNA
6924	19583	32412	3.33	1.0E-69	AB032873.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6924	19583	32413	3.33	1.0E-69	AB032873.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
10077	22572	35566	5.1	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2878

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10077	22572	35587	5.1	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP Homo sapiens cDNA clone TCBAP2878
10168	22684	35559	1.41	1.0E-69	AB014807.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10313	22807	35789	0.47	1.0E-69	BF628429.1	EST_HUMAN	602043782F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181325 5'
10751	23275		14.22	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
11745	24144	38768	1.81	1.0E-69	BF125887.1	EST_HUMAN	601782802F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12169	24408		4.69	1.0E-69	AJ809694.1	EST_HUMAN	wf64608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element: contains element MIR repetitive element:
2370	15464	27513	1.52	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4463	17049	29493	1.81	8.0E-70	L77566.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1849	14437	26983	1.85	7.0E-70	AJ497807.1	EST_HUMAN	bm86f01.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2165305 3'
1849	14437	26994	1.85	7.0E-70	AJ497807.1	EST_HUMAN	bm86f01.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2165305 3'
1974	14558	27115	1.64	7.0E-70	AA282956.1	EST_HUMAN	z15f904.1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:713239 5'
2109	14687		3.14	7.0E-70	5031988	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-IR) mRNA
4309	18695	29339	4.83	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5674	18301	30782	5.56	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5674	18301	30783	5.56	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7004	19502	32321	3.22	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
7745	20253	33147	0.87	7.0E-70	11417308	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
8370	20910	33829	2.87	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8370	20910	33830	2.87	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8858	21185	34114	3.59	7.0E-70	M74099.1	NT	Human displacement protein (CCAA1) mRNA
8858	21185	34115	3.59	7.0E-70	M74099.1	NT	Human displacement protein (CCAA1) mRNA
9084	21620	34555	3.99	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9084	21620	34556	3.99	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9356	20285	33184	3.84	7.0E-70	AF133715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9382	20320	33223	2.01	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9382	20320	33224	2.01	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9575	22075	35038	1.33	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
10199	22694	35886	0.81	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10199	22694	35887	0.81	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10953	23468	38492	1.59	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spepin) (SPG4), mRNA
10953	23468	38493	1.59	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spepin) (SPG4), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11468	23918	36986	2.2	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11468	23918	36987	2.2	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
904	13518	26036	2	6.0E-70	4502198	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2182	14756	27328	1.02	6.0E-70	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2551	15115	27685	1.42	6.0E-70	8923889	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2588	15470	27715	1.68	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2588	15470	27716	1.68	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
11758	24161	32255	3.78	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-508 HT0487 Homo sapiens cDNA
6851	19440	32255	163.58	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain, Stratagene (cat#0392806) Homo sapiens cDNA clone HFBDN25
6887	19822	32456	0.79	4.0E-70	AW793226.1	EST_HUMAN	CM4-UJ0003-010300-105-g08 UJ0003 Homo sapiens cDNA
6887	19822	32457	0.79	4.0E-70	AW793226.1	EST_HUMAN	CM4-UJ0003-010300-105-g08 UJ0003 Homo sapiens cDNA
1833	14225	28756	1.19	3.0E-70	BE071798.1	EST_HUMAN	RC0-BT0322-071289-011-e12 BT0322 Homo sapiens cDNA
1633	14225	28757	1.18	3.0E-70	BE071798.1	EST_HUMAN	RC0-BT0322-071289-011-e12 BT0322 Homo sapiens cDNA
6100	18716	31487	0.9	3.0E-70	A1831975.1	EST_HUMAN	W80603.X1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6511	19111	31897	2.36	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302808 5'
6511	19111	31898	2.36	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302808 5'
41	12720	25181	0.89	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
718	13339	25826	11.56	2.0E-70	N42161.1	EST_HUMAN	W07a10.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
718	13339	25827	11.56	2.0E-70	N42161.1	EST_HUMAN	W07a10.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
734	13354	25850	3.41	2.0E-70	A1246899.1	EST_HUMAN	q551h01.X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1059	13684	26175	1.89	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1226	13825	26340	1.29	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1226	13825	26341	1.29	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1776	14368	26912	1.48	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2359	14930		4.22	2.0E-70	AA054010.1	EST_HUMAN	Z48g04.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3698	16289	28758	2.21	2.0E-70	H37898.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3691	16490	28950	0.8	2.0E-70	AL133207.2	NT	Yp58004.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:191599 5'
4123	16716	29172	5.05	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X
							Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5708	18332	30836	8.49	2.0E-70	X72862.1	NT	H. sapiens gene for schwannomin (CS8)
5708	18332	30837	8.49	2.0E-70	X72862.1	NT	H. sapiens gene for schwannomin (CS8)
6351	18858	31735	1.22	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6745	18338	32144	1.97	2.0E-70	D12825.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6773	19365	32176	9.77	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6773	19365	32177	9.77	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7070	18059	30446	1.84	2.0E-70	11422842	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
7434	18958	32823	0.84	2.0E-70	AF288207.1	NT	Homo sapiens cystathionine synthetase mRNA, complete cds, alternatively spliced
7859	20401	33307	0.42	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8184	20705	33821	0.75	2.0E-70	11423599	NT	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
8584	21133	34571	0.8	2.0E-70	H47859.1	EST_HUMAN	y679g02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:183682 5'
9098	21632	35536	0.97	2.0E-70	11526355	NT	Homo sapiens dynactin p82 subunit (LOC51164), mRNA
10044	22539	35536	1.3	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10490	22884	35892	0.8	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
10950	23485	36487	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
10950	23485	36488	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11497	23948	37016	7.73	2.0E-70	4503620	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
12167	24397	30976	2.52	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12167	24397	30977	2.52	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3440	18048		2.73	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9204	21721		0.64	1.0E-70	W85785.1	EST_HUMAN	z555g05.1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:418024 5'
9714	22212		0.81	1.0E-70	AA442292.1	EST_HUMAN	z554g03.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
10814	23335	36348	15.93	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'
6089	18715	31465	9.2	9.0E-71	AI143870.1	EST_HUMAN	q604f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6089	18715	31466	9.2	9.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE. ;
6089	18715	31468	9.2	9.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE. ;
7098	19699	32508	1.82	9.0E-71	AI654903.1	EST_HUMAN	w652c05.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
11399	19699	32508	5.11	9.0E-71	AI654903.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11399	19699	32508	5.11	9.0E-71	AI654903.1	EST_HUMAN	w652c05.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
11399	19699	32508	5.11	9.0E-71	AI654903.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8000	21537		3.85	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.11 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143081 G1143081 STRAIN XA34 POL:
7410	19939	32800	7.39	7.0E-71	AA442230.1	EST_HUMAN	z60h08.1 Scores_NHT Homo sapiens cDNA clone IMAGE:768075 5'
8812	21151	34085	1.34	7.0E-71	AA705487.1	EST_HUMAN	z91a06.s1 Scores_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:462228 3'
11211	23714	36769	6.33	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2261	14825	27401	7.82	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4197	18787	29238	1.17	5.0E-71	AW818405.1	EST_HUMAN	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA
6041	18860	31388	1.72	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6768	18361	32170	1.8	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT1A7), mRNA
7000	19498	32318	0.8	5.0E-71	7692209	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7200	19731	32583	0.87	5.0E-71	11431580	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7520	20040	32908	2.84	5.0E-71	M38108.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7683	20202	33089	0.72	5.0E-71	11528445	NT	Homo sapiens MAGUK protein p65T; Protein Associated with Uns 2 (LOC51878), mRNA
7718	20224	33113	20.65	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8460	21000	33916	0.69	5.0E-71	5483777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8460	21000	33917	0.69	5.0E-71	5483777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
9826	22323		2.26	5.0E-71	X13487.1	NT	Human Prk4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10513	23051	36082	1.87	5.0E-71	6729600	NT	Homo sapiens (GF-II) mRNA-binding protein 3 (KOC1), mRNA
10859	23380	36398					Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PBPB), mRNA
11071	23583	36824	2.24	5.0E-71	11438089	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC883325), mRNA
11706	24119	37152	1.76	5.0E-71	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
108	12784	26287	1.08	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
372	13021	25508	118.83	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
372	13021	25507	116.83	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2911	15528	27898	3.25	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4619	17103	28549	5.18	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5123	17695	30132	6.54	4.0E-71	7857802	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
7977	20519		1.23	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043883 similar to contains PTR5.3 PTR5
							nl45h10.s1 NCI CGAP_P44 Homo sapiens cDNA clone IMAGE:1043883 similar to contains PTR5.3 PTR5
10572	23107	36121	4.09	3.0E-71	AA857683.1	EST_HUMAN	repetitive element;
1273	13889	26389	6.26	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
5623	18155	30570	6.94	2.0E-71	DB7492.1	NT	Human mRNA for KIAA0272 gene, partial cds
5523	18155	30571	6.94	2.0E-71	DB7492.1	NT	Human mRNA for KIAA0272 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10478	22972	36979	2.97	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10478	22972	35980	2.97	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10574	23109	36122	3.75	2.0E-71	BE018477.1	EST_HUMAN	bb31a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN
11454	23904	36971	1.96	2.0E-71	R55926.1	EST_HUMAN	P54727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B ;
11826	24163		10.18	2.0E-71	T05489.1	EST_HUMAN	y177611.r1 Soares breast 2NBH8at Homo sapiens cDNA clone IMAGE:154772 5'
696	13280	26771				EST_HUMAN	yo15a03.s1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:120520 5'
977	13689	26104	2.23	1.0E-71	A1077927.1	EST_HUMAN	contains LOR1.b2 LOR1 repetitive element ;
1139	13742	26261	4.37	1.0E-71	AF205890.1	NT	Homo sapiens neuronal cell death-related protein (LOC51816), mRNA
1395	13978	26506	10.24	1.0E-71	AF012872.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
2129	14707	27278	1.38	1.0E-71	AB017007.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2129	14707	27278	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L18 mRNA, partial cds
2717	15274	27840	3.73	1.0E-71	7657153	NT	Homo sapiens PMS2L18 mRNA, partial cds
3549	16153	28635	1.24	1.0E-71	AF119685.1	NT	Homo sapiens helix/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3668	16269	28730	6.17	1.0E-71	AF248219.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3656	16259	28731	6.17	1.0E-71	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3710	16311	28778	0.95	1.0E-71	BE122850.1	EST_HUMAN	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3710	16311	28778	0.95	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3804	16404	28698	2.11	1.0E-71	AF218904.1	NT	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
4599	17152	28598	2.19	1.0E-71	D28476.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19
4695	17277	28723	0.61	1.0E-71	H23176.1	EST_HUMAN	Human mRNA for KIAA0045 gene, complete cds
6840	18430	32246	1.64	1.0E-71	11426182	NT	ym56h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
7144	19877	32517	1.33	1.0E-71	AB011131.1	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog-like 2 (GCN5L2), mRNA
7352	19878	32743	11.94	1.0E-71	U80793.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
8089	20630	33543	0.87	1.0E-71	AF105287.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8110	20651	33559	2.11	1.0E-71	11426430	NT	Homo sapiens glycyl-protein 2 (GPC2) mRNA, complete cds
8383	20923	33842	3.93	1.0E-71	8922811	NT	Homo sapiens myomesin (M-protein) 2 (185KD) (MYOM2), mRNA
8393	20923	33843	3.93	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9155	21600	34834	0.97	1.0E-71	S72393.1	NT	GSNK2A1-casain kinase II (CKII) subunit alpha [human, Genomic, 18982 nt]
9920	22416	35391	7.06	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
9980	22476		4.9	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10431	22825	35931	1.57	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
10663	23195		6.4	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10762	23286	36288	2.09	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11026	23539	36574	1.82	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11026	23539	36575	1.82	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12208	24432		16.2	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
432	13065	25550	1.33	9.0E-72	A857635.1	EST_HUMAN	w495g03.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element
432	13065	25560	1.33	9.0E-72	A857635.1	EST_HUMAN	w495g03.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element
8259	19868	31638	0.87	8.0E-72	BF035752.1	EST_HUMAN	601458747F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862451 5'
10990	23504	36533	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
10990	23504	36534	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
10990	23504	36535	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4180	18779	29225	1.48	7.0E-72	4501888	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4180	18779	29228	1.48	7.0E-72	4501888	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4180	18779	29227	1.48	7.0E-72	4501888	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7178	19710	32558	3.23	7.0E-72	S41694.1	NT	(pseudogene) PTMAIP2-prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12339	24521		1.9	7.0E-72	F26259.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051G02
8324	20865		4.31	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
67	12746	25223	1.56	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
67	12746	25224	1.56	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
68	12746	25223	10.23	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
68	12746	25224	10.23	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1178	13780		2.72	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7030	18564	32391	1.36	5.0E-72	AU128594.1	EST_HUMAN	AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8711	21260	34173	3.18	5.0E-72	AW181274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782584 5' similar to
9871	22388	35348	0.62	5.0E-72	AV724632.1	EST_HUMAN	TR:Q99788 Q99785 HYPOTHEICAL 32.4 KD PROTEIN; contains element MSR1 repetitive element;
11122	23630	36672	3.44	5.0E-72	BF331671.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAK801 5'
11122	23630	36672	3.44	5.0E-72	BF331671.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11500	23949	37018	1.02	5.0E-72	BE208545.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11500	23949	37019	1.62	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823808 5'
11895	25047		2.89	5.0E-72	BE928845.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823808 5'
4948	17523		1.21	4.0E-72	11034844	NT	QV1-BT0632-280800-342-010 BT0632 Homo sapiens cDNA
5422	17979	30387	1.05	4.0E-72	AB033104.1	NT	Homo sapiens hypothetical protein dJ1057820.2 (DJ1057820.2), mRNA
5668	18283	30781	0.72	4.0E-72	AF170025.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
6674	19270	32075	0.81	4.0E-72	T87847.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-65 (ZFP65) mRNA, alternatively spliced, complete cds
7439	19683	32829	3.01	4.0E-72	5728887	NT	yd83a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
8898	22188	35171	1.64	4.0E-72	8823669	NT	SP:AA4282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;
							Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10318	22812	35807	0.98	4.0E-72	A1248798.1	EST_HUMAN	qh87c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to
11402	23853	36918	7.8	4.0E-72	H79421.1	EST_HUMAN	TR:Q14488 Q14488 SPLICING FACTOR, (1); contains Alu repetitive element; contains element L1 repetitive element;
11528	23978	37048	2.48	4.0E-72	T81910.1	EST_HUMAN	yu28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
12283	24473	30933	4.5	4.0E-72	AJ277548.2	NT	yd28d08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109849 3'
22	12701	25157	3.55	3.0E-72	5031976	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
838	13549		1.46	3.0E-72	AA723823.1	EST_HUMAN	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
							ah03a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310280 3'
1186	13787	26307	7.76	3.0E-72	U18308.1	NT	Homo sapiens chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1186	13797	26308	7.76	3.0E-72	U18308.1	NT	Homo sapiens chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1235	13834	26348	1.33	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1235	13834	26349	1.33	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1567	14189	26890	0.98	3.0E-72	BE242161.1	EST_HUMAN	TCAAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1252
3110	16725	28186	13.28	3.0E-72	AJ228043.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3317	18927	28404	2.84	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3885	18494	28856	2.71	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4508	17093	28540	0.94	3.0E-72	AF143892.1	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4509	17093	28541	0.94	3.0E-72	AF143892.1	NT	Homo sapiens thioredoxin-like protein (TXNL) gene, exon 3
4843	17223	28879	2.89	3.0E-72	11416186	NT	Homo sapiens thioredoxin-like protein (TXNL) gene, exon 3
6711	18337		1.07	3.0E-72	4759093	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
6134	18748	31504	1.88	3.0E-72	AF073387.1	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6134	18748	31505	1.88	3.0E-72	AF073387.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6314	18921	31897	4.49	3.0E-72	AB078004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6314	18921	31898	4.49	3.0E-72	AB078004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6728	18320	32125	3.59	3.0E-72	4826987	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7685	20100	32975	1.92	3.0E-72	U80017.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
8118	20657	33568	1.52	3.0E-72	6031892	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
10328	22822	35818	1.87	3.0E-72	X98289.1	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
12174	24413	30948	2.03	3.0E-72	AB011399.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
8113	18729	31482	1.41	2.0E-72	11426871	NT	Homo sapiens gene for AF-8, complete cds
8025	21862	34491	0.76	2.0E-72	BF308580.1	EST_HUMAN	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
10818	23161	36163	2.52	2.0E-72	AA789277.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
12260	24470	30930	4.78	2.0E-72	BF308580.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
2120	14898	27267	1.03	1.0E-72	AA846225.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
5940	18560	31288	4.04	1.0E-72	7857878	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone 1391609 3' similar to gb:U02087 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
6878	18272	32078	1.18	1.0E-72	11321878	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
6878	18272	32077	1.18	1.0E-72	11321878	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
6744	24768	32143	1.3	1.0E-72	AV751818.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
7633	20146	33028	3.81	1.0E-72	BE175434.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
7633	20145	33027	3.81	1.0E-72	BE175434.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9510	22010	34888	7.2	1.0E-72	AF222742.1	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9510	22010	34866	7.2	1.0E-72	AF222742.1	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
1508	14100	26837	1.28	9.0E-73	AW374868.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6190	18900	31670	0.98	9.0E-73	11525893	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
10828	23350		27.89	9.0E-73	11424069	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1078	13680	28160	1.62	8.0E-73	AW071785.1	EST_HUMAN	wa55cd06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q69050
3332	18942	28417	0.61	8.0E-73	11435180	NT	Q58050 HYPOTHETICAL PROTEIN MJ1656 ;
5783	18394	31108	0.76	8.0E-73	4805798	NT	Homo sapiens gephyrin (GPH), mRNA
6687	19283	32088	4.21	8.0E-73	11423469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A), mRNA
8039	20581	33488	2.58	8.0E-73	AF113129.1	NT	Homo sapiens lysocysteine homologue (LOC57151), mRNA
						NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9275	21801	34751	5.4	8.0E-73	BE018900.1	EST_HUMAN	bb82a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:XD4098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9656	22184	35123	1.83	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9655	22154	35124	1.83	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12324	24511	30919	7.07	8.0E-73	11418189	NT	Homo sapiens thyroid autotransferin 70kD (Ku antigen) (G22P1), mRNA
1173	13776	26285	1.37	7.0E-73	8823280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3340	15950	28428	1.27	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
						NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
4298	18884	29329	2.59	7.0E-73	AF018413.1	NT	Homo sapiens chromosome 21 segment HS21C082
5079	17652		1.64	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C018
169	12832		2.14	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C082
7224	19755	32810	3.52	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0404-020300-137-403 HT0404 Homo sapiens cDNA
8460	18095	30413	1.78	4.0E-73	11422169	NT	Homo sapiens HELG protein (FAM4A1), mRNA
1902	14487	27048	1.78	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1802	14487	27049	1.78	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
						NT	zn195604.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:585950 3' similar to
8789	19390	32205	1.03	3.0E-73	AA136403.1	EST_HUMAN	gb:Z23084_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8993	21232	34152	0.83	3.0E-73	AV728428.1	EST_HUMAN	AV728428 HTC Homo sapiens cDNA clone HTCAAF071 5'
8993	21232	34153	0.83	3.0E-73	AV728428.1	EST_HUMAN	AV728428 HTC Homo sapiens cDNA clone HTCAAF071 5'
11478	23928		1.68	3.0E-73	A1004040.1	EST_HUMAN	cu11d02.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1825955 3'
12579	24875		1.34	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12683	24877		1.87	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
884	13488	26018	2.4	2.0E-73	AF136897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1889	14571		2.46	2.0E-73	AW89081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
3215	18827	28305	2.05	2.0E-73	4502592	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3804	18208	28886	0.68	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3604	18208	28887	0.68	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
8607	19204	32011	6.35	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1561 protein, partial cds
8601	18392	32207	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
8601	18392	32208	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
9451	21977	34928	0.68	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9451	21977	34929	0.68	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10320	22814	36810	1.46	2.0E-73	4604168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10391	22885	35880	1.18	2.0E-73	11469980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10391	22885	35881	1.18	2.0E-73	11469980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10633	23461	36472	3.48	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10633	23461	36473	3.48	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10662	23477	36502	1.85	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1069 protein, partial cds
12098	14571		2.75	2.0E-73	AW89081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
12665	24735	30825	1.41	2.0E-73	AB029016.1	NT	Homo sapiens mRNA for KIAA1063 protein, partial cds
1818	14408	28853	1.74	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2626	16089	27681	0.97	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
6500	19100	31885	1.05	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-111199-042-h10 HT0282 Homo sapiens cDNA
9419	21928	34874	1.41	1.0E-73	AU147427.1	EST_HUMAN	qg81b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838637 5' similar to contains element
11325	23023	38032	3.93	1.0E-73	BE385477.1	EST_HUMAN	MER22 repetitive element
770	13389	28888	2.42	8.0E-74	4557428	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6073	18690	31435	1.87	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3428 nt]
6073	18690	31436	1.87	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3428 nt]
1982	14574	27133	3.28	7.0E-74	AJ001989.1	NT	Homo sapiens NKG2D gene, exon 10
3371	19979	28458	1.18	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
9187	21744	34687	2.49	7.0E-74	BE967432.1	EST_HUMAN	601849284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932897 5'
12323	24510	30918	6.87	7.0E-74	BE268305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
1181	13764	28276	4.55	6.0E-74	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14261	26764	0.9	6.0E-74	AW263177.1	EST_HUMAN	3x78q07.x1 Spares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700638 3'
2355	14926	27469	10.83	6.0E-74	BE398280.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2355	14928	27500	10.83	6.0E-74	BE398280.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2889	15508	27977	1.22	6.0E-74	AW014039.1	EST_HUMAN	U1H-B10-aah-h-03-O-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3'
2889	15508	27978	1.22	6.0E-74	AW014039.1	EST_HUMAN	U1H-B10-aah-h-03-O-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3'
3775	16375	28840	1.64	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3775	16375	28841	1.64	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5177	17744	30172	0.85	6.0E-74	4759135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5177	17744	30173	0.85	6.0E-74	4759135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5568	18169	30847	3.28	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
938	13551	26067	1.37	5.0E-74	AW020988.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2728	15281		4.42	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5603	18232	30682	1.98	6.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5681	18583	31317	11.6	5.0E-74	X89870.1	NT	H. sapiens mRNA for TPCR18 protein
6004	18624	31359	8.99	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, end translated products
6087	18684	31426	2.33	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6087	18684	31427	2.33	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6978	19582	32377	3.35	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7880	20522	33428	3.2	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10614	23147	36158	1.98	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10614	23147	36159	1.98	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
301	12956	26446	2.66	4.0E-74	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
895	13489	26017	9.19	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
2005	14587	27146	2.26	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2005	14587	27147	2.26	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2117	14695	27263	2.03	4.0E-74	4506182	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2117	14695	27264	2.03	4.0E-74	4506182	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2178	14755	27325	1.21	4.0E-74	AB032684.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2471	15038	27606	0.89	4.0E-74	AJ008978.1	NT	Homo sapiens PUP gene

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3127	15741	28210	4.58	4.0E-74	AJ009376.1	NT	Homo sapiens PLP gene
3580	16184	28868	1.14	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4136	16728	29181	1.01	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4856	17237	28892	1.71	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4720	17301	29748	0.79	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
6168	17737	30184	0.61	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
8486	21025		21.13	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8510	21049	33971	0.47	3.0E-74	8986912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
9294	21894	34841	2.47	3.0E-74	M78884.1	EST_HUMAN	EST01132 Subretinal Hippocampus, Stragena (cat. #838205) Homo sapiens cDNA clone HHCPF01
10241	22736	35728	2.42	3.0E-74	AA801493.1	EST_HUMAN	not7g05.at NC1_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100884 3'
993	13606	28119	172.8	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
993	13606	28120	172.8	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1217	13817	28332	0.82	2.0E-74	AF020082.1	NT	Human endogenous retrovirus HERV-K-T47D
1287	13882	26407	1.64	2.0E-74	A1950528.1	EST_HUMAN	W051607.x1 NC1_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG95_HUMAN
1639	14231	28784	4.17	2.0E-74	4885188	NT	W08379 GOLGIN-95, contains element MER22 repetitive element
1639	14231	28785	4.17	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
6149	17719	30149	2.97	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
6149	17719	30150	2.97	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
6155	17725	30158	3.93	2.0E-74	J02863.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5968	24752	31322	1.72	2.0E-74	BE711134.1	EST_HUMAN	RC8-HT0878-220500-011-Q03 HT0878 Homo sapiens cDNA
6055	24755	31412	2.03	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6055	24755	31413	2.03	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6120	24755	31412	2.72	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6120	24755	31413	2.72	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
7180	19692	32538	1.3	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
7881	20423	33331	1.88	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1305 protein, partial cds
8304	21904	34953	7.78	2.0E-74	AA163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12033	24323		3.9	2.0E-74	AA198181.1	EST_HUMAN	zp86a08.a1 Stragena muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
12005	24889	30882	1.89	2.0E-74	BF665568.1	EST_HUMAN	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276569 5'
67	12737	28207	2.04	1.0E-74	7657334	NT	Homo sapiens Mississippin/NIK-related Kinase (MINK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
359	13008	25491	4.11	1.0E-74	AW818405.1	EST_HUMAN	QV4-ST0234-181189-037-405 ST0234 Homo sapiens cDNA
526	13157	26639	0.92	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028). mRNA
532	13163	25844	10.17	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
627	13264	26728	1.88	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1037	13647	26159	2.13	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2268	14842	27419	3.73	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3173	15786	28268	2.7	1.0E-74	4758997	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3684	16682	28064	0.63	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3694	16592	28065	0.63	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4040	16638	28108	6.11	1.0E-74	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C068
4137	16729	28182	0.78	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-408 BT0642 Homo sapiens cDNA
4354	16941	28383	0.75	1.0E-74	BE487786.1	EST_HUMAN	h273h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:80511.12
6361	17911	30326	1.87	1.0E-74	D53327.1	NT	CE17351 ;
6808	18387	32211	1.51	1.0E-74	M89914.1	NT	Homo sapiens DCCR1 mRNA, partial cds
7622	20135	33013	1.23	1.0E-74	11417977	NT	Human neurofibromin (NF1) gene, complete cds
8000	20542	33444	0.74	1.0E-74	BE549106.1	EST_HUMAN	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8000	20542	33445	0.74	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456280 5'
8740	21279	34202	7.81	1.0E-74	AF214592.1	NT	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8768	21307	34230	0.81	1.0E-74	BF351951.1	EST_HUMAN	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
10378	22870	35863	1.37	1.0E-74	11420549	NT	MRO-HT0559-230500-021-403 HT0559 Homo sapiens cDNA
11659	24096	37144	1.95	1.0E-74	11417856	NT	Homo sapiens hypothetical protein FLJ10783). mRNA
11748	24145		3.39	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12400	24560		1.59	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
2870	15228		4.08	8.0E-75	AF176228.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12056	24338		2.18	8.0E-75	AL163202.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5376	17895		1.01	6.0E-75	AA789285.1	EST_HUMAN	Homo sapiens DNA cytosine-6 methyltransferase 3B (DNMT3B) mRNA, complete cds
8839	21378	34301	2.15	5.0E-75	BE272325.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
9045	21552	34511	0.82	5.0E-75	AA132611.1	EST_HUMAN	q128c06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391828 3' similar to TR:Q16377 Q16377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN ;
9122	21658	34589	0.8	5.0E-75	BE561655.1	EST_HUMAN	2017403.1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
9122	21658	34600	0.8	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9295	21895	34842	1.39	5.0E-75	BF690254.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687459 5'
							602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10133	22628	36816	2.5	5.0E-76	A1838623.1	EST_HUMAN	131c12.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2242380 3' similar to TR:P07381 P07381
117	12788	28270	1.81	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN ;
484	13117		1.21	4.0E-75	N36757.1	EST_HUMAN	QV1-BT0632-210200-079-402 BT0632 Homo sapiens cDNA
1802	14392	28837	1.43	4.0E-76	AW897230.1	EST_HUMAN	y80h08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA IMAGE:268055 5'
2874	15482	27882	5.4	4.0E-76	BE40484.1	EST_HUMAN	CMQ-NN0007-150400-335-411 NN0007 Homo sapiens cDNA
5720	18346	31048	0.71	4.0E-76	11417948	NT	601303868F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5720	18346	31048	0.71	4.0E-76	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8415	18018	31801	5.28	4.0E-75	5578487	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8856	18444	32281	1.84	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10585	23101	38115	8.22	4.0E-76	7689606	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1040	13850	28162	2.75	3.0E-76	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1041	13850	28162	9.08	3.0E-76	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1878	14492	27019	2.54	3.0E-76	AB011163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2158	14735	27308	1.47	3.0E-76	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
2487	15034	27601	3.11	3.0E-75	4759163	NT	Homo sapiens synaptosomal-associated protein, 28kD (SNAP28) mRNA
3056	16672	28148	0.65	3.0E-76	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3223	16835	28313	1.12	3.0E-76	AB011163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3393	16001	28480	0.83	3.0E-76	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3393	16001	28481	0.83	3.0E-76	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4530	17114	28558	0.67	3.0E-75	7682421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5387	17927		0.61	3.0E-76	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5458	18068	30408	1.01	3.0E-76	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5458	18068	30410	1.01	3.0E-76	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6867	19601	32432	1.42	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6867	19601	32433	1.42	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7189	19721	32568	4.6	3.0E-75	7682209	NT	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA
7189	19721	32568	4.6	3.0E-75	7682209	NT	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA
7618	20131	33008	3.35	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7618	20131	33007	3.35	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8915	21453	34374	1.23	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9598	22098	35059	0.85	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKLCHL), mRNA
10435	22928	36936	3.76	3.0E-75	11436430	NT	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
5853	18477		1.45	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cDABED02 5'
8686	21224	34144	2.43	2.0E-75	AI311783.1	EST_HUMAN	q981602.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916898 3' similar to TR:Q68386 Q68388
2341	14912	27485	4.05	1.0E-75	AW168135.1	EST_HUMAN	POLJENV GENE:
2973	15589	28072	3.23	1.0E-75	X62221.1	NT	x68002.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2832707 3' similar to contains P TR7.11
6366	17816	30331	0.57	1.0E-75	BE894192.1	EST_HUMAN	PTR7 repetitive element:
8353	20893		13.67	1.0E-75	AA390270.1	EST_HUMAN	H sapiens ERCC2 gene, exons 1 & 2 (partial)
9348	21863	34812	4.14	1.0E-75	BF313646.1	EST_HUMAN	z157603.s1 Soares_besla_NHT Homo sapiens cDNA clone IMAGE:3922303 5'
9348	21863	34813	4.14	1.0E-75	BF313646.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
10763	23287		6.58	1.0E-75	AA684377.1	EST_HUMAN	601600284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128878 5'
10970	23485	36513	3.06	1.0E-75	AF223391.1	NT	601600284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128878 5'
11945	17916	30331	2.58	1.0E-75	BE894192.1	EST_HUMAN	ac77608.s1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:8685599 3'
48	12728	25191	2.19	9.0E-76	AI652848.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
48	12728	25192	2.19	9.0E-76	AI652848.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
9815	22313	35294	62.44	9.0E-76	M12637.1	NT	w630b10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
154	12817	25305	9	8.0E-76	AF154830.1	NT	TRAP1;
974	13588	26100	10.38	8.0E-76	4504374	NT	Human ferritin Heavy subunit mRNA, complete cds
974	13588	26101	10.38	8.0E-76	4504374	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
2935	15551	28028	1.25	8.0E-76	7706724	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
6319	18926	31703	5.69	8.0E-76	11421442	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
7500	20022	32885	1.84	8.0E-76	1143215	NT	Homo sapiens mediator (Sur2), mRNA
7507	20064	32860	0.84	8.0E-76	11419212	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
8237	20778	33699	0.81	8.0E-76	11419981	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
10280	22775	35784	1.25	8.0E-76	M13702.1	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
10546	23083	36097	7.28	8.0E-76	10442821	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
12305	24501		2.28	8.0E-76	11417862	NT	Homo sapiens adenosine deaminase (ADA) gene, complete cds
							Homo sapiens baculoviral IAP repeat-containing 8 (BIRC8), mRNA
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
808	13425	26931	2.84	7.0E-78	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (OLD) mRNA
3333	15943	28418	3.23	7.0E-78	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3339	18949	28426	6.78	7.0E-78	4505052	NT	Homo sapiens lymphocyte antigen 76 (LY76) mRNA, and translated products
3378	15988	28487	1.89	7.0E-78	4797915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2, translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4481	17047	29480	6.32	7.0E-78	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4481	17047	29481	6.32	7.0E-78	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1277	13872		30.59	6.0E-78	BE390253.1	EST_HUMAN	601312010F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11340	23038	36047	2.97	6.0E-78	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508029 5'
1988	14568	27128	8.39	6.0E-78	D83874.1	NT	Human mRNA for HMG-1, complete cds
1988	14568	27129	8.39	5.0E-78	D83874.1	NT	Human mRNA for HMG-1, complete cds
1988	14568	27130	8.39	5.0E-78	D83874.1	NT	Human mRNA for HMG-1, complete cds
3242	16884	28336	0.88	4.0E-78	BE814096.1	EST_HUMAN	QV3-BN0047-270700-263-g08 BN0047 Homo sapiens cDNA
5474	18108	30427	1.22	4.0E-78	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3974470 5'
9937	22432	35407	5.79	4.0E-78	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujwara) Homo sapiens cDNA clone GEN-178G01 5'
9937	22432	35408	6.79	4.0E-78	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujwara) Homo sapiens cDNA clone GEN-178G01 5'
657	13280	25759	1.63	3.0E-78	BF516282.1	EST_HUMAN	UI-H-BW1-anz-b-04-Q-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083882 3'
657	13280	25760	1.63	3.0E-78	BF516282.1	EST_HUMAN	UI-H-BW1-anz-b-04-Q-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083882 3'
1643	14235	26769	7.45	3.0E-78	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1643	14235	26770	7.45	3.0E-78	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3476	16082	28556	5.2	3.0E-78	BF376689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3476	16082	28556	5.2	3.0E-78	BF376689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5447	18018	37140	2.41	3.0E-78	Z41314.1	EST_HUMAN	HSC2QD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
5908	18530	31255	1.08	3.0E-78	AA160811.1	EST_HUMAN	z673c07.1 Stragene pancreas (#837209) Homo sapiens cDNA clone IMAGE:692624 5' similar to gb:L32878 MIXED LINEAGE KINASE 1 (HUMAN);
8508	19108	31891	7.49	3.0E-78	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
8091	20632	33545	1.03	3.0E-78	N42871.1	EST_HUMAN	W20g10.r1 Soares melanocyte 2NbfHM Homo sapiens cDNA clone IMAGE:271842 5'
9832	22132	35097	2.91	3.0E-78	AW286353.1	EST_HUMAN	xe49h01.s1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
9836	22155	35125	1.11	3.0E-78	AA442309.1	EST_HUMAN	z64d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2773009 3'
9836	22155	35126	1.11	3.0E-78	AA442309.1	EST_HUMAN	z64d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2773009 3'
11849	24884	30708	1.73	3.0E-78	AW987984.1	EST_HUMAN	EST380058 IMAGE resequences, MAGI Homo sapiens cDNA
11760	25090	30501	4.85	3.0E-78	AW658455.1	EST_HUMAN	EST388525 IMAGE resequences, MAGD Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
303	12958	25448	1.1	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
364	13013	25495	2.12	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
364	13013	25496	2.12	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
486	13119		1.12	2.0E-76	4557602	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
616	13243	25717	1.45	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1088	13873	26186	1.57	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1583	14178	26708	0.89	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1583	14178	26709	0.89	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1972	14556	27113	1.04	2.0E-76	AA253954.1	EST_HUMAN	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2867	15485	27958	2.64	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3336	15946	28422	2.3	2.0E-76	AA448992.1	EST_HUMAN	z66402.81 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:760988 3' similar to SW:ITB5_HUMAN
3336	15946	28423	2.3	2.0E-76	AA448992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3832	16431	28893	0.7	2.0E-76	AA40700.1	EST_HUMAN	z66402.81 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:760988 3' similar to SW:ITB5_HUMAN
4215	12958	25448	0.62	2.0E-76	D84295.1	NT	CE00281 ;
5082	17855	30096	7.33	2.0E-76	AW879818.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
5512	18145		0.88	2.0E-76	AF127845.1	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5803	18428	31147	4.95	2.0E-76	AB028004.1	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
7442	18968	32833	0.72	2.0E-76	11421326	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7658	20170	33057	1.84	2.0E-76	11427410	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
10182	22677	35670	7.63	2.0E-76	11437211	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
10801	23324	36334	2.79	2.0E-76	7548807	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
4385	16972	29420	4.17	1.0E-76	D63874.1	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA
4385	16972	29421	4.17	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5639	18268	30741	5.55	1.0E-76	BE786537.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
6391	18994		0.7	1.0E-76	AA333207.1	EST_HUMAN	601589898F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
7003	19501	32320	4.41	9.0E-77	BE86525.1	EST_HUMAN	EST37301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
11116	23625	36687	1.88	9.0E-77	4508022	NT	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
12474	24598		1.9	9.0E-77	BE410384.1	EST_HUMAN	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C) mRNA
200	12860	25344	1.36	8.0E-77	R83144.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636783 5'
							yp1102.1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:187155 5' similar to
							SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4620	17203	29652	1.27	8.0E-77	BF205181.1	EST_HUMAN	60186828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5844	18273	30747	2.93	8.0E-77	4508230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mow04 homolog) (P3MMD7) mRNA
11264	23792	36849	2.67	8.0E-77	AA019770.1	EST_HUMAN	2862602.1 Source refina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11264	23792	36850	2.67	8.0E-77	AA019770.1	EST_HUMAN	2862602.1 Source refina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12451	24595	30916	21.88	8.0E-77	R00245.1	EST_HUMAN	y63904.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ;
1973	14557	27114	2.58	7.0E-77	AA625755.1	EST_HUMAN	zu81g01.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:746392 3'
2455	15022	27593	1.98	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2455	15022	27594	1.98	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
284	12940	25426	3.62	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1181	13783	26293	3.04	6.0E-77	AW957753.1	EST_HUMAN	EST368823 MAGE resequences, MAGE Homo sapiens cDNA
1500	14183	26716	2.97	6.0E-77	AI204098.1	EST_HUMAN	q67h12.x1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1745083 3'
156	12819	25307	3.77	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
160	12819	25308	3.77	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1279	13874	26394	1.69	5.0E-77	AF041016.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1404	13997	26526	1.93	5.0E-77	4557260	NT	Homo sapiens diantegrin and metalloprotease domain 10 (ADAM10) mRNA
2792	15345	27914	0.98	5.0E-77	4503180	NT	Homo sapiens cullin 1 (CUL1) mRNA
3574	16178	28691	1.03	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4813	17361	29842	1.08	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4813	17361	29843	1.08	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3) mRNA
5071	17844	30088	2.22	6.0E-77	AL043953.1	EST_HUMAN	DKF2p434G1728_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKF2p434G1728 5'
5419	17976	30384	1.77	6.0E-77	AA861184.1	EST_HUMAN	elk33a05.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1407728 3' similar to contains Alu repetitive element; contains element PTR7 PTR7 repetitive element ;
8879	19813	32447	0.71	6.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7365	19892	32765	0.68	6.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
7592	19892	32765	0.75	6.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8309	20850	33773	1.07	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8309	20850	33774	1.07	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9489	21945	34893	3.52	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9489	21945	34894	3.52	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10385	22879	35972	0.51	6.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
10385	22879	35973	0.51	6.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
2015	14597	27160	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA

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2015	14597	27161	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and maf-like transposase fusion gene (SETMAR) mRNA
10189	22884	35675	0.82	3.0E-77	H65187.1	EST_HUMAN	y64g01.r1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10189	22884	35678	0.82	3.0E-77	H65187.1	EST_HUMAN	y64g01.r1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10493	22887	35994	0.51	3.0E-77	A1017333.1	EST_HUMAN	ox31h07.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10493	22887	35995	0.51	3.0E-77	A1017333.1	EST_HUMAN	ox31h07.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10754	23278	36291	4.39	3.0E-77	BF350917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1396	13990	28517	1.82	2.0E-77	AV784817.1	EST_HUMAN	AV784817 MDS Homo sapiens cDNA clone MDSBT10 5'
1479	14072	28611	3.43	2.0E-77	AW697712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
2138	14718	27283	1.24	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2151	14728	27301	2.37	2.0E-77	7708316	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2830	18471	27780	2.28	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2830	18471	27781	2.28	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4103	18689	28153	1.36	2.0E-77	BE044318.1	EST_HUMAN	h043005.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2 HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4504	17088	28538	0.85	2.0E-77	A1813519.1	EST_HUMAN	hw22g02.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2280466 3' similar to TR:O65245
4504	17088	28537	0.85	2.0E-77	A1813519.1	EST_HUMAN	hw22g02.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2280466 3' similar to TR:O65245
4701	17283		1.38	2.0E-77	4504089	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4883	17458	28910	4.3	2.0E-77	AA653025.1	EST_HUMAN	ns88g12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL28_HUMAN
6108	18725	31478	1.78	2.0E-77	BE288940.1	EST_HUMAN	P47914 80S RIBOSOMAL PROTEIN L28, [1]: contains element MSR1 repetitive element ;
6320	18827	31704	1.88	2.0E-77	BE787143.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
7226	19757	32612	14.03	2.0E-77	A1833003.1	EST_HUMAN	601478802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878505 5'
8468	21008	33924	0.9	2.0E-77	A1362707.1	EST_HUMAN	at74809.x1 Barrelet colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
9447	21873	34824	4.56	2.0E-77	U50321.1	NT	Q13311 TAX1-BINDING PROTEIN TXBP151, [1]:
9447	21873	34825	4.56	2.0E-77	U50321.1	NT	qy70c08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F28D11.1
9808	22403	35377	0.55	2.0E-77	BF310349.1	EST_HUMAN	CE05769 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
						NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
						NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
						EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'

Table 4

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9008	22403	35378	0.55	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
47	12726	25197	1.39	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
47	12726	25198	1.39	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
294	12950	25437	2.09	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nehdn-ii, Alzheimer disease) (APP), mRNA
294	12950	25438	2.09	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nehdn-ii, Alzheimer disease) (APP), mRNA
908	15428	26041	2.96	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nehdn-ii, Alzheimer disease) (APP), mRNA
908	15428	26042	2.96	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nehdn-ii, Alzheimer disease) (APP), mRNA
1963	14547	27104	1.41	1.0E-77	AW058119.1	EST_HUMAN	ww63605.xt Soares_thymus_NHFTn Homo sapiens cDNA clone IMAGE:2356160 3'
2488	15053	27626	0.89	1.0E-77	AB026024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3081	15698	28188	2.82	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4445	17031	29472	3.95	1.0E-77	7708290	NT	Homo sapiens CGI-60 protein (LOC31626), mRNA
4622	17205	29854	20.39	1.0E-77	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21 q22; segment 1/3
4755	17336	29780	3.41	1.0E-77	9552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-axon4, mRNA
6098	17180	29827	0.59	1.0E-77	4768093	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
6228	17792	30211	1.05	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
6228	17792	30212	1.05	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5387	17946	31449	4.13	1.0E-77	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6086	18702	31450	1.46	1.0E-77	AF088944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6108	18808	31577	1.4	1.0E-77	M25844.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6575	19173	31972	1.45	1.0E-77	4885182	NT	Human von Willebrand factor gene, exon 20
7114	19454	32270	15.68	1.0E-77	5881412	NT	Homo sapiens diaphanous (Draophila, homolog) 1 (DIAPH1), mRNA
7881	20173	33080	0.92	1.0E-77	11420159	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7740	20248	33141	0.78	1.0E-77	X04671.1	NT	Homo sapiens cullin 1 (CUL1), mRNA
9189	21708	34648	1.31	1.0E-77	X94354.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9189	21708	34650	1.31	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10416	22910	35909	1.01	1.0E-77	AB026898.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10416	22910	35910	1.01	1.0E-77	AB026898.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10958	23471	36498	2.92	1.0E-77	11433426	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10444	22938	36948	2.4	9.0E-78	AW753302.1	EST_HUMAN	Homo sapiens malingoma expressed antigen 8 (colled-ool proline-rich) (MGEA8), mRNA
							RC3-CT0294-280898-011-905 GT0254 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6574	19172	31970	4.74	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6574	19172	31971	4.74	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e08 ET0023 Homo sapiens cDNA
89	12785	26248	1.48	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
89	12785	26249	1.48	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3356	16994	28441	0.72	6.0E-78	BF344101.1	EST_HUMAN	602016926F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4162511 5'
6877	19273		2.29	6.0E-78	11422710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
234	12894	25377	4.78	6.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2597	16159	27727	4.1	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2600403 5' similar to WP:Y48B8A.6
3432	16040	28522	3.88	5.0E-78	M59596.1	NT	CE22121:
6807	18236	30686	2.29	5.0E-78	AF038536.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5764	18390	31102	24.58	5.0E-78	11416885	NT	Homo sapiens Basal's macular dystrophy related protein mRNA, partial cds
7208	19739	32593	2.2	5.0E-78	AW93120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kd (TGFB1), mRNA
9012	21549	34478	6.88	5.0E-78	U60899.1	NT	EST368160 MAGE resequences, MAGB Homo sapiens cDNA
9013	21550	34479	3.6	5.0E-78	BE860836.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manB) gene, exon 7
1178	13778	26288	1.64	4.0E-78	AL043314.2	EST_HUMAN	601648081F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1565	14157	26898	1.99	4.0E-78	AL355841.1	NT	DKFZp434N0323_J1 434 (synonym: hras3) Homo sapiens cDNA clone DKFZp434N0323 5'
2357	14928	27602	2.97	4.0E-78	AF107405.1	NT	Novel human gene mapping to chromosome 22
4414	16998	29441	1.23	4.0E-78	7656876	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4887	17462	29915	1.91	4.0E-78	4505806	NT	Homo sapiens sycylin (LOC30818), mRNA
4887	17482	29916	1.91	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5941	18561	31280	0.97	4.0E-78	11420732	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
7502	20024	32888	0.77	4.0E-78	4508736	NT	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
8787	21326	34250	1.51	4.0E-78	AF012872.1	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
8787	21326	34251	1.51	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9290	21890	34837	0.61	4.0E-78	11417251	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
10341	22835	35829	2.03	4.0E-78	11560161	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10341	22835	35830	2.03	4.0E-78	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10841	23173	36185	1.67	4.0E-78	11428810	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11297	23749	36808	2.09	4.0E-78	AF169748.1	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (RFXANK), mRNA
11432	23882	36848	4.15	4.0E-78	X05944.1	NT	Homo sapiens e-Cadherin (CABP1) mRNA, complete cds
12337	24520	30923	4.58	4.0E-78	AB011399.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
172	12836	26318	2.42	3.0E-78	AF095601.1	NT	Homo sapiens gene for AF-6, complete cds
							Homo sapiens eRF1 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
172	12835	25319	2.42	3.0E-78	AF085901.1	NT	Homo sapiens eRF1 gene, complete cds
3827	16427		1.16	3.0E-78	AU140804.1	EST_HUMAN	AU140804 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
4180	16486	28947	0.76	3.0E-78	4507334	NT	Homo sapiens synapocin 1 (SYN1), mRNA
10188	22881		5.78	3.0E-78	BE144758.1	EST_HUMAN	QMO-HT0180-041088-065-c07 HT0180 Homo sapiens cDNA
10860	23381	38400	6.65	3.0E-78	BE166318.1	EST_HUMAN	QMO-HT0387-150200-114-q08 HT0387 Homo sapiens cDNA
3155	18769		2.54	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4086	16882		1.8	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7483	20006	32870	1.38	2.0E-78	AW402308.1	EST_HUMAN	UI-HF-BKO-est-g-10-q-UJr1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7483	20006	32871	1.38	2.0E-78	AW402308.1	EST_HUMAN	UI-HF-BKO-est-g-10-q-UJr1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7714	20223	33110	3.47	2.0E-78	BF889800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288599 5'
7884	20526	33432	1.73	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8389	20929	33848	1.8	2.0E-78	AI557409.1	EST_HUMAN	P2.1_16_B07.7 tumor2 Homo sapiens cDNA 3'
8389	20929	33849	1.8	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16_B07.7 tumor2 Homo sapiens cDNA 3'
10659	23474	38499	3.39	2.0E-78	AI97897.1	EST_HUMAN	q150H05.X1 NCL CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1859981 3' similar to WP:R60.1
11003	23517	36552	3.47	2.0E-78	N68951.1	EST_HUMAN	CE083235 PROTEIN KINASE;
6508	18141	30553	2.83	1.0E-78	11417304	NT	za48f12.e1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:285823 3'
7039	18055	30478	1.91	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51308), mRNA
8100	20841		2.25	1.0E-78	U52373.1	NT	AV648699 GLC Homo sapiens cDNA clone GLCBMC01 3'
11832	24197	31037	2.17	1.0E-78	11430460	NT	Human serine/threonine Kinase MNB (mnb) mRNA, complete cds
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11828	24261	31014	1.41	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC53140), mRNA
4808	17388	29836	4.05	9.0E-79	11825891	NT	Homo sapiens peptide YY (PYY), mRNA
4888	17562	30008	3.34	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-080300-014-c12 BN0074 Homo sapiens cDNA
5024	18253	30722	13.77	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6482	18083	31864	2.48	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
6731	18025	32129	1.43	9.0E-79	11430822	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA
7388	24781		0.88	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7576	20091	32968	0.89	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7575	20091	32969	0.89	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7612	20125	33002	0.72	9.0E-78	D30858.1	NT	Human T-cell mRNA for glycyl tRNA synthetase, complete cds
8287	20828	33748	0.56	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8287	20828	33749	0.56	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8993	21631	34460	7.08	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8993	21531	34461	7.08	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9302	21902	34851	0.61	9.0E-79	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10297	22762	35749	0.69	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10316	22810	35803	2.32	9.0E-79	AF082348.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10316	22810	35804	2.32	9.0E-79	AF082348.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10948	23462	36484	2.73	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11388	23840	36804	3.26	9.0E-79	11423827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
11388	23840	36805	3.26	9.0E-79	11423827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
12548	24654	39090	2.05	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3805	18405	28869	1.17	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11747	18035	30495	1.3	8.0E-79	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
3291	15902	28382	10.29	7.0E-79	BE118948.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875857 3'
11676	24095		2.07	9.0E-79	AA898829.1	EST_HUMAN	TR-Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
11368	23820	36882	3.85	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
5159	17728	30157	2.24	4.0E-79	BF210889.1	EST_HUMAN	601874522F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101245 5'
335	12987	25474	2.46	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1014	13624	28139	4.44	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
3133	18747	28218	1.91	3.0E-79	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5292	17854	30278	0.84	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5292	17854	30279	0.94	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5584	18165	30841	8.78	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5898	18520	31245	1.72	3.0E-79	AB020689.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5922	18544	31270	1.01	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884564 5'
5922	18544	31271	1.01	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884564 5'
5942	18562	31281	3.6	3.0E-79	11428770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5942	18562	31282	3.6	3.0E-79	11428770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6843	19433	32248	0.76	3.0E-79	BE266893.1	EST_HUMAN	601112035F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7120	19460	32276	3.07	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0820 protein, partial cds
7120	19460	32276	3.07	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0820 protein, partial cds
8105	20848	33555	1.58	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9324	21838	34789	0.71	3.0E-79	10835039	NT	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA
10249	22744		0.62	3.0E-79	AV688115.1	EST_HUMAN	AV688115 GKc Homo sapiens cDNA clone GKCAHE11 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10740	23265	36280	1.97	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10740	23265	36281	1.97	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
309	12984		1.08	2.0E-79	H83129.1	EST_HUMAN	y4803.81 Scarsa fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:208541 3'
682	13288	25787	1.38	2.0E-79	BE379926.1	EST_HUMAN	601159419F2 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:3311107 5'
863	13574	26090	0.94	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1020	13630	26145	0.91	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1020	13630	26146	0.91	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1073	13678		1.08	2.0E-79	A1523747.1	EST_HUMAN	th18h07.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2118855 3'
1824	14413	26958	1.21	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1824	14413	26959	1.21	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1918	14503	27060	1.01	2.0E-79	7682255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2193	14768	27341	10.78	2.0E-79	4585983	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2193	14769	27342	10.78	2.0E-79	4585983	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2382	14923	27488	2.42	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2741	15286	27863	0.99	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
3985	18583	29054	0.85	2.0E-79	AJ170482.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4246	18833	29284	1.24	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4800	17378	29828	0.82	2.0E-79	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C008
5851	18475		1.16	2.0E-79	AA312223.1	EST_HUMAN	EST182928 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
5901	18523	31248	0.9	2.0E-79	11181768	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6390	18983	31773	1.1	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7040	18080	30482	0.96	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7219	19750	32605	1.76	2.0E-79	7392479	NT	Homo sapiens Rho GTPase activating protein 6 (RHGAP6), transcript variant 4, mRNA
7219	19750	32606	1.76	2.0E-79	7392479	NT	Homo sapiens Rho GTPase activating protein 6 (RHGAP6), transcript variant 4, mRNA
8044	20586	33482	1.22	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8454	20994	33912	2.52	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8701	21240	34183	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8701	21240	34184	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8834	21472	34391	0.99	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) membrane sector associated protein MB-9 (H. sapiens) (LOC883981), mRNA
10004	22499	35488	1.94	2.0E-79	S72889.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10004	22499	35489	1.94	2.0E-79	S72889.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10908	23427	38444	5.07	2.0E-79	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10908	23427	38445	5.07	2.0E-79	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
11718	18033	30483	5.59	2.0E-79	7882367	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
11808	24181	31028	5.85	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12038	24326	30994	2.81	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6701	24768		3.27	1.0E-79	BF363071.1	EST_HUMAN	MRO-NIN0087-260800-017-b10 NIN0087 Homo sapiens cDNA
8187	20728	33640	0.74	1.0E-79	BE394211.1	EST_HUMAN	601311617F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632809 5'
11487	23936	37008	2.11	1.0E-79	BF087405.1	EST_HUMAN	QV2-HT0540-120800-358-e05 HT0540 Homo sapiens cDNA
11834	25021		1.84	1.0E-79	AI480116.1	EST_HUMAN	ai79a04.x1 Blathead colon HPLR87 Homo sapiens cDNA clone IMAGE:2151438 3'
3180	15793	28284	5.7	9.0E-80	AA725848.1	EST_HUMAN	ai23a05.a1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
3180	15793	28265	5.7	9.0E-80	AA725848.1	EST_HUMAN	ai23a05.a1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
9926	22422	35396	1.33	9.0E-80	BE788803.1	EST_HUMAN	601591652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938061 5'
11156	23883	38708	11.44	9.0E-80		NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11156	23883	38709	11.44	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3882	16284		1.19	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7600	20113	32889	2.92	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7600	20113	32890	2.92	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9323	21837	34787	1.07	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9323	21837	34788	1.07	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
933	13548	28083	1.84	8.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUJEM_HUMAN
1685	14277	26810	2.29	8.0E-80	U84888.1	NT	Q18795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
2337	14908	27479	2.88	6.0E-80	6831094	NT	Homo sapiens NRD convertase mRNA, complete cds
2337	14908	27480	2.88	6.0E-80	6831094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4372	18959	29403	0.98	6.0E-80	AB032881.1	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4372	18959	29404	0.98	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5689	18560	31325	2.15	6.0E-80	11421482	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6226	18835	31608	3.16	6.0E-80	AJ404483.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6378	18980	31759	4.09	6.0E-80	11436736	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6418	19021		0.88	6.0E-80	7882363	NT	Homo sapiens lubby like protein 3 (TULP3), mRNA
						NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6464	18065	31650	0.84	6.0E-80	M18533.1	NT	Homo sapiens dydrothelin (DMD) mRNA, complete cds
8768	21297	34217	2.43	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8758	21287	34218	2.43	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8849	21487	34409	1.6	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9281	21807	34759	0.88	6.0E-80	AF161495.1	NT	Homo sapiens HSPC148 mRNA, complete cds
9775	22273	38258	1.49	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exon 21
10820	23341	38358	2.08	6.0E-80	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11103	23613	38653	22.81	6.0E-80	AF226730.1	NT	Homo sapiens Cyt18 mRNA, complete cds
11593	24036	37105	1.93	6.0E-80	AF102285.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
11817	24896		1.84	6.0E-80	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12019	24316		6.01	6.0E-80	AB028900.1	NT	Homo sapiens GST gene for cerebroside sulfoxidase, exon 1, 2, 3, 4, 5
12543	25028		1.95	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2) gene
614	13241	25718	2.83	5.0E-80	4503228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit non-ATPase, 3 (PSMD3) mRNA
868	13483	25998	1.9	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
868	13483	25999	1.9	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1231	13630		1.16	5.0E-80	X91647.1	NT	H. sapiens next gene (exon 12)
1503	14095		2.88	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2389	14987	27540	1.08	5.0E-80	U89358.1	NT	Human (3) mbt protein homolog mRNA, complete cds
2474	15041	27609	2.86	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2820	16372	27941	2.87	5.0E-80	4504282	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4112	16708	29160	0.93	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4112	16708	29161	0.93	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
6089	17662	30102	1.29	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
8288	20639	33760	1.04	5.0E-80	8910283	NT	Mus musculus keratin complex 2, gene 6g (Krt-6g), mRNA
9182	21759	34705	15.52	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s400049F03
233	12693		11.18	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5034	17608		6.93	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040800-241-g10 BN0263 Homo sapiens cDNA
5986	18806	31340	2.04	3.0E-80	AI091676.1	EST_HUMAN	cc23e12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to
1833	14421	26871	6.34	2.0E-80	R35321.1	EST_HUMAN	TR:035780 O35790 PIG-L;
1900	14485	27046	1.4	2.0E-80	AI444821.1	EST_HUMAN	ig65e08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:39080 5'
2100	14879	27247	5.9	2.0E-80	AL043116.2	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
8303	18998	31775	0.71	2.0E-80	AI923972.1	EST_HUMAN	DKFZP434D1323.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D1323 6'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6393	18998	31776	0.71	2.0E-80	A1923872.1	EST_HUMAN	wn4ec10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448788 3'
6897	18631	32489	1.08	2.0E-80	AA682952.1	EST_HUMAN	nm8001.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1080177 3'
6893	19491	32312	1.89	2.0E-80	11421820	NT	Homo sapiens Gajji transport complex protein (80 kDa) (GTC90), mRNA
7298	19828	32885	1	2.0E-80	T75215.1	EST_HUMAN	yc8912.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to
8088	21822	34558	1.25	2.0E-80	AW684270.1	EST_HUMAN	SP-K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B;
9883	22182	35158	1.13	2.0E-80	AJ007379.1	NT	EST378343 MAGE resequences, MAGH Homo sapiens cDNA
10748	23272	38287	7.28	2.0E-80	AA383362.1	EST_HUMAN	Homo sapiens GGT gene, exon 6
382	13011		1.44	1.0E-80	AL163303.2	NT	z170112.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191316
832	13449	25856	1.39	1.0E-80	AF231820.1	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
1997	14879		3.73	1.0E-80	A1732858.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4945	17520	29982	0.71	1.0E-80	N99520.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
5530	18182		6.77	1.0E-80	BE386815.1	EST_HUMAN	nm01112.x5 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.t1 OFR
6126	18741	31494	5.8	1.0E-80	L10347.1	NT	repetitive element;
6824	19221	32028	1.67	1.0E-80	6174540	NT	z83907.r1 Soares fetal liver spleen 1N1F8 Homo sapiens cDNA clone IMAGE:284972 5' similar to contains
7258	19786	32642	1.39	1.0E-80	AJ224172.1	NT	Alu repetitive element;
7574	20090	32866	2.64	1.0E-80	A1948731.1	EST_HUMAN	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616433 5'
7574	20090	32867	2.64	1.0E-80	A1948731.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
8173	20714	33830	1.25	1.0E-80	11421211	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial
8634	21173	34091	0.98	1.0E-80	11421211	NT	protein, mRNA
8634	21173	34092	0.98	1.0E-80	11421211	NT	Homo sapiens mRNA for lipophilin B
8209	21726	34688	1.78	1.0E-80	AF245219.1	NT	nm25c05.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:2472288 3'
9209	21726	34689	1.78	1.0E-80	AF245219.1	NT	wq25c05.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:2472288 3'
10323	22817	35813	0.93	1.0E-80	D63478.2	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
10531	23068	36080	2.64	1.0E-80	11841276	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
10531	23068	36081	2.64	1.0E-80	11841276	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
12091	24359	30967	2.04	1.0E-80	11417801	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10564	23100	36113	3.66	8.0E-81	A1251762.1	EST_HUMAN	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10564	23100	36114	3.56	8.0E-81	A1251762.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11033	23547	36582	6.13	8.0E-81	BE394525.1	EST_HUMAN	Homo sapiens similar to rat myomegalin (LOC84182), mRNA
							Homo sapiens similar to rat myomegalin (LOC84182), mRNA
							Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
							qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854288 3'
							qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854288 3'
							601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7269	18927	32686	3.19	7.0E-81	AI822115.1	EST_HUMAN	zb97c08.x5 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289918 3'
4478	17061	29510	4.95	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352840 5'
4478	17061	29511	4.95	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352840 5'
5487	18121	30528	1.71	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5487	18121	30528	1.71	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9192	21697	34641	1.22	6.0E-81	AA360017.1	EST_HUMAN	EST69128 Fetal lung II Homo sapiens cDNA 5' end
12240	24453	30955	2.16	6.0E-81	BF879022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294801 5'
12240	24453	30956	2.16	6.0E-81	BF879022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294801 5'
2268	14832	27410	2.68	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8351	20892	33813	1.42	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8351	20892	33814	1.42	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9568	22068	35026	1.28	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9568	22068	35026	1.28	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11455	23905	36972	2.68	6.0E-81	9508834	NT	Homo sapiens hypothetical protein (FLJ11046), mRNA
238	12898	25381	1.3	4.0E-81	AF252237.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
731	19351	25848	1.34	4.0E-81	AI621435.1	EST_HUMAN	th80e12.x1 NCI_CGAP_OY23 Homo sapiens cDNA clone IMAGE:212702 3' similar to TR:Q85560 Q85560
3206	15818	28294	4.76	4.0E-81	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3690	16291	28760	0.98	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505289 3' similar to TR:O43815 O43815
4240	16928	29277	2.39	4.0E-81	AF263306.1	NT	STRATIN. ;
4240	16928	29278	2.39	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4481	17066	29516	1.08	4.0E-81	8923209	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7321	19848	32708	0.85	4.0E-81	4757853	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
8226	20770	33699	1.71	4.0E-81	X06989.1	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2), mRNA
8482	21021	33936	3.39	4.0E-81	U20197.1	NT	Human mRNA for amyloid A4(751) protein
8482	21021	33937	3.39	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9163	21698	34632	4.78	4.0E-81	AB018001.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
10012	22607	35498	1.79	4.0E-81	11435281	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10075	22570	35564	0.57	4.0E-81	11439068	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10076	22570	35565	0.57	4.0E-81	11439068	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11063	23575	36612	2.85	4.0E-81	4759085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11063	23575	36613	2.85	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11708	24981	30834	11.8	4.0E-81	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11708	24981	30835	11.8	4.0E-81	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12277	24481	30938	2.13	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12277	24481	30939	2.13	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12430	24572	30912	4.2	4.0E-81	11417874	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
1310	13904	26422	9.81	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1310	13904	26423	9.81	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2408	14977	27661	1.86	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3020	15636	28112	6.8	3.0E-81	4506280	NT	Homo sapiens plectrophilin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3020	15636	28113	6.8	3.0E-81	4506280	NT	Homo sapiens plectrophilin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
6143	17714	27653	2.95	3.0E-81	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
2859	15478	27653	2.07	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2859	15478	27654	2.07	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3841	16440	28902	0.75	2.0E-81	AW611642.1	EST_HUMAN	hg85cd1.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2852384 3'
12591	16440	28902	2.77	2.0E-81	AW611642.1	EST_HUMAN	hg85cd1.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2852384 3'
1488	14080	28595	0.92	1.0E-81	W28599.1	EST_HUMAN	3393 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4813	17196	29842	1.81	1.0E-81	AA040370.1	EST_HUMAN	2k45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4750	17331	29774	8.65	1.0E-81	BE047098.1	EST_HUMAN	PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly;
5049	17622	30087	1.14	1.0E-81	AW182428.1	EST_HUMAN	tz45cd4.y1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281528 5'
5448	18017	37139	3.85	1.0E-81	U87828.1	NT	442a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2859852 3'
5556	18188	30603	3.68	1.0E-81	11432868	NT	Human acetylcholinesterase (ACO2) gene, exon 3
5556	18188	30604	3.68	1.0E-81	11432868	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5693	18319	30818	0.77	1.0E-81	AA255889.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5835	18459	31180	3.92	1.0E-81	U52351.1	NT	z65cd08.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:682476 5' similar to SW:PR12_HUMAN
5835	18459	31181	3.92	1.0E-81	U52351.1	NT	P49843 DNA PRIMASE 58 KD SUBUNIT;
6296	18903	31674	1.82	1.0E-81	BF874841.1	EST_HUMAN	Homo sapiens arm-repeat protein NPRAP/neurexophilin (CTNND2) mRNA, partial cds
6838	19426	32242	0.73	1.0E-81	AJ133289.1	NT	Homo sapiens arm-repeat protein NPRAP/neurexophilin (CTNND2) mRNA, partial cds
7749	20258	33151	7.93	1.0E-81	11432868	NT	Homo sapiens arm-repeat protein NPRAP/neurexophilin (CTNND2) mRNA, partial cds
7762	20270	33168	0.72	1.0E-81	AJ250408.1	NT	602137804F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274635 5'
							Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
							Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
							Homo sapiens GLI3 gene for GLI3 protein

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9891	22190	35163	13.75	1.0E-81	BE958278.1	EST_HUMAN	601845051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9891	22190	35164	13.75	1.0E-81	BE958278.1	EST_HUMAN	601845051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9879	22378	35353	4.13	1.0E-81	BE5584387.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885483 5'
							ac14d06.a1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:358427 3' similar to SW:YB36_YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.;
10014	22509	35500	1.16	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10016	22511	35502	2.64	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10016	22511	35503	2.64	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10402	22898	35882	1.47	1.0E-81	AW887650.1	EST_HUMAN	CMS-NN0059-140400-147-412 NN0059 Homo sapiens cDNA
10887	23482	36508	2.02	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0008-260568-019 CT0008 Homo sapiens cDNA
10887	23482	36509	2.02	1.0E-81	AW844988.1	EST_HUMAN	MRO-CT0008-260568-019 CT0008 Homo sapiens cDNA
10871	23486	36514	1.57	1.0E-81	AW788167.1	EST_HUMAN	RC3-UM0046-260200-011-408 UM0046 Homo sapiens cDNA
10871	23486	36515	1.57	1.0E-81	AW788167.1	EST_HUMAN	RC3-UM0046-260200-011-408 UM0046 Homo sapiens cDNA
11182	18027	30489	2.07	1.0E-81	AW960658.1	EST_HUMAN	EST372728 MAGI resequences, MAGI Homo sapiens cDNA
11398	23850	36816	2.34	1.0E-81	BF204263.1	EST_HUMAN	601887714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
11920	24266	31012	3.39	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
14	12693	25149	13.13	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
111	12893	25149	8.9	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
285	12841	25427	1.89	8.0E-82	U09898.1	NT	Human CRFB4 gene, partial cds
847	13483	25971	2.2	8.0E-82	U08898.1	NT	Human CRFB4 gene, partial cds
920	13533	26061	1.5	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1537	14128	26685	1.12	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1937 protein, partial cds
							Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
1687	14290	26826	1.42	8.0E-82	8716601	NT	mRNA
4328	16914	29358	0.77	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1496	14091		1.45	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
2794	16347	27916	1.21	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
12395	24555		1.37	7.0E-82	AA516512.1	EST_HUMAN	m88e11.1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:826168 3'
1710	14303	28840	20.15	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
6888	18314	30812	0.83	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120800-382-08 HT0540 Homo sapiens cDNA
6888	18314	30813	0.83	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120800-382-08 HT0540 Homo sapiens cDNA
							wp76c06.x1 NCL_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2487824 3' similar to TR:O76278
11563	24010	37080	5.53	4.0E-82	AI837300.1	EST_HUMAN	O75276 PKD1;
12170	24415		5.68	4.0E-82	AF029701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
268	12855	25444	14.77	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nadn-II, Alzheimer disease) (APP), mRNA
732	13352	25847	2.11	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
820	13437	25944	8.87	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
803	13517	26035	3.37	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nadn-II, Alzheimer disease) (APP), mRNA
1088	13704		39.08	3.0E-82	AA725848.1	EST_HUMAN	al23605.s1 Soares, testis, NHT Homo sapiens cDNA clone 1343848.3
1398	13883	26522	1.11	3.0E-82	AW875073.1	EST_HUMAN	RC8-PT0001-180100-021-802 PT0001 Homo sapiens cDNA
1515	14107	26843	2.16	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1845	14528	27085	1.58	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-280700-018-g04 BN0005 Homo sapiens cDNA
2050	14631	27202	1.18	3.0E-82	4501922	NT	Homo sapiens adenylyate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
3310	15921		2.54	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
5047	17820	30065	0.82	3.0E-82	AA135679.1	EST_HUMAN	z83604.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:555711 5' similar to SW:PAGT_BOVIN Q07537 POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE:
8093	20834	33546	2.5	3.0E-82	11428208	NT	Homo sapiens ankryrin-like with transmembrane domains 1 (ANKTM1), mRNA
8491	21030	33949	0.82	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8481	21030	33950	0.82	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9738	22236	35216	5.18	3.0E-82	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
9738	22236	35216	5.18	3.0E-82	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
623	13250	25723	2.48	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
623	13250	25724	2.48	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1724	14315	26857	1.52	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117.1 434 (synonym: h1553) Homo sapiens cDNA clone DKFZp434M117.6
3637	16436	26898	1.47	2.0E-82	M88878.1	NT	H. sapiens plasminogen-apolipoprotein (a) gene family, exon for 1st kingle 4 repeat
3913	16511	26873	1.03	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4095	16690	26146	0.62	2.0E-82	U78833.1	NT	Human Integral membrane serine protease Seprease mRNA, complete cds
4317	16903	26347	0.68	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4658	17238	26893	1.38	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1086 protein, partial cds
4658	17238	26894	1.38	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1086 protein, partial cds
4985	17599	30013	2.59	2.0E-82	AF046555.1	NT	Homo sapiens whsc71 (WBSCR1) and whsc5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5239	17803	30223	1.36	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
6238	17803	30224	1.36	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5320	17882	30301	1.3	2.0E-82	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
5662	18289	30787	3.76	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6322	18929	31705	4.77	2.0E-82	AF234882.1	NT	Homo sapiens FAM44A1 splice variant a (FAM44A1) mRNA, complete cds
7673	25121		1.02	2.0E-82	A1476428.1	EST_HUMAN	hm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7771	20280	33177	0.71	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8247	20788	33707	1.82	2.0E-82	11321570	NT	Homo sapiens sirt (Drosophila) homolog 3 (SIRT3), mRNA
10018	22513	35505	1.45	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10018	22513	35506	1.45	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11149	23657	36699	1.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11149	23657	36700	1.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11155	23662	36707	2.35	2.0E-82	11417106	NT	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA
11188	23693	36741	8.98	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11188	23693	36742	8.88	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11737	24140		4.92	2.0E-82	N94950.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
12299	24496		2.45	2.0E-82	AA011278.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
618	13246	26718	1.69	1.0E-82	11648921	NT	Homo sapiens CAGF9 mRNA, partial cds
1250	13847		1.26	1.0E-82	BE885108.1	EST_HUMAN	z031d10.s1 Soares_parathyroid_tumor_1NFLS_S1 Homo sapiens cDNA clone IMAGE:306203 3'
1329	13923	26443	2.7	1.0E-82	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1330	13924	26444	0.84	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
8872	21411	34334	1.31	1.0E-82	AB037638.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9571	22071	35032	0.48	1.0E-82	AB014562.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10143	22638		1.19	1.0E-82	BF16638.1	EST_HUMAN	U1H-BW1-acc-f03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
10524	23158	36169	2.41	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10887	23408	36425	1.55	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8849	21188	34108	4.39	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
10175	22870	35694	0.78	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357734 5'
1469	14051	28583	4.93	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1721	15394	26852	2.5	8.0E-83	N68951.1	EST_HUMAN	z048f12.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
1401	13995	28523	1	7.0E-83	AW385626.1	EST_HUMAN	QV4-LT0018-271289-088-H11 LT0018 Homo sapiens cDNA
							no12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
2890	15507		1.75	7.0E-83	AA584656.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y318 Q9Y318
4940	17515		6.84	7.0E-83	BF221813.1	EST_HUMAN	DJ207H1.1 ;
6202	19812	31582	0.69	7.0E-83	11428657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
428	13061	25555	3.97	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-28
1822	14411	26956	2.07	6.0E-83	AW573088.1	EST_HUMAN	h31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034. ;
3087	15702		0.81	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3819	16222	28700	1.18	6.0E-83	11430241	NT	Homo sapiens hypodermal protein FLJ10378 (FLJ10378), mRNA
5497	16131	30539	2.35	6.0E-83	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6174	18785	31553	1.18	6.0E-83	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7613	20034	32850	1.98	6.0E-83	11422024	NT	Homo sapiens mit proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9594	22064	35058	3.97	6.0E-83	4505314	NT	Homo sapiens myosin (M-protein) 2 (185kD) (MYOM2), mRNA
9894	22183	35157	2.77	6.0E-83	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
9894	22183	35158	2.77	6.0E-83	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
11405	23856		6.84	6.0E-83	AA489108.1	EST_HUMAN	ab14410.x1 Stragene lung (8237210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.12 THR repetitive element ;
11688	24102		6.52	6.0E-83	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
982	13594		10.4	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2084	15397		1.12	5.0E-83	AF006308.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3700	16301	28789	0.98	6.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3977	16575	28045	0.84	5.0E-83	4885180	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
4527	17111	29555	0.6	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6238	17802	30221	13.17	6.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5238	17802	30222	13.17	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
688	13292	25773	1.34	4.0E-83	AF224689.1	NT	Homo sapiens maritoxidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3564	16188	28850	1.07	4.0E-83	BE88078.1	EST_HUMAN	601511680F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
1035	13845		3.47	3.0E-83	AA368311.1	EST_HUMAN	EST179542 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
6692	19288		0.68	3.0E-83	AI217223.1	EST_HUMAN	q773e06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1835	14423	28973	1.31	2.0E-83	AA883492.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0218. ;
1835	14423	28974	1.31	2.0E-83	AA883492.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0218. ;
1909	14553	27109	2.88	2.0E-83	N68951.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0218. ;
2876	15494	27884	1.06	2.0E-83	BE828894.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0218. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3307	15918		2.83	2.0E-83	11430834	NT	Homo sapiens <i>cd</i> (Drosophila)-like 1 (SALL1), mRNA
3842	18441		0.78	2.0E-83	AL183202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4429	17015	29457	4.01	2.0E-83	AF202878.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4758	17337	28781	4.54	2.0E-83	7708398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51876), mRNA
4758	17337	28782	4.54	2.0E-83	7708398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51876), mRNA
5475	18109	30518	0.8	2.0E-83	U06870.1	NT	Human carcinoembryonic antigen gene family member 18 (GCM18) gene, exons A1 and B1
6119	18735	31488	1.28	2.0E-83	BE885401.1	EST_HUMAN	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809088 5'
7482	18985	32850	6.08	2.0E-83	AF128533.1	NT	Homo sapiens F-box protein Fb13b (FBL3B) mRNA, partial cds
7784	20327	33232	0.53	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7784	20327	33233	0.53	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7928	20470	33379	1.84	2.0E-83	U06870.1	NT	Rattus norvegicus desmin-180 mRNA, complete cds
8258	20787	33714	2.17	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8258	20787	33715	2.17	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8787	22265	35278	0.85	2.0E-83	BF128748.1	EST_HUMAN	601811127F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053894 5'
9847	22442	35419	2.41	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
9847	22442	35420	2.41	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10028	22820	35516	1.12	2.0E-83	AU117859	EST_HUMAN	UI-HF-BNO-amd-4-07-J-U1r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3081852 5'
10092	22887	35590	0.78	2.0E-83	AW50500.1	EST_HUMAN	UI-HF-BNO-amd-4-07-J-U1r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3081852 5'
10729	23285	36271	4.96	2.0E-83	11438448	NT	Homo sapiens KIAA0886 protein (KIAA0886), mRNA
10808	23329	36340	1.95	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
10808	23328	36341	1.95	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
12342	24523		4.52	2.0E-83	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
1457	14048	26580	2.83	1.0E-83	4504328	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoadenyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1457	14048	26581	2.83	1.0E-83	4504328	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoadenyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1508	14098	26635	15.48	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1508	14098	26638	15.48	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2084	14844	27218	1.11	1.0E-83	4503852	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2681	15239	27807	1.08	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808754 5'
3217	15828	28308	0.69	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0868), mRNA
3938	16834	29000	5.8	1.0E-83	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
4328	16915	29359	2.45	1.0E-83	Z75822.1	NT	H. sapiens gene for mitochondrial dodecanoyl-CoA delta-isomerase, exon 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6797	19388	32204	1.58	1.0E-83	AI027614.1	EST_HUMAN	α98b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M84241 QM PROTEIN (HUMAN);
3884	18482	26926	3.57	7.0E-84	BE901208.1	EST_HUMAN	601876023F1 NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3958853 5'
1338	13932	26451	3.5	6.0E-84	BE83884.1	EST_HUMAN	RC2-FN0119-200600-011-q05 FN0119 Homo sapiens cDNA
1338	13932	26452	3.5	6.0E-84	BE83884.1	EST_HUMAN	RC2-FN0119-200600-011-q05 FN0119 Homo sapiens cDNA
2441	15008	27580	21.62	6.0E-84	AA778574.1	EST_HUMAN	es88a03.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5448	18019		2.84	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322.1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434H0322 5'
6706	18336	30840	1.74	6.0E-84	AA897339.1	EST_HUMAN	el47g03.s1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5841	18485	31189	1.06	6.0E-84	11426718	NT	Homo sapiens apolipoprotein LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
5841	18485	31190	1.06	6.0E-84	11426718	NT	Homo sapiens acyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7489	20012	32878	3.2	6.0E-84	BE810371.1	EST_HUMAN	PMO-LT0019-190900-004-F02 LT0019 Homo sapiens cDNA
7878	20180	33079	0.63	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP18) mRNA, complete cds
8018	20560	33481	1.85	6.0E-84	BE770196.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
11409	23860		2	6.0E-84	AW368812.1	EST_HUMAN	IL0-BT0188-081188-138-c08 BT0188 Homo sapiens cDNA
743	13363	25856	0.69	5.0E-84	AA382811.1	EST_HUMAN	EST98084 Testis I Homo sapiens cDNA 5' end
3048	15684		1.4	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
11419	23870	36931	2.7	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11508	23955	37024	1.95	5.0E-84	AB032857.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11508	23955	37026	1.95	5.0E-84	AB032857.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1456	14048	26579	2.3	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC HUMAN O43847 NARDILYSIN PRECURSOR;
5086	17668	30089	0.79	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5086	17668	30100	1.62	4.0E-84	AF089601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5761	18377	31087	1.42	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5761	18377	31088	1.42	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6414	19017	31800	2.16	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7843	20195	33041	13.58	4.0E-84	11421326	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8842	21381	34305	1.06	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8842	21381	34306	1.06	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10788	23321	38331	5.78	4.0E-84	AB032858.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
336	12960	25477	1.97	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1194	13796	26304	0.88	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2003	14596	27144	1.93	3.0E-84	5493855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2061	14682	27203	1.94	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger G2H2 type domains
3812	16411	28876	5.94	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschialis precursor protein (XURS1) mRNA, complete cds
10768	23282		10.78	3.0E-84	A1983801.1	EST_HUMAN	wu20405.x1 Soares_Dieckgraefe_codon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:U05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2153	14730	27304	6.68	2.0E-84	BE68397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2163	14730	27305	6.68	2.0E-84	BE68397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2870	16598	28068	11.8	2.0E-84	AF039943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
2888	16606	28085	1.3	2.0E-84	X68211.1	NT	H. sapiens DNA for endogenous retroviral like element
5717	18343	30849	1.02	2.0E-84	BF511575.1	EST_HUMAN	UHH-B14-ed-a-02-UJ.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
5717	18343	30850	1.02	2.0E-84	BF511575.1	EST_HUMAN	UHH-B14-ed-a-02-UJ.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6748	19341	32148	1.04	2.0E-84	H63370.1	EST_HUMAN	yr56a11.s1 Soares_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:208324 3'
8001	20543		1.51	2.0E-84	A1298874.1	EST_HUMAN	qm87c08.x1 NCJ_CGAP_Ly5 Homo sapiens cDNA clone IMAGE:1898728 3'
9289	21795	34744	0.89	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
9847	22146	35117	0.55	2.0E-84	H22841.1	EST_HUMAN	ym49a11.r1 Soares_infant brain 1N1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP:APOH_RAT
11954	24279	31021	1.69	2.0E-84	BF448000.1	EST_HUMAN	P26844 BETA-2-GLYCOPROTEIN I;
11954	24279	31022	1.69	2.0E-84	BF448000.1	EST_HUMAN	nee30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
334	12896	26473	1.61	1.0E-84	AF114488.1	NT	TR:Q8UGS3 Q8UGS3 DJ766G23.1;
575	13205	25685	7.74	1.0E-84	4507952	NT	Homo sapiens interectin short isoform (ITSN) mRNA, complete cds
749	13369		4	1.0E-84	11427631	NT	Homo sapiens tyrosine 3-monooxygenase/hypophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
1336	13630	26449	3.89	1.0E-84	AA084379.1	EST_HUMAN	Homo sapiens complement component 5 (C5), mRNA
2099	14978	27248	2.49	1.0E-84	BE392137.1	EST_HUMAN	am85b11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1828885 3'
2285	14839	27415	1.21	1.0E-84	11427197	NT	601308008F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626267 5'
2945	15561	28035	1.09	1.0E-84	4507848	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
2945	15561	28036	1.09	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3814	16414	28878	2.82	1.0E-84	AA720851.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4608	17092	29539	6.08	1.0E-84	AJ228041.1	NT	nm12e08.s1 NCJ_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4809	17387	28837	3.09	1.0E-84	AL043314.2	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4809	17387	28837	3.09	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4809	17387	28838	3.09	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5037	17082	28539	3.8	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6076	18698	31443	0.81	1.0E-84	11430422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA uterine water channel-28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6337	18943	31722	1.46	1.0E-84	S73482.1	NT	Novel human gene mapping to chromosome 13
6961	19538	32361	1.63	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
6961	19538	32362	1.63	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7162	19694	32540	2.39	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7488	20009	32875	3.27	1.0E-84	8393994	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7565	20082	32858	1.18	1.0E-84	11430848	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7598	20082	32858	2.45	1.0E-84	11430848	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8454	21680	35159	4.5	1.0E-84	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
8695	22184	28035	0.58	1.0E-84	AF224511.1	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 8 and partial cds
8708	15561	28035	2.37	1.0E-84	4607848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9705	15561	28036	2.37	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
11833	24198		2.44	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
11843	24274	31017	3.97	1.0E-84	11418185	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
1002	13613		4.54	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1111	13715	28224	8.29	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1111	13715	28225	6.26	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1424	14017	28546	1.35	9.0E-85	4758569	NT	Homo sapiens leupadin (LDPL), mRNA
1622	14215	28746	9.44	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1622	14215	28747	9.44	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1714	14308	28845	2.45	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
4338	16925	28368	0.97	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5008	17678	30023	0.98	9.0E-85	5501970	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5038	17611	30055	1.02	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1175	13777	26287	10.28	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11489	23948		11.38	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11284	23746	36803	3.15	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11284	23746	36804	3.15	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2371	14941	27514	1.09	5.0E-85	AL163264.2	NT	Homo sapiens chromosome 21 segment HS21C084

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4525	17109		0.89	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds
5642	18271	30744	1.42	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3882402 5'
5642	18271	30745	1.42	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3882402 5'
10998	23512	36545	1.95	5.0E-85	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12589	17109		3.17	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds
6287	18905	31876	1.83	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6287	18905	31878	1.83	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
10484	22958		1.84	4.0E-85	BE079283.1	EST_HUMAN	RC1-BT0823-120200-011-c07 BT0823 Homo sapiens cDNA
1342	13837	26458	0.88	3.0E-85	AF096187.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1816	14406	26850	5.06	3.0E-85	T87495.1	EST_HUMAN	ye53g08.r1 Soares fetal liver spleen T1N1LS Homo sapiens cDNA clone IMAGE:121504 5'
4405	16990	28434	0.93	3.0E-85	BE287188.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533816 5'
5025	17599	30043	1.44	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5025	17599	30044	1.44	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
6283	18891	31659	6.49	3.0E-85	7682309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6283	18891	31660	6.49	3.0E-85	7682309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7032	18566		7.22	3.0E-85	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9) gene
7428	18952	32817	0.95	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0821 protein (KIAA0821), mRNA
7813	20356	33284	1.55	3.0E-85	U44983.1	NT	Homo sapiens DIEN mRNA, complete cds
8445	20885	33900	0.78	3.0E-85	11525828	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
8908	21447	34399	3.75	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9230	21952	34901	1.32	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
9230	21952	34902	1.32	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
10377	22871	35984	0.81	3.0E-85	AF088842.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11380	23832	36895	2.25	3.0E-85	6031660	NT	Homo sapiens EGF-like repeats and discordin I-like domains 3 (EDIL3), mRNA
12470	24595		2.19	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
698	13609	26124	3.12	2.0E-85	7687268	NT	Homo sapiens KIAA0829 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
1078	13683	26194	2.1	2.0E-85	AF248540.1	NT	Homo sapiens interectin 2 (SH3D1B) mRNA, complete cds
1460	14042	26570	3.85	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1485	14057	26590	32.65	2.0E-85	5174776	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA

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1465	14057	26591	32.65	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2274	14948	27424	2.27	2.0E-86	U0525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2650	13978		8.53	2.0E-85	7687488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3057	15973	28149	1.18	2.0E-85	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4427	17013	29455	7.95	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4664	17246	29700	8.24	2.0E-85	4826977	NT	Homo sapiens reelin (RELN) mRNA
5036	17610	30094	1.19	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5313	17875	30287	1.73	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARG1) mRNA
9197	21714	34658	1.33	2.0E-85	A1760820.1	EST_HUMAN	w187h08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2388431 3' similar to contains element
9567	22067	35027	0.84	2.0E-85	A1914459.1	EST_HUMAN	MSR1 repetitive element;
10163	22858	35654	1.38	2.0E-85	A1898384.1	EST_HUMAN	w184d12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:243607 3'
2328	14897		2.43	1.0E-85	BE704305.1	EST_HUMAN	601591418F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3945818 5'
2437	15004	27676	8.29	1.0E-85	BE5618392.1	EST_HUMAN	601482817F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3868021 5'
2437	15004	27677	8.29	1.0E-85	BE5618392.1	EST_HUMAN	601482817F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3868021 5'
9698	22185	35188	2.03	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:3350553 5'
10804	23327	36337	2.67	1.0E-85	AA778785.1	EST_HUMAN	z45f03.s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:463245 3'
10804	23327	36338	2.67	1.0E-85	AA778785.1	EST_HUMAN	z45f03.s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:463245 3'
10878	23397	36413	2.59	1.0E-85	BF311562.1	EST_HUMAN	601897003F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4128440 5'
10878	23397	36414	2.59	1.0E-85	BF311562.1	EST_HUMAN	601897003F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4128440 5'
10943	23459	36482	2.48	1.0E-85	Y00052.1	NT	Human mRNA for T-cell cyclophilin
11605	24048	37114	2.17	1.0E-86	A1188420.1	EST_HUMAN	q156a07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1860468 3'
11838	24363	30969	4.42	1.0E-85	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12098	24363	30969	5.48	1.0E-85	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1475	14087		17.55	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2867690 5'
6275	18893	31651	1.65	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
11543	23991	37063	1.65	8.0E-86	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
244	12903	26384	0.88	7.0E-86	7682247	NT	Homo sapiens KIAA0880 gene product (KIAA0880), mRNA
972	13583	26086	1.08	7.0E-86	AA860801.1	EST_HUMAN	q186f08.s1 Scores_perathyroid_tumor_NbH1PA Homo sapiens cDNA clone IMAGE:1403559 3'
972	13583	26097	1.08	7.0E-86	AA860801.1	EST_HUMAN	q186f08.s1 Scores_perathyroid_tumor_NbH1PA Homo sapiens cDNA clone IMAGE:1403559 3'
6343	18949	31726	1.01	7.0E-86	9966888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6343	18949	31727	1.01	7.0E-86	9966888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7053	18072	30463	5.8	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
8879	21218	34138	3.41	7.0E-86	L38557.1	NT	Homo sapiens galactoseoxidase (GALC) gene, exon 15

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22116		1.53	7.0E-88	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9873	22172	35148	1.82	7.0E-88	11526307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCRC6), mRNA
10841	23382	38377	2.38	7.0E-88	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10841	23382	38378	2.38	7.0E-88	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11638	24077	37137	2.7	7.0E-88	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1337	13931	26450	2.34	6.0E-86	4505492	NT	Homo sapiens coagulation factor XI (F11) (F11), mRNA
226	12888	28373	2.48	4.0E-86	BE547173.1	EST_HUMAN	601072584F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:345830 5'
6185	18795	31563	10.88	4.0E-86	BE285943.1	EST_HUMAN	601176885F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
11120	12888	28373	1.88	4.0E-86	BE547173.1	EST_HUMAN	601072584F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:345830 5'
4377	18884	28410	0.64	3.0E-88	BE887703.1	EST_HUMAN	601443282F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5782	18407	31123	6.23	3.0E-86	AW340946.1	EST_HUMAN	x282112.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8205	20748	33658	1.15	3.0E-88	AV723229.1	EST_HUMAN	AV723229 HTB Homo sapiens cDNA clone HTBBS004 5'
10121	22816	35608	3.12	3.0E-86	BE88479.1	EST_HUMAN	601509686F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10121	22816	35607	3.12	3.0E-86	BE88479.1	EST_HUMAN	601509686F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11312	23010	36018	10.63	3.0E-88	AI682240.1	EST_HUMAN	1u18p02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2251371 3'
11808	24893		3.18	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688763 5'
288	12844	26429	2.08	2.0E-88	AA308284.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
439	13072		2.33	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1232	13831	26345	2.16	2.0E-86	N58977.1	EST_HUMAN	yz18a08.r1 Saccharomyces cerevisiae 2NbhMSP Homo sapiens cDNA clone IMAGE:263478 5'
2233	14808	27381	1.95	2.0E-88	9635487	NT	Human endogenous retrovirus, complete genome
3462	16069	28542	1.38	2.0E-86	AW968142.1	EST_HUMAN	EST378215 MAGI resequencing, MAGI Homo sapiens cDNA
3809	16408	28872	2.89	2.0E-88	AF158776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3809	16408	28873	2.89	2.0E-88	AF158776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4113	16707		3.01	2.0E-86	AW516742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2816542 3'
4904	17479	29837	3.25	2.0E-88	AF056480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
6032	18651	31392	1.65	2.0E-88	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6032	18651	31393	1.55	2.0E-88	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7134	24773	32284	0.88	2.0E-88	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7952	20494	33403	0.6	2.0E-88	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8453	20863		0.54	2.0E-86	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8509	21048	33869	2.19	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-coagulation factor diacylglycerol (gamma-butyrobetaine hydroxylase) (BBOX), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8509	21048	33970	2.19	2.0E-88	11437136	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8834	21373	34288	1.28	2.0E-88	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9242	21768	34717	2.08	2.0E-88	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10344	22838	35833	2.82	2.0E-88	11548848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10344	22838	35834	2.82	2.0E-88	11548848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10347	22841	35837	1.85	2.0E-88	11417120	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
10397	22891	35885	0.85	2.0E-88	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10784	23308	36315	1.94	2.0E-88	4769061	NT	Homo sapiens ribosomal protein S8 kinase, 90kD, polypeptide 5 (RPS8KAS), mRNA
12289	24476	30835	3.82	2.0E-88	11418188	NT	Homo sapiens gene for AF-6, complete cds
12462	24588		3.36	2.0E-88	AB011399.1	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1), mRNA
1841	14233	28767	1.33	1.0E-88	4828855	NT	Homo sapiens fibulin 5 (FBLN5), mRNA
3198	15810	28283	1.64	1.0E-88	5453848	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3272	15894	28368	3.1	1.0E-88	20482.1	NT	Homo sapiens chromosome 21 segment HS21C009
3335	15945	28420	1.24	1.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3335	15945	28421	1.24	1.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4018	16818	29090	0.98	1.0E-88	7708181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4018	16818	29091	0.98	1.0E-88	7708181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4351	16938	29380	5.98	1.0E-88	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5042	17615	30059	0.9	1.0E-88	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
5741	18387	31074	1.62	1.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5559	18191		1.72	9.0E-87	AI150703.1	EST_HUMAN	kb77c09.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1708128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
7472	19894	32857	1.78	9.0E-87	4767721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7472	19894	32858	1.78	9.0E-87	4767721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
505	13137	25625	84.08	8.0E-87	X62245.1	NT	O.cuniculus mRNA for elongation factor 1 alpha
2335	14908	27477	2.29	7.0E-87	BF083211.1	EST_HUMAN	7H85R0.2.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2335	14908	27478	2.29	7.0E-87	BF083211.1	EST_HUMAN	7H85R0.2.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6533	18133	31928	0.86	7.0E-87	AW890336.1	EST_HUMAN	MRO-NT0038-020500-004-a11 NT0039 Homo sapiens cDNA
8130	20671	33581	2.87	7.0E-87	BF552778.1	EST_HUMAN	IL3-HT0619-080700-188-D10 HT0619 Homo sapiens cDNA
8375	20314	33216	0.87	7.0E-87	BET12881.1	EST_HUMAN	IL6-HT0702-160800-103-088 HT0702 Homo sapiens cDNA
9983	22478	35460	3.7	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323 5'
9983	22478	35461	3.7	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10770	23294	36299	11	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
10770	23294	36300	11	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3579	16163	28685	0.82	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
6553	19151	31947	1.54	6.0E-87	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10603	23137		8.8	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC83102), mRNA
1200	13901	26313	2.58	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
12100	13801	26313	2.47	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
1001	13812	26126	0.86	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1214	13814	26328	11.73	4.0E-87	AB037635.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1476	14088	28605	3.14	4.0E-87	R76133.1	EST_HUMAN	y80f10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contig Alu repetitive element
2466	15033	27589	2.57	4.0E-87	7708299	NT	Homo sapiens CGI-60 protein (LOC51628), mRNA
2466	15033	27600	2.57	4.0E-87	7708298	NT	Homo sapiens CGI-60 protein (LOC51628), mRNA
3511	16116	28595	1.82	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11b22)) homolog; translocated to, 4 (MLLT4) mRNA
5439	17894		0.92	4.0E-87	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5637	18268	30738	11.09	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5925	18547	31273	0.72	4.0E-87	U85426.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6106	18806	31575	4.42	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4061 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
11044	23658	36594	6.04	4.0E-87	M80676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11623	24065	37130	2.12	4.0E-87	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC83184), mRNA
12202	24947	30623	1.81	4.0E-87	11417682	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12202	24947	30624	1.81	4.0E-87	11417682	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12371	24541		17.18	4.0E-87	11417612	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RX1), mRNA
2805	15357	27624	2.34	2.0E-87	4888420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2975	15591		1.1	2.0E-87	BF327620.1	EST_HUMAN	QVQ-BND148-050600-254-e03 BND148 Homo sapiens cDNA
3852	18450	28913	0.78	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
6039	17612	30058	0.6	2.0E-87	BF376911.1	EST_HUMAN	GM0-TN0038-160800-552-n08 TN0038 Homo sapiens cDNA
5842	18468	31161	12.69	2.0E-87	BE734190.1	EST_HUMAN	GM0-TN0038-160800-552-n08 TN0038 Homo sapiens cDNA clone IMAGE:3843730 5'
5842	18468	31162	12.69	2.0E-87	BE734190.1	EST_HUMAN	GM0-TN0038-160800-552-n08 TN0038 Homo sapiens cDNA clone IMAGE:3843730 5'
6468	19069		6.41	2.0E-87	BE567193.1	EST_HUMAN	601568041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6800	19391	32208	2.12	2.0E-87	N48128.1	EST_HUMAN	601341383F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3883348 5'
							WY21607.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243388 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6877	18611	32444	0.93	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04 3'
7225	19758	32811	1.43	2.0E-87	BE29432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531611 5'
7277	19805	32864	0.76	2.0E-87	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7476	19968	32863	31.97	2.0E-87	N48128.1	EST_HUMAN	Y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 6'
7678	20187	33075	33.12	2.0E-87	N48128.1	EST_HUMAN	Y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
8334	20875	33767	15.83	2.0E-87	X62851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9700	22189		6.14	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 6'
1224	15392		1.68	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1478	14070	26607	1.21	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0285-141089-001-g04 CT0285 Homo sapiens cDNA
1478	14070	26608	1.21	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0285-141089-001-g04 CT0285 Homo sapiens cDNA
3772	16373	28838	6.15	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3708	16398	28861	2.65	1.0E-87	4758827	NT	Homo sapiens neuradin III (NRXN3) mRNA
5283	17846	30272	1.14	1.0E-87	U50949.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
6374	18978	31756	2.17	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6374	18978	31757	2.17	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7228	19760	32815	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotrophin-releasing factor type 1 receptor gene, exon 8
7228	19760	32816	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotrophin-releasing factor type 1 receptor gene, exon 8
7235	19765	32821	1	1.0E-87	4508788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7430	19954	32819	1.18	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8059	20801	33511	10.74	1.0E-87	AF214582.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8840	21379	34302	1.01	1.0E-87	AB022818.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8840	21379	34303	1.01	1.0E-87	AB022818.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9551	22051	35013	3.71	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA
9551	22051	35014	3.71	1.0E-87	BE818183.1	EST_HUMAN	RC9-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA
10275	22770	35758	0.89	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' and
10611	23144	36155	2.84	1.0E-87	5728987	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
10878	23399		1.82	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12108	25098		2.92	1.0E-87	7667632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
955	13597	26081	5.21	9.0E-88	6463897	NT	Homo sapiens protease inhibitor 4 (kallistatin) (PI4) mRNA
1145	13748	26257	8.78	9.0E-88	AF107485.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1393	13987	26514	2.74	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1393	13987	26515	2.74	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3689	16280	28759	1.7	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4356	16943	29385	3.11	9.0E-88	X91926.1	NT	H. sapiens ECE-1 gene (exon 9)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4356	16943	29386	3.11	9.0E-88	X01920.1	NT	H.sapiens ECE-1 gene (exon 9)
5146	17718	30147	1.11	9.0E-88	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8861	21488	34412	3.16	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1893	14454		0.86	6.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2688	15224	27787	2.31	5.0E-88	N89399.1	EST_HUMAN	K9718F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3031	15847	28125	0.77	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3044	15860	28140	0.81	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3044	15860	28141	0.91	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3436	18044		2.81	5.0E-88	AI693217.1	EST_HUMAN	wd8808.1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:236799 3' similar to contains Alu repetitive element/contains element MER22 MER22 repetitive element
3598	18192	28876	0.78	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
4843	17421	28874	0.79	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
6868	18602	32434	2.89	5.0E-88	H10632.1	EST_HUMAN	ym06b10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
7870	20412	33318	1.73	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment H621C084
9236	21782	34708	0.54	5.0E-88	BF680208.1	EST_HUMAN	602154938F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4285775 5'
11842	14454		1.37	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1374	13988	26495	1.93	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-110 TN0028 Homo sapiens cDNA
1374	13988	26496	1.93	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-110 TN0028 Homo sapiens cDNA
7292	19820	32679	2.25	4.0E-88		NT	Homo sapiens transforming growth factor, beta-induced, 88kd (TGFB1), mRNA
10788	23312	36320	1.93	4.0E-88		NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11362	23814	36874	2.42	4.0E-88		NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11362	23814	36875	2.42	4.0E-88		NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
761	13380	25877	0.96	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1848	14439		2.59	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2874	15560	28073	4.78	3.0E-88	N68051.1	EST_HUMAN	294812.11 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:285823 3'
4325	16911	28352	0.64	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4326	16911	28353	0.64	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4376	17159		4.33	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5502	18136	30546	2.95	3.0E-88	11429667	NT	Homo sapiens valosin-containing protein (VCP), mRNA
6773	18398	31112	4.24	3.0E-88	8868888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5882	18504	31230	3.86	3.0E-88	11420697	NT	Homo sapiens viral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6309	18916	31690	1.3	3.0E-88	11417370	NT	Homo sapiens Interleukin 13 (IL13), mRNA
6545	24764	31638	0.99	3.0E-88	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6545	24764	31639	0.99	3.0E-88	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7125	19495	32283	15.2	3.0E-88	AF276286.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7548	20066	32840	5.75	3.0E-88	11435400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
7891	20403	33310	9.25	3.0E-88	11421728	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8137	20878	33589	1.57	3.0E-88	AF034374.1	NT	Homo sapiens myoblastum cofactor biosynthesis protein A and myoblastum cofactor biosynthesis protein C mRNA, complete cds
9355	20284	33183	2.09	3.0E-88	11528282	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9841	22339	35320	0.67	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9841	22339	35321	0.67	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9857	22364	35343	0.89	3.0E-88	11439085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11928	24263		5.35	3.0E-88	11417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
11944	24954	30828	1.28	3.0E-88	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12668	24738	30828	1.41	3.0E-88	11528140	NT	Homo sapiens procaspase, serine, 7 (entelokinase) (PRSS7), mRNA
1074	13879	26186	1.87	2.0E-88	7305198	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1665	14258	26782	1.57	2.0E-88	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1798	14378	26920	4.58	2.0E-88	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4318	17100	29547	2.07	2.0E-88	6031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
6070	18887	31430	5.11	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aaa-d04-Q-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6070	18887	31431	5.11	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aaa-d04-Q-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6753	18346	32153	22.7	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6753	18346	32154	22.7	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7176	19708	32556	1.3	1.0E-88	AI069034.1	EST_HUMAN	wq70a12.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2476006 3'
7238	19766	32622	4.05	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851
9166	21743	34686	0.9	1.0E-88	AA180368.1	EST_HUMAN	zp87c02.11 Stralagene HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:827170 5' similar to SW:POL1_HUMAN P10288 RETROVIRUS-RELATED POL POLYPROTEIN ;
9499	21899	34956	3.09	1.0E-88	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hhas3) Homo sapiens cDNA clone DKFZp434N0323 5'
11319	23017	36026	6.14	1.0E-88	AA891479.1	EST_HUMAN	cs91g03.s1 NCL CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
12160	24400		5.38	1.0E-88	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
10830	23351	36366	3.56	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2763	16317	27884	1.05	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508188 5'
7012	10610	32331	1.07	8.0E-89	11421514	NT	Homo sapiens similar to beta domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83232), mRNA
458	13092	25955	1.26	7.0E-89	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
458	13092	25588	1.26	7.0E-89	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
6012	17688	30026	2.51	7.0E-89	4657390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
5064	17637	30080	6.15	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E248_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E248 5'
5623	18252	30720	1.26	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete cds
5623	18252	30721	1.26	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete cds
6483	18084	31865	1.06	7.0E-89	7548808	NT	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
6483	18084	31866	1.06	7.0E-89	7548808	NT	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
7510	20031	32898	1.88	7.0E-89	11420764	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
7820	20362	33268	0.51	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7820	20362	33270	0.51	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8415	20955	33872	0.83	7.0E-89	J02923.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10423	22917	35917	1.3	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10423	22917	35918	1.3	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10440	22934	35942	0.97	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10440	22934	35943	0.97	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
12804	24905	26177	1.86	7.0E-89	J05235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
1081	13666	26177	1.41	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2254	14928	27404	1.24	6.0E-89	4508124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2477	15044	27611	1.37	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2477	15044	27612	1.37	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3577	16181	28683	0.91	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4743	17324	29785	3	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4743	17324	29786	3	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5366	17926	30340	0.82	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5366	17926	30341	0.82	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5234	17798	30216	2.68	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pro-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5234	17798	30217	2.68	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pro-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7587	20102	32977	0.91	4.0E-89	BE762749.1	EST_HUMAN	QV9-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11020	23634	36570	1.69	4.0E-89	AI708972.1	EST_HUMAN	w691c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2901	13518	27988	2.21	3.0E-89	AW976181.1	EST_HUMAN	EST388290 IMAGE resequences, MAGN Homo sapiens cDNA
7194	18726	32575	1.5	3.0E-89	AI217359.1	EST_HUMAN	qh17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844815 3'
10678	23210	36221	2.24	3.0E-89	N57357.1	EST_HUMAN	yw66e11.1 Soares_placenta_8b0dweels_2NkHP8b9W Homo sapiens cDNA clone IMAGE:259148 5'
12270	24840	30789	2.82	3.0E-89	AV708431.1	EST_HUMAN	similar to SW:P14K_HUMAN P42359 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
12384	24637	30902	1.32	3.0E-89	AV706749.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
132	13066	25561	0.74	2.0E-89	7708670	NT	AV706749 ADB Homo sapiens cDNA clone ADBBGA01 6'
132	13066	25562	0.74	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
433	13066	25561	0.65	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
433	13066	25562	0.65	2.0E-89	7708670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
1828	14415	26982	1.71	2.0E-89	AJ238277.1	NT	Homo sapiens mRNA for cancer-testis-associated protein (CtP11 gene)
2805	19522	27892	1.84	2.0E-89	AI222095.1	EST_HUMAN	qg98c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3608	18212	28691	0.67	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
3608	18212	28692	0.67	2.0E-89	AA759149.1	EST_HUMAN	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4228	18814	28281	1.18	2.0E-89	AF089897.1	NT	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4233	18821	28271	5.23	2.0E-89	X59742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4233	18821	28272	5.23	2.0E-89	X59742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4441	17027	29467	0.7	2.0E-89	AL163203.2	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4598	17179	29628	1.52	2.0E-89	AJ007378.1	NT	Homo sapiens chromosome 21 segment HS21C003
5548	18178		1.07	2.0E-89	BE841744.1	EST_HUMAN	Homo sapiens GGT gene, exon 6
5672	18289	30780	3.13	2.0E-89	AB007448.1	NT	601065896F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3482423 5'
5960	18582	31318	1.44	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6358	18882	31739	0.7	2.0E-89	AL163285.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7664	20176	33063	4.46	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C086
7875	20417	33225	3.22	2.0E-89	11428801	NT	Human GT24 (GT24) mRNA, partial cds
8356	20898	33816	1	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
9177	21754	34701	0.69	2.0E-89	AB037754.1	NT	Homo sapiens partial mRNA for PEX5-related protein
8724	22222	35167	0.65	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
9724	22222	35168	0.65	2.0E-89	AF170814.1	NT	Homo sapiens CABP5 (CABP5) gene, exon 5
						NT	Homo sapiens CABP5 (CABP5) gene, exon 6

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11252	23782	36838	2.58	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11444	23804	36959	5.1	2.0E-89	11433873	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
11564	24011	37081	2.25	2.0E-89	U10692.1	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11449	23896	36965	6.8	1.0E-89	BF198052.1	EST_HUMAN	h181d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -JUKE 2 PROTEIN ;
11449	23898	36966	6.8	1.0E-89	BF198052.1	EST_HUMAN	h181d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -JUKE 2 PROTEIN ;
8169	20710	33826	1.59	8.0E-90	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8169	20710	33827	1.59	9.0E-90	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1101	13708	28214	1.9	8.0E-90	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1102	13708	28214	2.3	8.0E-90	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1375	18439	28497	4.58	8.0E-90	BE870581.1	EST_HUMAN	7a38f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1375	18439	28498	4.58	8.0E-90	BE870581.1	EST_HUMAN	7a38f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8495	21034	33955	0.88	8.0E-90	BE177850.1	EST_HUMAN	RC1-HT0598-120400-022-b08 HT0598 Homo sapiens cDNA
10579	23114	36127	1.81	8.0E-90	A122095.1	EST_HUMAN	qp86c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10579	23114	36128	1.81	8.0E-90	A122095.1	EST_HUMAN	qp86c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
889	13484		4.48	7.0E-90	AF223301.1	NT	spliced
8363	20903		1.73	7.0E-90	AA782877.1	EST_HUMAN	ai83d08.s1 Scores_testis_NHT Homo sapiens cDNA clone 1375503 3'
8898	21434	34357	1.47	7.0E-90	BE982525.2	EST_HUMAN	601855837R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855824 3'
8898	21434	34358	1.47	7.0E-90	BE982525.2	EST_HUMAN	601855837R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855824 3'
10042	22537	35533	2.15	7.0E-90	H88849.1	EST_HUMAN	yr86e04.s1 Scores fetal liver spleen TNFHS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10042	22537	35534	2.15	7.0E-90	H88849.1	EST_HUMAN	yr86e04.s1 Scores fetal liver spleen TNFHS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10352	22846	35840	0.89	7.0E-90	BF526089.1	EST_HUMAN	SP:C1TC_HUMAN P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
3104	15719	28189	1.18	6.0E-90	X91928.1	NT	602071208F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4214257 5'
3104	15719	28190	1.18	6.0E-90	X91928.1	NT	H. sapiens ECE-1 gene (exon 6)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4311	16897	26341	8.68	6.0E-00	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4311	16897	26342	8.68	6.0E-00	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6137	18751	31508	3.08	6.0E-00	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6137	18751	31509	3.08	6.0E-00	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8269	20810	33730	3.18	6.0E-00	4504794	NT	Homo sapiens Insitol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8269	20810	33731	3.18	6.0E-00	4504794	NT	Homo sapiens Insitol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
166	12829		24.28	6.0E-00	AB035344.1	NT	Homo sapiens TCE6 gene, exon 1-10b
1234	13833	26347	2.38	5.0E-00	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1858	14448	27002	2.57	5.0E-00	A122095.1	EST_HUMAN	q98c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
1858	14448	27003	2.57	5.0E-00	A122095.1	EST_HUMAN	q98c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
2591	15153	27720	4.08	5.0E-00	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
4638	17220	28674	10.01	6.0E-00	4506364	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4680	17242	28696	0.84	5.0E-00	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5777	18402	31118	2.63	5.0E-00	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5871	18493	31220	1.13	5.0E-00	AB016617.1	NT	Homo sapiens ELKS mRNA, complete cds
5939	18402	31118	2.21	5.0E-00	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7267	19795	32651	2.56	6.0E-00	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7267	19795	32652	2.58	6.0E-00	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7564	20081	32857	13.89	5.0E-00	4557258	NT	Homo sapiens adenylylate cyclase 9 (ADCY9) mRNA
8234	20775	33697	4.57	5.0E-00	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9598	22098	35081	1.24	6.0E-00	11418428	NT	Homo sapiens similar to ecdonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
10181	22676	35669	0.71	5.0E-00	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10311	22805	35797	0.53	5.0E-00	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10311	22805	35798	0.53	5.0E-00	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10343	22837	35832	8.78	5.0E-00	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10399	22893	35887	0.51	5.0E-00	7882051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10399	22893	35888	0.51	5.0E-00	7882051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10795	23318	36328	3.38	6.0E-00	D49387.1	NT	Human mRNA for NADP dependent leukotriene b4 12-hydroxydehydrogenase, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12421	24807		1.9	5.0E-90	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
12471	24598		5.4	6.0E-90	AI523368.1	EST_HUMAN	ar78h05.x1 Barsted acta HPLRB8 Homo sapiens cDNA clone IMAGE:2128761 3'
324	12078	25468	1.81	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
324	12978	25467	1.81	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1125	13728	28239	4.34	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1727	14318	28861	8.55	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 18
3024	15840	28117	0.97	4.0E-90	AF007544.1	NT	Homo sapiens prostate-specific membrane antigen (PSM) gene, complete cds
4781	17342	28780	3.77	4.0E-90	DB7875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4916	17490	28944	2.2	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4943	17518	28960	1.82	4.0E-90	AB5987.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 8
6098	17669		0.7	3.0E-90	AI370788.1	EST_HUMAN	q289d08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2041743 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);
7794	20337	33244	1.07	3.0E-90	BF516168.1	EST_HUMAN	U1-H-BW1-amy-04-0-U1.x1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
7794	20337	33245	1.07	3.0E-90	BF516168.1	EST_HUMAN	U1-H-BW1-amy-04-0-U1.x1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11491	23940	37011	33.84	3.0E-90	BE563833.1	EST_HUMAN	60133524F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 3'
230	12890	25376	4.32	2.0E-90	BE537813.1	EST_HUMAN	60106737F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1215	13815	26328	16.28	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1215	13815	26330	16.29	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
2420	14988		1.78	2.0E-90	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;
3912	16510	28972	2.37	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_868weeks_2NbhP88t0W Homo sapiens cDNA clone IMAGE:1713410 3'
4798	17378	28827	1.18	2.0E-90	AB008827.1	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5035	17809	30053	10.95	2.0E-90	5728855	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5948	18569	31300	0.72	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5948	18569	31301	0.72	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5955	18577	31311	4.78	2.0E-90	AW672686.1	EST_HUMAN	be49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2893881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN.;
9705	22204	35176	8.36	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9705	22204	35177	8.36	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9870	22367	35344	0.92	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
9870	22367	35345	0.92	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11345	23043	36053	4.12	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
288	12854	25443	3.2	1.0E-60	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nepril-in, Alzheimer disease) (APP), mRNA
397	15386	25533	2.02	1.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
398	15386	25533	1.38	1.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
724	13344	25835	1.49	1.0E-60	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
724	13344	25835	1.49	1.0E-60	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
758	13378	25874	13.32	1.0E-60	AF284760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
758	13378	25875	13.32	1.0E-60	AF284760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1149	13752		3.05	1.0E-60	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1349	13944	26487	2.48	1.0E-60	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1349	13944	26488	2.48	1.0E-60	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1707	14300		1.38	1.0E-60	BE379884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1948	14530	27086	2.82	1.0E-60	11420514	NT	Homo sapiens similar to SALL1 (see Drosophila-like) (LOC57187), mRNA
2878	15486	27987	7.6	1.0E-60	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3918	16516	28980	0.98	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds
3918	16516	28981	0.98	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds
4514	17098	29545	1.84	1.0E-60	AF187340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5855	18478	31201	1.88	1.0E-60	AB014533.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds
6002	18622	31357	0.95	1.0E-60	11426810	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7133	19473	32293	0.68	1.0E-60	U91834.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7665	20177	33064	2.52	1.0E-60	11426768	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6755	21284	34214	4.17	1.0E-60	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9217	21734		0.97	1.0E-60	AF183884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9239	21765	34712	1.33	1.0E-60	11422108	NT	Homo sapiens CGI-15 protein (LOC51008), mRNA
9239	21765	34713	1.33	1.0E-60	11422109	NT	Homo sapiens CGI-15 protein (LOC51008), mRNA
4274	16880	26309	8.54	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line, Homo sapiens cDNA clone s381 3'
8248	20789	33708	2.74	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10201	22686	35680	0.74	7.0E-91	AI804151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
3521	16126	28808	1.52	6.0E-91	AA702784.1	EST_HUMAN	z90804.s1 Sources fetal liver spleen 1NFS S1 Homo sapiens cDNA clone IMAGE:448015 3'
4614	17197	29843	1.21	6.0E-91	AU149339.1	EST_HUMAN	AU149339 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4614	17197	29844	1.21	5.0E-91	AU149339.1	EST_HUMAN	AU149339 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4931	17508	29952	0.68	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4931	17508	29953	0.68	5.0E-01	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6728	19323	32128	1.08	5.0E-01	A1878995.1	EST_HUMAN	au49f08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW-ASPG_FLAME Q47898 N4-(BETA-N-ACETYL-GLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR ;
8147	20688	33801	1.82	5.0E-01	BF314682.1	EST_HUMAN	601801824F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8895	21234	34155	1.4	5.0E-01	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
8895	21234	34156	1.4	5.0E-01	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
12443	24578		1.78	5.0E-01	A1183568.1	EST_HUMAN	q70f11.x1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR.b2 MIR repeat element ;
3238	15848	28328	1.25	4.0E-01	AF156778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAA1-delta) mRNA, complete cds
3238	15848	28328	1.25	4.0E-01	AF156778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAA1-delta) mRNA, complete cds
10810	23333	36346	3.98	4.0E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11882	24229	31001	3.09	4.0E-01	M77094.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #838206) Homo sapiens cDNA clone HHCMC80 similar to
11882	24228	31047	3.09	4.0E-01	M77094.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #838206) Homo sapiens cDNA clone HHCMC80 similar to
12181	24417	30947	1.38	4.0E-01	M77094.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #838206) Homo sapiens cDNA clone HHCMC80 similar to
12181	24417	30948	1.38	4.0E-01	M77094.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #838206) Homo sapiens cDNA clone HHCMC80 similar to
1680	14253	28787	4.84	3.0E-01	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1680	14253	28788	4.84	3.0E-01	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3383	15992	28470	1.4	3.0E-01	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3509	18114	28592	3.17	3.0E-01	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3509	18114	28593	3.17	3.0E-01	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3896	16494	28918	1.2	3.0E-01	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4693	17275	29722	4.38	3.0E-01	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5115	17687	30124	1.19	3.0E-01	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C086
5115	17687	30125	1.19	3.0E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5885	18487	31211	1.5	3.0E-01	11434984	NT	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA
6446	18048		2.85	3.0E-01	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6897	19293	32097	4.48	3.0E-01	11497811	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6897	19293	32098	4.48	3.0E-01	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7634	20146	33028	4.04	3.0E-01	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7634	20146	33029	4.04	3.0E-01	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7837	20426	33338	0.46	3.0E-01	6601569	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8708	21245	34198	2.6	3.0E-01	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9212	21726	34672	0.8	3.0E-01	AB011168.1	NT	Homo sapiens mRNA for KIAA0694 protein, partial cds
12504	18025	30406	9.31	3.0E-01	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12504	18025	30407	9.31	3.0E-01	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
62	12732	26169	2.37	1.0E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1288	13833	26408	6.6	1.0E-01	AW449746.1	EST_HUMAN	UI-HB13-alka-d-01-Q-U1.3T NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5608	18237	30687	0.84	1.0E-01	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6930	19589	32419	1.76	1.0E-01	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6930	19589	32420	1.76	1.0E-01	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
1284	13880	26402	9.65	9.0E-02	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1284	13880	26403	9.65	9.0E-02	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5389	17947	30359	0.59	9.0E-02	AB020940.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5654	18281	30760	4.15	9.0E-02	UJ03007.1	NT	Human Na ⁺ /K ⁺ ATPase alpha-subunit mRNA, partial cds
6790	18416	31131	2.63	9.0E-02	11427149	NT	Homo sapiens hypothetical protein FLJ20280 (FLJ20280), mRNA
6581	19179	31979	4	9.0E-02	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7798	20341	33249	0.75	9.0E-02	AJ250598.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
7798	20341	33250	0.76	9.0E-02	AJ250598.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8315	20856	33781	1.11	9.0E-02	AB040945.1	NT	Homo sapiens mRNA for KIAA1612 protein, partial cds
8315	20856	33782	1.11	9.0E-02	AB040945.1	NT	Homo sapiens mRNA for KIAA1612 protein, partial cds
9198	21715	34659	1.84	9.0E-02	11422086	NT	Homo sapiens brafadin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
98	12772	25254	11	8.0E-02	W26367.1	EST_HUMAN	2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
307	12882	25451	6.03	8.0E-02	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1860	14448	27005	1.03	8.0E-02	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
1860	14448	27006	1.03	8.0E-02	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
4306	16892	29335	0.86	8.0E-02	AA09167.1	EST_HUMAN	om13e02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1540922 3' similar to contains L1.b2 L1 repetitive element;
5285	17827	30251	2.02	8.0E-02	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
5591	18222	30671	0.76	8.0E-02	AB048820.1	NT	Homo sapiens mRNA for KIAA1800 protein, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5690	18316	30815	0.98	8.0E-92	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6666	19282	32066	1.25	8.0E-92	AJ000979.1	NT	Homo sapiens MCP-4 gene
6668	19265	32066	0.72	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase α catalytic subunit variant 1 (REV3L) mRNA, complete cds
7747	20265	33148	5.03	8.0E-92	X69336.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
7747	20265	33150	5.03	8.0E-92	X69338.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
8035	20577		0.68	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8364	20904	33822	4.86	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8364	20904	33823	4.98	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8461	21001	33918	0.67	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
8982	21630	34459	2.47	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
9939	22434	35410	1.78	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
10883	23214	36226	6.17	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11239	23770	36828	2.58	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
257	15411	25402	1.61	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
257	15411	25403	1.61	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
617	13244		1.09	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Secrase truncated isoform mRNA, complete cds
1323	13917	26439	3.02	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2228	14804	27375	1.25	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2228	14804	27376	1.25	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2598	15181	27728	1.45	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2751	15306	27870	2.14	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2781	15334	27904	1.03	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3389	18003	28474	0.65	7.0E-92	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3389	18003	28475	0.65	7.0E-92	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4687	17269	28718	1.08	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
4687	17269	28719	1.08	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
5147	17717	30148	1.16	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5350	17910	30325	1.12	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5498	18101	30419	4.93	7.0E-92	AA446206.1	EST_HUMAN	zw68d121 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1631	14223		1.18	5.0E-02	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3806018 5'
2763	15348	27815	2.12	3.0E-02	BE009714.1	EST_HUMAN	601601242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
6036	18655	31397	7.84	3.0E-02	AA378336.1	EST_HUMAN	EST01020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
10845	23177	36189	2.86	3.0E-02	X15804.1	NT	Human mRNA for alpha-actinin
10845	23177	36190	2.86	3.0E-02	X15804.1	NT	Human mRNA for alpha-actinin
12358	25103		1.76	3.0E-02	BF367198.1	EST_HUMAN	RC1-GN0021-240800-012-011 GN0021 Homo sapiens cDNA
28	12707	25184	1.57	2.0E-02	4501888	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
153	12816	25304	29.76	2.0E-02	AF184830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
191	12851	25334	3.47	2.0E-02	11422848	NT	Homo sapiens hypothetical protein dJ462023.2 (Dj462023.2), mRNA
191	12851	25336	3.47	2.0E-02	11422848	NT	Homo sapiens hypothetical protein dJ462023.2 (Dj462023.2), mRNA
779	13398	25900	12.47	2.0E-02	BE288190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
779	13398	25901	12.47	2.0E-02	BE288190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1782	14342		1.42	2.0E-02	S78663.1	NT	mtg=mas-related [human, Genomic, 2418 nt]
1980	14563	27122	4.27	2.0E-02	AB181819.1	EST_HUMAN	wk27407.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1980	14563	27123	4.27	2.0E-02	AB181819.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2092	14872	27242	4.82	2.0E-02	4508860	NT	wk27407.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2683	15241	27809	21.03	2.0E-02	8912457	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2687	14287	26823	1.16	2.0E-02	11418424	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
2857	14287	26824	1.16	2.0E-02	11418424	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3673	16274	28740	1.13	2.0E-02	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3673	16274	28741	1.13	2.0E-02	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3749	16350	28818	6.13	2.0E-02	5803180	NT	Homo sapiens chromosome 21 unknown mRNA
4376	16983	29409	1.46	2.0E-02	M10976.1	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4868	17444	29895	0.75	2.0E-02	AF136623.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5133	17705		4.94	2.0E-02	AL040437.1	EST_HUMAN	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
6444	19048		0.68	2.0E-02	4504756	NT	DKFZp434C0414.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5'
6727	19321	32126	2.75	2.0E-02	AB028591.1	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
7489	20005		0.76	2.0E-02	U87780.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
8789	21328	34253	1.78	2.0E-02	AW340174.1	EST_HUMAN	Human NPY Y1-like receptor pseudogene mRNA, complete cds
							h020202.x1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:Q02711
							Q02711 PRO-POL-OUTPASE POLYPROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10639	23171	36182	6.98	2.0E-02	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
10928	23444	38486	1.92	2.0E-02	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
11022	23638	36571	1.84	2.0E-02	AW838260.1	EST_HUMAN	CM4-LT0028-161289-082-g08 LT0028 Homo sapiens cDNA
11022	23838	36572	1.84	2.0E-02	AW838260.1	EST_HUMAN	CM4-LT0028-161289-082-g08 LT0028 Homo sapiens cDNA
12248	24459	30980	2.99	2.0E-02	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12533	18241	27809	98.37	2.0E-02	6912497	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1890	14476	27034	1.8	1.0E-02	R78078.1	EST_HUMAN	y80608.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1890	14475	27035	1.8	1.0E-02	R78078.1	EST_HUMAN	y80608.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2118	14698	27285	10.49	1.0E-02	4506888	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8189	20730	33842	1.01	1.0E-02	BE438826.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
9091	21827	34563	4.16	1.0E-02	A1380358.1	EST_HUMAN	ig01b02.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; contains Alu repetitive element; contains element MER17 repetitive element;
9091	21827	34564	4.16	1.0E-02	A1380356.1	EST_HUMAN	ig01b02.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; contains Alu repetitive element; contains element MER17 repetitive element;
2078	14898	27228	3.52	9.0E-03	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2086	14897		10.78	9.0E-03	AA316723.1	EST_HUMAN	EST189414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2673	15231		1.18	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3674	18275	28742	1.02	9.0E-03	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603632 5'
11501	23950		18.44	9.0E-03	11418528	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6705	19300	32104	4.23	8.0E-03	BF036384.1	EST_HUMAN	601480521F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863808 5'
267	12924	25410	8.58	7.0E-03	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3111	15726	28197	0.59	6.0E-03	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6782	19373	32189	1.17	6.0E-03	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
6998	19494	32315	1.37	6.0E-03	AF085771.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
1423	14016	26545	1.82	5.0E-03	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
1453	14045	26574	6.35	5.0E-03	A1874184.1	EST_HUMAN	wc08c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1453	14045	26575	6.35	5.0E-03	A1874184.1	EST_HUMAN	wc08c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1523	14116		0.97	5.0E-03	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
1862	15482	27008	0.9	5.0E-03	AJ287710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3270	15932	28384	2.6	5.0E-03	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5987	18598	31323	0.93	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogenes, complete cds
8257	18888		1.49	5.0E-93	AF045555.1	NT	Homo sapiens wbscr1 (WBSR1) and wbscr5 (WBSR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7700	20209	33088	3.68	5.0E-93	AF067138.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8541	21080	34000	0.88	5.0E-93	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8541	21080	34001	0.88	5.0E-93	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9541	22041	35002	2.28	5.0E-93	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9721	22219	35194	2.87	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
9882	22477	35459	1.58	5.0E-93	AF068313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
10705	23234	38247	2.14	5.0E-93	11439889	NT	Homo sapiens nucleobindin 2 (NUCB2) mRNA
12145	24731	30858	2.11	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
91	12767		6.55	4.0E-93	AA458633.1	EST_HUMAN	z60608.at Soares testis_NHT Homo sapiens cDNA clone IMAGE:705688 3' similar to SW:CLPA_RAT
470	13103	25595	1.56	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
470	13103	25598	1.68	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
804	13421	25928	2.39	4.0E-93	7857454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
804	13421	25927	2.39	4.0E-93	7857454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1225	13824	26339	1.5	4.0E-93	8923858	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2020	14602	27167	5.25	4.0E-93	AF047877.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in Intron 5
2638	15197	27771	1.41	4.0E-93	7658972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3624	16227	28705	0.8	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4122	16715	28711	2.14	4.0E-93	4504854	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5171	16227	28705	0.88	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5825	18449	31172	6.27	4.0E-93	T48894.1	EST_HUMAN	y694c12.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
11013	23527	36563	14.54	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKCDRF07 5'
3713	18314	28781	8.68	3.0E-93	BF690630.1	EST_HUMAN	602248554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
3713	18314	28782	8.68	3.0E-93	BF690630.1	EST_HUMAN	602248554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
4319	18805		6.51	3.0E-93	AF225898.1	NT	Homo sapiens brain mRNA, complete cds
6878	19275	32078	1.28	3.0E-93	11428182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10880	23212	36223	4.85	3.0E-03	AB24829.1	EST_HUMAN	w502d05.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2304489 3'
204	12865	25349	26.58	2.0E-03	AB015810.1	NT	Chlorocibus aethiops mRNA for ribosomal protein S4X, complete cds
204	12865	25350	26.58	2.0E-03	AB015810.1	NT	Chlorocibus aethiops mRNA for ribosomal protein S4X, complete cds
345	12997	25483	10.26	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
348	12997	25483	8.69	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1687	14250	26784	7.56	2.0E-03	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2527	15091	27684	1.01	2.0E-03	BE252982.1	EST_HUMAN	601117588F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5611	18240	30889	6.13	2.0E-03	AW964385.1	EST_HUMAN	EST1376458 IMAGE resequences, MAGH Homo sapiens cDNA
5818	18442	31184	1.06	2.0E-03	11430039	NT	Homo sapiens hypothetical protein (LOC61318), mRNA
5832	18458	31177	0.76	2.0E-03	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-89
6785	18378		1.21	2.0E-03	AW50202.1	EST_HUMAN	UHF-BNO-aka-g-09-0-UJ,r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078329 5'
12032	24322		2.49	2.0E-03	AA126735.1	EST_HUMAN	z28c10.81 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503348 3'
12119	24378		2.81	2.0E-03	L41826.1	NT	Homo sapiens CYP17 gene, 5' end
12404	24962		6.69	2.0E-03	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3682088 5'
107	12783	25265	33.31	1.0E-03	AF238987.1	NT	Homo sapiens CTR1 pseudogene
107	12783	25268	33.31	1.0E-03	AF238987.1	NT	Homo sapiens CTR1 pseudogene
944	13178	25686	7.63	1.0E-03	7687018	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
626	13263	26727	3.51	1.0E-03	AI148755.1	EST_HUMAN	o/84b08.x1 NCI_CGAP_CLL.1 Homo sapiens cDNA clone IMAGE:1672903 3' similar to TR:Q82384 Q82384
905	13519	26037	5.19	1.0E-03	D87675.1	NT	ZINC FINGER PROTEIN. ;
1280	13875	26395	6.4	1.0E-03	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1280	13875	26396	6.4	1.0E-03	8923270	NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA
1389	13983	26509	1.09	1.0E-03	AB049783.1	NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA
2375	14945	27518	1.57	1.0E-03	AF231981.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
2503	15097	27841	2.67	1.0E-03	AF050086.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2848	13833	26483	1.93	1.0E-03	BE297399.1	EST_HUMAN	Homo sapiens MHC class 1 region
2849	13933	26454	1.93	1.0E-03	BE297399.1	EST_HUMAN	60117688F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632965 5'
2860	15576	28055	1.99	1.0E-03	D87876.1	NT	60117688F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632965 5'
3262	15964		1.51	1.0E-03	AF231981.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4620	17104	28550	1.82	1.0E-03	AL163284.2	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
5755	18381	31092	1.38	1.0E-03	U78509.1	NT	Homo sapiens chromosome 21 segment HS21C084
5755	18381	31093	1.38	1.0E-03	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6938	18659	31288	0.89	1.0E-03	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6074	18691	31437	9.28	1.0E-03	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6344	18950	31728	1.02	1.0E-03	7892241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6888	18921	32455	2.18	1.0E-03	11431560	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7207	19825	32684	5.6	1.0E-03	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8203	20744	33857	2.4	1.0E-03	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8480	21018	33834	1.1	1.0E-03	Y10163.1	NT	H. sapiens mRNA for MEMD protein
8983	21122	34042	1.28	1.0E-03	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9373	20312	33214	1.84	1.0E-03	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9377	20316	33218	1.28	1.0E-03	AF091395.1	NT	Homo sapiens Trlo isoform mRNA, complete cds
9507	22007	34963	4.34	1.0E-03	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9507	22007	34964	4.34	1.0E-03	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9841	22141	35108	0.89	1.0E-03	AL046801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10050	22545	35540	0.51	1.0E-03	11433848	NT	Homo sapiens ryandoline receptor 3 (RVR3), mRNA
11888	24822	30763	1.37	1.0E-03	AI288282.1	EST_HUMAN	qin03c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880768 3' similar to WP:119B4.4 CE13742
12301	24488		2.08	1.0E-03	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12397	24557		5.43	1.0E-03	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12668	24687	30874	1.72	1.0E-03	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12584	25080		2.21	1.0E-03	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10484	22978		1.17	8.0E-04	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4034	16632	28101	2.19	6.0E-04	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
12524	24840		1.31	6.0E-04	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5570	18201	30650	3.71	5.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5570	18201	30651	3.71	5.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
6188	18808	31578	6.6	5.0E-04	AA722434.1	EST_HUMAN	zq87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3'
7091	19653	32491	1.45	5.0E-04	A1015900.1	EST_HUMAN	ci83b005.s1 Soares_fetal_heart_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1623369 3'
8573	21112	34031	0.78	5.0E-04	BF529115.1	EST_HUMAN	602042163F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
10852	23373	36331	1.97	5.0E-04	11423982	NT	Homo sapiens adenylyate kinase 2 (AK2), mRNA
10852	23373	36392	1.97	5.0E-04	11423982	NT	Homo sapiens adenylyate kinase 2 (AK2), mRNA
12010	25083	30517	4.38	5.0E-04	T89398.1	EST_HUMAN	y88b04.s1 Soares_fetal_liver_spleen_1N1FLS Homo sapiens cDNA clone IMAGE:116239 3'
1882	14488		9.28	4.0E-04	LO5084.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4827	17405	28859	3.19	4.0E-04	A1591312.1	EST_HUMAN	hw11101.x1 NCI CGAP Bm52 Homo sapiens cDNA clone IMAGE:2269403 3' similar to TR:Q16285 Q16286 PROTEIN TYROSINE PHOSPHATASE ;
6594	19191	31696	2.35	4.0E-04	11440870	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6594	19191	31696	2.35	4.0E-04	11440870	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6992	19490		0.89	4.0E-04	L27388.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11328	23026	36035	1.6	4.0E-04	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
11698	24041	37110	4	4.0E-04	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
639	13262	25738	3.74	3.0E-04	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
750	13370	25684	9.91	3.0E-04	4502806	NT	Homo sapiens complement component 6 (C6) mRNA
1778	14366	26910	1.19	3.0E-04	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1778	14366	26911	1.19	3.0E-04	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1808	14398	26944	5.11	3.0E-04	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
5851	18483	31207	4.01	3.0E-04	11496288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6299	18907	31678	1.07	3.0E-04	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6579	19177	31977	5.19	3.0E-04	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
8140	20681	33593	0.89	3.0E-04	AF152309.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8523	21092	33984	3.81	3.0E-04	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9511	22011	34970	7.24	3.0E-04	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
10979	23493	36523	1.64	3.0E-04	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11527	23975	37045	1.62	3.0E-04	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
9687	22166	35140	0.51	2.0E-04	AB10393.1	EST_HUMAN	w30h11.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
9687	22166	35141	0.51	2.0E-04	AB10393.1	EST_HUMAN	w30h11.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
160	12823	25311	2.34	1.0E-04	BE286714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3125	15739	28207	1.98	1.0E-04	BE253433.1	EST_HUMAN	601111698F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3125	15739	28208	1.98	1.0E-04	BE253433.1	EST_HUMAN	601111698F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4450	17036	29480	1.14	1.0E-04	9505692	NT	Homo sapiens hypothetical protein (FLJ20748), mRNA
6223	18932	31606	1.21	1.0E-04	AE000289.1	NT	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome
6412	19015	31797	1.32	1.0E-04	AL040518.1	EST_HUMAN	DKFZp334G0314.1_134 (synonym: hba3) Homo sapiens cDNA clone DKFZp334G0314 5'
6421	19024	31808	0.79	1.0E-04	H08270.1	EST_HUMAN	y8762.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
8057	20599	33507	0.58	1.0E-04	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8057	20599	33508	0.58	1.0E-04	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9180	21757	34703	2.29	1.0E-04	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9702	22201	36173	1.8	1.0E-04	BE780478.1	EST_HUMAN	801488748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872089 5'
10945	23461	36483	3.48	1.0E-04	U85590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11187	23702	36763	2.05	1.0E-04	AI272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q82846
11592	24035	37104	2.28	1.0E-04	11418871	NT	Q82846 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, ;
12133	12823	25311	1.34	1.0E-04	BE285714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
1625	14117	26684	2.12	8.0E-05	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3191	15803	28275	1.15	9.0E-05	7682027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3191	15803	28276	1.15	9.0E-05	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5601	18230	30879	1.89	9.0E-05	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5601	18230	30680	1.59	9.0E-05	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
8184	20735	33845	1.89	9.0E-05	AF274753.1	NT	M.musculus glyt1 gene (exons 1c and 2)
155	12818	25308	10.05	8.0E-05	AF164830.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4634	17217	29889	1.92	8.0E-05	AI700998.1	EST_HUMAN	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4634	17217	29870	1.92	8.0E-05	AI700998.1	EST_HUMAN	we08e04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
7028	19562	32388	0.7	8.0E-05	11419378	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7260	19818	32677	1.44	8.0E-05	11428528	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
7260	19818	32678	1.44	8.0E-05	11428528	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8138	20879	33590	1.83	8.0E-05	AF032897.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
9287	21887	34832	1.88	8.0E-05	11420944	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9287	21887	34833	1.88	8.0E-05	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9762	22260	35243	3.42	8.0E-05	6174844	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9763	22261		3.07	8.0E-05	AB037816.1	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
10134	22628	35817	0.76	8.0E-05	9845523	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10592	23127	36141	1.76	8.0E-05	AF112152.1	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
11357	23811	36871	2.34	8.0E-05	10894024	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
12365	24638		25.75	8.0E-05	AA828056.1	EST_HUMAN	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
287	12953	25441	8.43	7.0E-05	D87875.1	NT	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744849 3' similar to contains L1.11 L1 repetitive element ;
287	12953	25442	6.43	7.0E-05	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4456	17042	28486	5.84	7.0E-05	MB9708.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
							Homo sapiens Ly-8-like protein (CD58) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17099		1.35	7.0E-05	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C0.46
9144	21879	34823	0.92	4.0E-05	BE436626.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
11548	23998	37089	1.69	4.0E-05	AW950834.1	EST_HUMAN	EST382704 MAGC resequencing, MAGC Homo sapiens cDNA
11848	23998	37089	1.69	4.0E-05	AW950834.1	EST_HUMAN	EST382704 MAGC resequencing, MAGC Homo sapiens cDNA
224	12885	25370	8.53	3.0E-05	AV648381.1	EST_HUMAN	AV648381 GLC Homo sapiens cDNA clone GLC01F01 3'
5634	18283	30735	1.76	3.0E-05	BF528041.1	EST_HUMAN	602071148F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4214147 5'
5854	24760	31200	0.72	3.0E-05	4503384	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7404	18928	32782	1.38	3.0E-05	AW958121.1	EST_HUMAN	EST370191 MAGC resequencing, MAGC Homo sapiens cDNA
7404	18928	32783	1.38	3.0E-05	AW958121.1	EST_HUMAN	EST370191 MAGC resequencing, MAGC Homo sapiens cDNA
9277	21803	34763	1.71	3.0E-05	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9277	21803	34764	1.71	3.0E-05	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9882	22181	35134	0.87	3.0E-05	BF213448.1	EST_HUMAN	601845212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
10759	23283	36298	2.2	3.0E-05	R83190.1	EST_HUMAN	y87g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194468 5'
973	13585	28098	2.57	2.0E-05	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
1696	14278	26811	1.66	2.0E-05	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1696	14278	26812	1.55	2.0E-05	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1984	14588	27127	3.25	2.0E-05	4507612	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorcery fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1987	14589	27131	1.57	2.0E-05	BE383873.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3858862 5'
2470	15037	27604	1.23	2.0E-05	5453665	NT	Homo sapiens G protein-coupled receptor 18 (GPR18) mRNA
2470	15037	27605	1.23	2.0E-05	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2505	15069	27642	4.2	2.0E-05	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2554	16118	27688	1.05	2.0E-05	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2844	13584	26088	8.06	2.0E-05	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3193	15805	28278	2.64	2.0E-05	AF015462.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3821	16224	28701	2.98	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-16 (LOC51168), mRNA
3821	16224	28702	2.98	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3877	16278	28745	0.72	2.0E-05	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
3813	16413	28877	0.64	2.0E-05	AI290284.1	EST_HUMAN	qm01c02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP.T23G7.4 CE03705
4452	17038	29481	1.42	2.0E-05	7657185	NT	Homo sapiens hypothetical protein (H3322B1A), mRNA
5048	17621	30086	3.24	2.0E-05	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
5191	17766	30185	3.18	2.0E-05	7681878	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5251	17814	30237	1.89	2.0E-08	AA447831.1	EST_HUMAN	z11d07.r1 Soares fetal_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5251	17814	30238	1.89	2.0E-05	AA447831.1	EST_HUMAN	z11d07.r1 Soares fetal_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5971	18298	30778	5.38	2.0E-05	7705784	NT	Homo sapiens CGI-48 protein (LOC51098), mRNA
5971	18298	30779	5.38	2.0E-06	7705784	NT	Homo sapiens CGI-48 protein (LOC51098), mRNA
5978	18488	31223	1.21	2.0E-05	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5978	18488	31224	1.21	2.0E-06	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6291	18899	31870	3.33	2.0E-05	M69724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6577	19175	31874	1.08	2.0E-05	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6577	19175	31875	1.08	2.0E-05	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6885	19281	32084	2.42	2.0E-05	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH8) mRNA, complete cds
8881	19688	32428	1.8	2.0E-05	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
8089	21806	34537	1.85	2.0E-05	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10283	22778	35769	0.49	2.0E-05	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10602	23138	36180	2.21	2.0E-05	4767853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
11546	23864	37085	1.74	2.0E-05	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11546	23864	37086	1.74	2.0E-05	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	24365	30871	2.56	2.0E-05	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12220	24442	30890	1.41	2.0E-05	11417860	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
12534	24846	30890	8.02	2.0E-05	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5789	18424	31140	7.88	1.0E-05	AA284651.1	EST_HUMAN	z123104.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
5789	18424	31141	7.88	1.0E-05	AA284651.1	EST_HUMAN	z123104.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
7523	20043	32912	4.16	1.0E-05	BF370000.1	EST_HUMAN	RC6-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
7523	20043	32913	4.18	1.0E-05	BF370000.1	EST_HUMAN	RC6-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8135	20876	33588	1.51	9.0E-06	BE897289.1	EST_HUMAN	601437232F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922423 5'
497	15415	25592	1.19	8.0E-06	BE897607.1	EST_HUMAN	601497608F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3898781 5'
497	15415	25593	1.19	8.0E-06	BE897607.1	EST_HUMAN	601497608F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3898781 5'
5702	18328	AW836047.1	2.71	8.0E-06	AW836047.1	EST_HUMAN	PMO-L10019-090300-002-d09 L10019 Homo sapiens cDNA
3980	18578	28048	0.99	7.0E-06	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3360	15988	28445	1.65	6.0E-06	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3528	16134	28814	11.83	6.0E-06	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3 end

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5820	18444	31166	0.85	6.0E-06	11422842	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
11420	23871	36932	2.52	6.0E-06	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11420	23871	36933	2.52	6.0E-06	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11461	23911	36978	1.96	6.0E-06	6923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
342	12894	25478	2.95	5.0E-06	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
875	13489	26005	3.61	5.0E-06	AB032908.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
876	13489	26006	3.61	5.0E-06	AB032908.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2650	15209		0.91	5.0E-06	11416707	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
3061	15677	28151	0.59	5.0E-06	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
5030	17604		1.8	6.0E-06	X60812.1	NT	H. sapiens DNA for monomelic odense type A (7) (partial)
6758	18351	32180	1.1	5.0E-06	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6878	19612	32445	4.05	5.0E-06	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6878	19612	32446	4.05	5.0E-06	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7090	18661	32501	0.78	5.0E-06	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7524	20044	32914	1.7	5.0E-06	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8050	20692	33489	1.62	5.0E-06	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8050	20692	33500	1.62	5.0E-06	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
11618	24080	37124	1.68	5.0E-06	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4269	16855		8.01	3.0E-06	H88668.1	EST_HUMAN	y87h12.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
440	13073		3.68	2.0E-06	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
777	13398	26887	1.52	2.0E-06	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4871	17447	26898	1.56	2.0E-06	BE149074.1	EST_HUMAN	RC3-H10230-040500-110-q02 HT0230 Homo sapiens cDNA
8911	21449		5.45	2.0E-06	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCFCMD07 5'
11795	24176		1.71	2.0E-06	AW249440.1	EST_HUMAN	2818351.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818351 5'
699	13321	25808	2.62	1.0E-06	Y18990.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1817	14407	26951	3.32	1.0E-06	AW95054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1817	14407	26952	3.32	1.0E-06	AW95054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
2272	14946	27421	1.3	1.0E-06	M75997.1	NT	Human hepatocyte growth factor gene, exon 1
2272	14946	27422	1.3	1.0E-06	M75997.1	NT	Human hepatocyte growth factor gene, exon 1
2306	15398	27459	1.1	1.0E-06	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
7045	18065	30455	1.08	1.0E-06	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8154	20695	33608	0.9	1.0E-06	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8154	20695	33609	0.9	1.0E-06	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8650	21189	34107	22.03	1.0E-08	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC883214), mRNA
8784	21323	34247	2.21	1.0E-08	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10064	22559	35553	0.87	1.0E-08	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10064	22559	35554	0.87	1.0E-08	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
11781	18023	30404	2.58	1.0E-08	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
11781	18023	30405	2.58	1.0E-08	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3370	15978	28455	0.62	6.0E-07	BF249240.1	EST_HUMAN	801863712F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4081202 5'
7558	20076	34327	2.78	6.0E-07	BE141849.1	EST_HUMAN	IL6-HT0117-011098-004-D07 HT0117 Homo sapiens cDNA
8864	21403	34327	0.74	6.0E-07	BE88012.1	EST_HUMAN	801440317F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3925133 5'
8864	21403	34328	0.74	6.0E-07	BE88012.1	EST_HUMAN	801440317F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3925133 5'
10486	22980	35987	0.62	6.0E-07	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
10486	22980	35988	0.62	6.0E-07	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
11284	23737	36763	1.8	6.0E-07	X15804.1	NT	Human mRNA for alpha-actinin
7957	20496	33409	2.45	5.0E-07	AL043314.2	EST_HUMAN	DKFZp434N0323_J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8085	20826	33540	12.84	5.0E-07	AA18026.1	EST_HUMAN	z07e12.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
9593	22093	35057	2.67	5.0E-07	BFT54912.1	EST_HUMAN	G1304125 PMS4 MRNA ;
11421	23872	36834	1.89	5.0E-07	BE148597.1	EST_HUMAN	RCO-BT0812-250900-032-e09 BT0812 Homo sapiens cDNA
11421	23872	36835	1.89	5.0E-07	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
975	13587	29102	6.69	4.0E-07	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
1953	14537	27093	0.97	4.0E-07	5453572	NT	CMO-BN0106-170300-293-e08 BN0106 Homo sapiens cDNA
5764	18380	31091	17.27	4.0E-07	4557328	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5912	19571	32389	6.05	4.0E-07	Y11339.2	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
5912	19571	32400	6.05	4.0E-07	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7086	19859	32498	1.01	4.0E-07	7710126	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7128	19488	32286	1.01	4.0E-07	11422166	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7778	20288	33186	0.74	4.0E-07	10947053	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
7778	20288	33187	0.74	4.0E-07	10947053	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8078	20820	33533	0.84	4.0E-07	4597708	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8268	20840	33761	1.57	4.0E-07	11421763	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8555	21094	34014	0.73	4.0E-07	11423233	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
							Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9172	21749	34692	1.23	4.0E-07	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9172	21749	34693	1.23	4.0E-07	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10333	22827	35922	0.75	4.0E-07	11431080	NT	Homo sapiens N-myc (end STAT) Interactor (NMI), mRNA
11042	23556	36591	1.85	4.0E-07	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11042	23556	36592	1.85	4.0E-07	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11977	24288		4.75	4.0E-07	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
264	12922	25408	2.37	3.0E-07	AB032908.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
807	13521	26039	8.51	3.0E-07	4502160	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nadn-ii, Alzheimer disease) (APP), mRNA
907	13521	26040	8.61	3.0E-07	4502160	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nadn-ii, Alzheimer disease) (APP), mRNA
1490	15443	26823	2.15	3.0E-07	4758813	NT	Homo sapiens N-myc (end STAT) Interactor (NMI), mRNA
2483	15400	27618	1.38	3.0E-07	U39255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3205	15817	28293	37.82	3.0E-07	K02212.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3296	15910	28389	1.48	3.0E-07	5174478	NT	Homo sapiens perlecanin (PCNT) mRNA
3893	16492	28952	1.04	3.0E-07	AF136523.1	NT	Homo sapiens bile-salt export pump (BSEP) mRNA, complete cds
4804	17469	29925	28.9	1.0E-07	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6556	19156	31952	2.38	1.0E-07	BE689486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881821 5'
9365	20304	33206	0.8	1.0E-07	AW379976.1	EST_HUMAN	RCQ-H10258-211188-011-q05 HT0258 Homo sapiens cDNA
9365	20304	33207	0.8	1.0E-07	AW379976.1	EST_HUMAN	RCQ-H10258-211188-011-q05 HT0258 Homo sapiens cDNA
9878	22178	33193	1.21	1.0E-07	R10897.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
10584	23119	36134	4.07	1.0E-07	11427767	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
10584	23119	36135	4.07	1.0E-07	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11189	23684	36743	3.63	1.0E-07	AA663781.1	EST_HUMAN	n128g02.s1 NCL_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014862 3'
11343	23041	36050	18.96	1.0E-07	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11343	23041	36051	18.96	1.0E-07	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
834	13547	26064	5.55	9.0E-08	BE00973.1	EST_HUMAN	PM4-B10724-010400-008-e12 BT0724 Homo sapiens cDNA
1319	13913	26434	1.41	9.0E-08	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6445	19047		0.67	9.0E-08	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
7865	20407	33314	7.35	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7865	20407	33315	7.35	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8044	21581	34510	2	9.0E-08	X06989.1	NT	Human mRNA for amyloid A4(751) protein
9151	21686	34629	1.94	9.0E-08	11321680	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9216	21733	34676	1.46	9.0E-08	AB037786.1	NT	Homo sapiens mRNA for KIAA1955 protein, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9282	21788		1.25	9.0E-08	AF057728.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9288	21889	34835	1.15	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9289	21899	34836	1.15	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10101	22896	35651	0.54	9.0E-08	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10288	22763	35750	0.5	9.0E-08	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
10883	23404	36422	2.37	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10883	23404	36423	2.37	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11894	13547	26064	4.28	9.0E-08	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-e12 BT0724 Homo sapiens cDNA
27	12706		0.82	8.0E-08	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1607	14199	26732	1.04	8.0E-08	5031810	NT	Homo sapiens IL2-Inducible T-cell kinase (ITK), mRNA
1607	14199	26733	1.04	8.0E-08	5031810	NT	Homo sapiens IL2-Inducible T-cell kinase (ITK), mRNA
1764	14354	26800	1.84	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1764	14354	26801	1.84	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3883	16461	28925	7.16	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5276	17838		1.43	8.0E-08	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21G001
6233	18842	31614	1.18	5.0E-08	BE883873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3609097 5'
12308	24558	30908	1.88	4.0E-08	BE348727.1	EST_HUMAN	h88802.x1 NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151899 3'
2222	14787	27370	1.16	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
2639	15198	27772	1.67	3.0E-08	AB014807.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2777	15330		1.97	3.0E-08	AA077498.1	EST_HUMAN	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7818H01
7028	19560	32368	1.66	3.0E-08	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7028	19560	32387	1.66	3.0E-08	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8686	21225	34145	3.05	3.0E-08	H46898.1	EST_HUMAN	yo17g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:176240 5'
9221	21737	34679	0.77	3.0E-08	8922098	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
9798	22296	35278	1.8	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
9798	22296	35280	1.8	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
10399	22863	35856	0.86	3.0E-08	BE000464.1	EST_HUMAN	60187388F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
10831	23352	36387	3.79	3.0E-08	U59309.1	NT	Human fumarylase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
12508	24685		5.13	3.0E-08	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
785	13384	-26883	0.81	2.0E-08	BE281694.1	EST_HUMAN	60114948F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2124	14702	27272	3.38	2.0E-08	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2279	14853	27431	1.37	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4384	16971	29419	0.74	2.0E-08	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4432	17018	29458	4.85	2.0E-08	4768331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4953	17528	29988	0.86	2.0E-08	AF218802.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 18
4953	17528	29988	0.98	2.0E-08	AF218802.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 18
5579	18210	30660	4.83	2.0E-08	7706812	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6761	19354	32163	1.03	2.0E-08	4505788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7619	20132	33008	1.13	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7619	20132	33009	1.13	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8544	21083	34004	3.84	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8544	21083	34005	3.84	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8625	21164	34078	0.82	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8625	21164	34079	0.82	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8456	21982	34824	3.9	2.0E-08	X12684.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10312	22808		1.31	2.0E-08	7705888	NT	Homo sapiens AIM-1 protein (LOC51161), mRNA
11078	23590	38828	1.6	2.0E-08	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
11989	24305	30988	1.82	2.0E-08	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
430	13063	28558	67.20	1.0E-08	AI982007.1	EST_HUMAN	hw36b04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2281743 3' similar to SW:RL2B_HUMAN
480	13113	25603	2.18	1.0E-08	AW988811.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A. ;
1832	14420	26970	13.48	1.0E-08	N49818.1	EST_HUMAN	PMO-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
5520	18152	30598	3.14	1.0E-08	AA19854.1	EST_HUMAN	y23705.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to
5758	18384	31087	1.12	1.0E-08	BE390827.1	EST_HUMAN	PIR:S54204 S54204 ribosomal protein L28 - human ;
5758	18384	31088	1.12	1.0E-08	BE390827.1	EST_HUMAN	z988c09.r1 Strategene muscle 607209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G808562
6928	21466	34383	8.27	1.0E-08	AF141349.1	NT	G808562 NEBULIN. ;
6928	21466	34384	8.27	1.0E-08	AF141349.1	NT	601284988F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608892 5'
6984	18804	31338	0.93	9.0E-08	AI905004.1	EST_HUMAN	601284988F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608892 5'
6984	18804	31339	0.93	9.0E-08	AI905004.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
6191	18801	31571	4.33	9.0E-08	AW988835.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
11001	23515	36548	3.39	9.0E-08	AK478829.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
							QV-B7073-161289-012 B7073 Homo sapiens cDNA
							QV-B7073-161289-012 B7073 Homo sapiens cDNA
							EST380711 IMAGE resequences, MAGJ Homo sapiens cDNA
							hm69h07.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
							P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11001	23515	36550	3.39	9.0E-09	A1478829.1	EST_HUMAN	hm90h07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2183421 3' similar to SW:BD_HUMAN
11292	23744	36801	1.97	9.0E-09	AA134604.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11627	24059	37133	2.11	9.0E-09	AJ271736.1	NT	zn80d02.f1 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
8861	21200	34118	1.59	8.0E-09	9635487	NT	TR:G862294 G862294 GPI-ANCHORED PROTEIN P137. ;
5999	18619	31355	10.3	7.0E-09	AF033808.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
11477	23927	36898	2.62	7.0E-09	AF001896.1	NT	Human endogenous retrovirus, complete genome
497	13129	25818	0.57	6.0E-09	U10991.1	NT	Homo sapiens oscillin (hLn) gene, exon 6
4859	17437	29887	1.3	6.0E-09	4502660	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
5382	17941	30355	1.01	6.0E-09	8923244	NT	Human G2 protein mRNA, partial cds
8711	19305	32109	1	6.0E-09	7706136	NT	Homo sapiens CD34 antigen (CD34) mRNA
6760	18371	32187	1.39	6.0E-09	L43810.1	NT	Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA
8048	20590	33497	1.11	6.0E-09	X99101.1	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
8700	21239	34182	1.88	6.0E-09	AB030429.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8797	21336	34261	4.03	6.0E-09	AF080255.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8797	21336	34262	4.03	6.0E-09	AF080255.1	NT	H. sapiens mRNA for estrogen receptor
8854	21393	34315	0.62	6.0E-09	11431894	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
8854	21393	34316	0.62	6.0E-09	11431894	NT	Homo sapiens luteal protein mRNA, complete cds
10588	23132	36146	4.18	6.0E-09	11526299	NT	Homo sapiens luteal protein mRNA, complete cds
853	13565	26077	9.63	5.0E-09	U35484.1	NT	Homo sapiens Incisal 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
953	13565	26078	9.63	5.0E-09	U35484.1	NT	Homo sapiens Incisal 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
2007	14589	27149	1.33	6.0E-09	Y11865.1	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
4663	17245	28696	1.44	5.0E-09	AF089650.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
12009	24311		2.1	5.0E-09	BE890177.1	EST_HUMAN	Human protein C inhibitor (PCI-B) mRNA, complete cds
8263	20804		5.49	3.0E-09	M85586.1	NT	H. sapiens IMPA gene, exon 8
1282	13878		15.39	2.0E-09	AW274782.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
3297	15908	28388	1.27	2.0E-09	M30938.1	NT	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
4641	17223	28677	1.67	2.0E-09	AF095703.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
7697	20179	33086	1.28	2.0E-09	AF257737.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
							XP00608.x1 NCL_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
							LIGHT CHAIN ALKAL, NON-MUSCLE ISOFORM (HUMAN);
							Human Ku (p70/p80) subunit mRNA, complete cds
							Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
							encoding mitochondrial protein, complete cds
							Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21180	34100	9.83	2.0E-99	W2507.1	EST_HUMAN	zb4808.r1 Scores fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306835 5' similar to
8078	21815	34550	0.63	2.0E-99	R78284.1	EST_HUMAN	gbM18182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
10984	23498	36528	3.8	2.0E-99	AF247487.2	NT	y81b09.r1 Scores placenta Nb24P Homo sapiens cDNA clone IMAGE:145625 5'
11617	24059	37123	1.61	2.0E-99	AF247487.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
337	12989	25476	1.46	2.0E-99	AF114487.1	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
402	13048	25537	1.21	1.0E-99	11628160	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
1498	14058	26592	2.52	1.0E-99	M30698.1	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1803	14195	28726	2.14	1.0E-99	AF192523.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1803	14195	28726	2.14	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1971	14555	27111	0.91	1.0E-99	4503730	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1971	14555	27112	0.91	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (39kD) (FKBP6) mRNA, and translated products
3121	15735	28204	0.9	1.0E-99	J03171.1	NT	Homo sapiens FK506-binding protein 6 (39kD) (FKBP6) mRNA, and translated products
4469	17055	28499	2.98	1.0E-99	AF098018.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4469	17055	28500	2.98	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6896	18630	32487	2.18	1.0E-99	11421007	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6896	18630	32488	2.18	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7183	24778	32574	0.8	1.0E-99	X98022.1	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
9127	21862		1.04	1.0E-99	11419721	NT	Homo sapiens EB-AP gene exon 2
9439	21985	34914	1.81	1.0E-99	AW340174.1	EST_HUMAN	Homo sapiens ALEX1 protein (LOC51309), mRNA
11084	23678	36814	1.82	1.0E-99	5901979	NT	h002h02.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:002711
11255	23785	36841	2.94	1.0E-99	AB023222.1	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN;
11557	24005	37077	1.8	1.0E-99	AF223391.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11637	24078	37138	1.57	1.0E-99	AF223391.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11764	24155		9.06	1.0E-99	AF240786.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1	12682	25138	1.19	1.0E-100	AL163247.2	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2	12682	25138	1.73	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
72	12750	25227	1.35	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
72	12750	25228	1.35	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
90	12768	25250	0.79	1.0E-100	AW276237.1	EST_HUMAN	Homo sapiens Testis-specific XK-related protein on Y (XXRY), mRNA
							Homo sapiens Testis-specific XK-related protein on Y (XXRY), mRNA
							xv78b11.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824805 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
180	12842	25326	1.18	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
339	12891	25478	1.76	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
365	13014	25497	2.08	1.0E-100	T05087.1	EST_HUMAN	EST02875 Fetal brain, Striatogene (cat#938206) Homo sapiens cDNA clone HFBOR32
482	13086		1.84	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
515	13148		8.1	1.0E-100	X99631.1	NT	G.gorilla DNA for ZNF80 gene homolog
535	13166	25847	1.78	1.0E-100	BE180609.1	EST_HUMAN	RC3-H10825-040500-022-509 HT0825 Homo sapiens cDNA
1057	13662	26172	3.18	1.0E-100	7681688	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA
1057	13662	26173	3.18	1.0E-100	7681689	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA
1483	14076	26614	0.83	1.0E-100	BF530735.1	EST_HUMAN	602072064F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215039 5'
1594	14187		2.49	1.0E-100	AW207655.1	EST_HUMAN	UI-H-B1-afk-e-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1698	14190	26721	1.32	1.0E-100	AI200857.1	EST_HUMAN	q82009.x1 Scores_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81081 CYSTATIN
2284	14858		2.78	1.0E-100	D93349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2462	15046	27617	0.87	1.0E-100	X62468.1	NT	H sapiens mRNA for IFN-gamma (pKC-0)
2731	15286	27893	2.8	1.0E-100	11418978	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
3053	15689		3.92	1.0E-100	D11078.1	NT	Homo sapiens RG2 gene, retrovirus-like element
4289	18875	28324	1.83	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4320	18908	28348	2.66	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5253	17816	30239	3.18	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5253	17816	30240	3.18	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5493	18127	30535	1.55	1.0E-100	BF244218.1	EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080989 5'
5699	18326	30828	0.87	1.0E-100	AW076983.1	EST_HUMAN	xa8201.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
5878	18501	31227	1.93	1.0E-100	AJ118182.1	EST_HUMAN	PROTEIN PHPS1-2 (HUMAN);
5920	18542	31266	1.36	1.0E-100	AF135116.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6003	18623	31356	10.01	1.0E-100	X14690.1	NT	Human mRNA for plasma inter-alpha-tryptin inhibitor heavy chain H(9)
6311	18918	31892	1.06	1.0E-100	4557598	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6311	18918	31893	1.06	1.0E-100	4557598	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6566	19184		1.29	1.0E-100	5728837	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
6623	19220	32025	5.02	1.0E-100	AJ140214.1	EST_HUMAN	AU140214 PLAGE2 Homo sapiens cDNA clone PLAGE2000137 5'
6787	19378	32193	1.46	1.0E-100	R0887.1	EST_HUMAN	y93808.s1 Scores fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:128134 3'
6866	19600	32431	2.42	1.0E-100	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6928	19588	32417	1.2	1.0E-100	AA498841.1	EST_HUMAN	aa33b08.r1 Gesseler Wilms tumor Homo sapiens cDNA clone IMAGE:897687 6' similar to TR:G487418
6929	19588	32418	1.2	1.0E-100	AA498841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
6986	19543	32386	1.25	1.0E-100	BF376478.1	EST_HUMAN	aa33b08.r1 Gesseler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6986	19543	32387	1.25	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
6974	19550	32375	8.47	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-006 TN0046 Homo sapiens cDNA
8498	21009	33926	12.09	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0046-060900-004-005 TN0046 Homo sapiens cDNA
8503	21042		4.61	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8944	21482	34404	0.67	1.0E-100	AU116951.1	EST_HUMAN	601847357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 6'
8944	21482	34405	0.67	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9159	21694	34636	3.35	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9234	21956		1.98	1.0E-100	A1972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9354	20263	33192	1.65	1.0E-100	AW898611.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9407	21916		1.74	1.0E-100	AU127720.1	EST_HUMAN	Homo sapiens mRNA for KIAA1485 protein, partial cds
9504	22004	34061	2.84	1.0E-100	AB046848.1	NT	MR22 repetitive element ;
9504	22004	34062	2.84	1.0E-100	AB046848.1	NT	PM0-BN0066-100300-001-008 BN0066 Homo sapiens cDNA
9757	22255	35237	1.81	1.0E-100	AW630487.1	EST_HUMAN	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9757	22255	35238	1.81	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1628 protein, partial cds
9917	22413	35396	0.6	1.0E-100	AV732101.1	EST_HUMAN	Homo sapiens mRNA for KIAA1628 protein, partial cds
10366	22860	35863	1.46	1.0E-100	BF347519.1	EST_HUMAN	hb83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868396 5'
10452	22946		1.38	1.0E-100	Y10391.1	NT	hb83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868396 5'
10638	23170	36181	7.36	1.0E-100	BF327282.1	EST_HUMAN	AV732101 HTF Homo sapiens cDNA clone HTF81G01 6'
11196	23673	36719	2.59	1.0E-100	X94633.1	NT	602020554F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156165 5'
11196	23673	36720	2.59	1.0E-100	X94633.1	NT	Human endogenous retrovirus HERV-K, pol gene
11232	23763	36816	4.28	1.0E-100	AF111170.3	NT	MR0-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11232	23763	36819	4.28	1.0E-100	AF111170.3	NT	H. sapiens CD97 gene exon 4
11261	12682	25136	2.14	1.0E-100	AL163247.2	NT	H. sapiens CD97 gene exon 4
11529	23977		1.65	1.0E-100	AF268285.1	NT	Homo sapiens chromosome 21 segment HS21C047
11663	24100	37150	9.41	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12000	24308	30990	2.92	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12842	24717	30868	3.53	1.0E-100	11417874	NT	Homo sapiens transthyretin II; macrocytic anemia (TCN2), mRNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
81	12768	26240	2.04	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
81	12758	25241	2.04	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
715	13338	25922	1.77	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
733	13353	25848	6.28	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
733	13353	25849	5.28	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
803	13420	25925	3.37	1.0E-101	7857454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRC1 domain (PES1), mRNA
888	13500	26018	1.98	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycylamide formyltransferase, phosphoribosylglycylamide synthetase, phosphoribosylamimidazole synthetase (GART) mRNA
961	13572	26088	0.88	1.0E-101	Z20858.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1022	13632	26149	24.09	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1080	13695	26204	1.58	1.0E-101	A1221878.1	EST_HUMAN	gg98e06.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1843338 3'
1782	14372	26917	0.9	1.0E-101	7852183	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
1782	14372	26918	0.9	1.0E-101	7852183	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
1888	14570	27132	1.54	1.0E-101	4502998	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2101	14680	27248	1.83	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160900-018-109 ST0281 Homo sapiens cDNA
2388	15465	27528	1.24	1.0E-101	5728892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2648	15206	27778	10.93	1.0E-101	X72983.1	NT	H. sapiens EWS gene, exon 5
2771	15324	27891	2.71	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2771	15324	27892	2.71	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2882	15598	28330	10.39	1.0E-101	AJ262312.1	NT	Homo sapiens genomic downstream Rhesus box
3237	15949	28330	2.92	1.0E-101	4985270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3278	15889	28515	2.37	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3662086 5'
3427	16035	28515	1.94	1.0E-101	AW685556.1	EST_HUMAN	EST377620 MAGI resequences, MAGI Homo sapiens cDNA
3447	15324	27891	2.93	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3447	15324	27892	2.93	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3945	16543	28010	4.29	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5185	17750	30180	1.38	1.0E-101	5921400	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5185	17750	30181	1.38	1.0E-101	5921490	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5521	18153	30597	1.26	1.0E-101	AW685139.1	EST_HUMAN	EST377212 MAGI resequences, MAGI Homo sapiens cDNA
6154	18767	31530	3.48	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6154	18767	31531	3.48	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6768	19387	32203	1.06	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7317	18844	32203	1.18	1.0E-101	11645780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7361	19897	32749	4.87	1.0E-101	AF208870.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7361	19887	32750	4.87	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEGS) mRNA, alternative splice form 4, partial cds
7491	20014	32880	11.99	1.0E-101	AW008475.1	EST_HUMAN	w55f12.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7576	20092		1.86	1.0E-101	BE257394.1	EST_HUMAN	601109217F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3346801 5'
7707	20216	33104	7.87	1.0E-101	BF330769.1	EST_HUMAN	RC1-BT0313-220700-018-112 BT0313 Homo sapiens cDNA
7854	20368	33301	0.88	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346869 5'
7854	20368	33302	0.88	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346869 5'
7869	20541	33443	6.69	1.0E-101	BF029174.1	EST_HUMAN	601178488F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3868837 5'
8264	20805	33722	0.88	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143
8264	20805	33723	0.88	1.0E-101	AW630070.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8940	21478	34359	1.65	1.0E-101	AA036800.1	EST_HUMAN	zk29g08.l1 Soares_pregnant_uterus_NihPU Homo sapiens cDNA clone IMAGE:471868 5' similar to
8953	21778	34730	0.8	1.0E-101	AB037772.1	NT	PIR:S54840 S54840 YD9335.03c protein - yeast
9253	21778	34731	0.8	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9263	20321	33225	17.2	1.0E-101	X60069.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9263	20321	33228	17.2	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9396	21819	34769	16.05	1.0E-101	8845482	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9672	22171	35148	12.54	1.0E-101	BE619687.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9672	22171	35147	12.54	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875953 3'
9808	22308	35290	0.65	1.0E-101	10863960	NT	601472808T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875953 3'
10308	22802	35764	1.71	1.0E-101	11429127	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10337	22831	35825	6.18	1.0E-101	AI570283.1	EST_HUMAN	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10337	22831	35826	6.18	1.0E-101	AI570283.1	EST_HUMAN	to77d11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326
10442	22836	35945	0.85	1.0E-101	BE973848.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10442	22836	35946	0.85	1.0E-101	BE973848.1	EST_HUMAN	to77d11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326
10757	23281	36295	1.63	1.0E-101	S38327.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10988	23502	36532	1.68	1.0E-101	AB020628.1	NT	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11620	24082	37128	18.03	1.0E-101	A321318.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
12274	24478		16.89	1.0E-101	AW630061.1	EST_HUMAN	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
43	12722	25183	0.8	1.0E-102	AF012872.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
							EST:23783 Bone marrow Homo sapiens cDNA 5' end similar to defensin 1
							QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
							Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
363	13012	25494	4.36	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
848	13271	25749	1.2	1.0E-102	BE252470.1	EST_HUMAN	601108202F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344328 5'
807	13424	25930	1.24	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1156	13759	26269	6.78	1.0E-102	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1311	13905	26424	3.09	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1311	13905	26425	3.09	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1327	13921	26442	1.92	1.0E-102	4826977	NT	Homo sapiens reelin (RELN) mRNA
1484	14056	26589	184.12	1.0E-102	BE408447.1	EST_HUMAN	601268992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628801 5'
2348	14919	27483	1.34	1.0E-102	AI124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
2348	14919	27484	1.34	1.0E-102	AI124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3101	15716	28187	1.56	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3167	15781	28251	4.07	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3167	15781	28252	4.07	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4316	16802	28346	1.84	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4503	17087	29535	2.55	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5287	17849	30275	1.19	1.0E-102	R66488.1	EST_HUMAN	y32c04.1 Sources placenta Nb2HP Homo sapiens cDNA clone IMAGE:140834 5'
5574	18205	30658	1.68	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5923	18545		4.52	1.0E-102	AB034851.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5957	18579	31313	2.43	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5957	18579	31314	2.43	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5962	18584	31318	0.76	1.0E-102	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6435	19038	31825	2.89	1.0E-102	AI459825.1	EST_HUMAN	ar208.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52 ;
7190	19722	32570	0.97	1.0E-102	BE728323.1	EST_HUMAN	601681505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7217	19748	32604	0.63	1.0E-102	BE366108.1	EST_HUMAN	60127215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818243 5'
7392	19917	32781	7.37	1.0E-102	AJ238984.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7620	20133	33010	2.78	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAAD03 5'
8163	20708	33622	3.41	1.0E-102	BE763051.1	EST_HUMAN	GV3-NT0025-210600-236-J08 NT0026 Homo sapiens cDNA
8244	20785	33704	1.5	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3803145 5'
8431	20971	33883	1.65	1.0E-102	AV684817.1	EST_HUMAN	AV684817 GK Homo sapiens cDNA clone GKCEEE11 5'
8431	20971	33884	1.65	1.0E-102	AV684817.1	EST_HUMAN	AV684817 GK Homo sapiens cDNA clone GKCEEE11 5'
8539	21078	33997	0.52	1.0E-102	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8861	21400	34324	0.75	1.0E-102	BE388083.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805538 5'
8861	21400	34325	0.75	1.0E-102	BE388083.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805538 5'
9176	21752	34688	0.57	1.0E-102	A1762859.1	EST_HUMAN	wf63b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2397971 3' similar to contains MER4.11
9205	21722	34688	0.76	1.0E-102	A1765842.1	EST_HUMAN	MER4 MER4 repetitive element;
9245	21771	34719	2.15	1.0E-102	T70393.1	EST_HUMAN	AV766842 BM Homo sapiens cDNA clone BMFAUD08 5'
9245	21771	34720	2.15	1.0E-102	T70393.1	EST_HUMAN	y413d07.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:87021 5'
9332	21846	34758	3.3	1.0E-102	A1124626.1	EST_HUMAN	y413d07.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:87021 5'
10264	22778		0.54	1.0E-102	AF163715.1	NT	AU124628 NT2RM4 Homo sapiens cDNA clone NT2RM400308 5'
10365	22859	35851	3.54	1.0E-102	A1905037.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10366	22869	36852	3.64	1.0E-102	A1905037.1	EST_HUMAN	RC-B1074-260469-014 B1074 Homo sapiens cDNA
10422	22916	35916	1.58	1.0E-102	AA970786.1	EST_HUMAN	RC-B1074-260469-014 B1074 Homo sapiens cDNA
10949	23464	36486	1.83	1.0E-102	BE897488.1	EST_HUMAN	on57h04.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P61636 CAVEOLIN-2. [1];
10952	23467	36490	6.26	1.0E-102	4507822	NT	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924168 5'
10952	23467	36491	6.26	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11200	23705	36756	1.54	1.0E-102	AA888675.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11282	23735	36790	3.6	1.0E-102	BF359243.1	EST_HUMAN	ek48h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409347 3'
11555	24003	37078	3.66	1.0E-102	U41302.1	NT	RC8-ET0072-160800-011-F01 ET0072 Homo sapiens cDNA
11889	24105		8.01	1.0E-102	AL163280.2	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
12261	24471	30631	0.87	1.0E-102	AW300882.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12598	24681		1.79	1.0E-102	J05235.1	NT	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2866038 3'
73	12751	25228	2.49	1.0E-103	BE808166.1	EST_HUMAN	Human gamma-glutamyl transpeptidase mRNA, complete cds
104	12760	25262	8.29	1.0E-103	D97078.2	NT	601600405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802305 5'
222	12883	26368	2.74	1.0E-103	5453793	NT	601600405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802305 5'
1017	13827	26140	0.82	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
1268	13881	26408	10.5	1.0E-103	BE877641.1	EST_HUMAN	Homo sapiens nuclear protein (KKE/D repeat) (NOP56) mRNA
1640	14232	26766	2.26	1.0E-103	AF012872.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
2018	14600	27163	1.43	1.0E-103	4502428	NT	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887676 5'
2018	14600	27164	1.43	1.0E-103	4502428	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2343	14914	27488	1	1.0E-103	AJ134981.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2494	15058	27632	1.88	1.0E-103	AF060588.1	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
							AU134981 PLACE1 Homo sapiens cDNA clone PLACE1000865 5'
							Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	15192	27792	1.54	1.0E-103	BF528378.1	EST_HUMAN	602041882F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4179428 5'
2631	15192	27793	1.54	1.0E-103	BF528379.1	EST_HUMAN	602041882F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4179428 5'
3105	15720		2.9	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3428	16034	28514	3.71	1.0E-103	AW268245.1	EST_HUMAN	U1-H-BWO-gth-11-Q-U1.1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:2733165 3'
3487	16092	28584	1.19	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3818	18418		6.77	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3861	18459	28923	1.17	1.0E-103	AA485683.1	EST_HUMAN	ab10d12.s1 Strategene lung (8937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element:
4075	18871	29132	3.82	1.0E-103	T23883.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
4948	17821	29983	0.88	1.0E-103	BE590203.1	EST_HUMAN	601873135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
6091	18707	31455	0.73	1.0E-103	BF568527.1	EST_HUMAN	602186023F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4310573 5'
6097	18713	31483	1.8	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6413	18016	31798	0.71	1.0E-103	11435083	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6413	18016	31799	0.71	1.0E-103	11435083	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19184	31885	0.76	1.0E-103	AW954588.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6587	19184	31886	0.76	1.0E-103	AW954588.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6707	24767	32108	1.18	1.0E-103	AA781442.1	EST_HUMAN	q28e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391452 3'
6743	18337	32142	0.86	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6819	19409	32227	1.69	1.0E-103	AI590071.1	EST_HUMAN	hm58b05.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769
6819	19409	32228	1.69	1.0E-103	AI590071.1	EST_HUMAN	Q13769 ANONYMOUS.;
6833	18041	30484	1.67	1.0E-103	5032282	NT	hm58b05.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769
6833	18041	30485	1.67	1.0E-103	5032282	NT	Q13769 ANONYMOUS.;
6833	18041	30485	1.67	1.0E-103	5032282	NT	Q13769 ANONYMOUS.;
7047	18097	30457	1.07	1.0E-103	11431100	NT	Homo sapiens dyetrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS208, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7101	18871	32510	1.13	1.0E-103	AL289880.1	NT	Homo sapiens dyetrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS208, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7278	18808	32885	1.34	1.0E-103	AW965776.1	EST_HUMAN	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7372	18888	32769	3.38	1.0E-103	BE748158.1	EST_HUMAN	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
7748	20267	33182	4.44	1.0E-103	AI590071.1	EST_HUMAN	EST377849 MAGC resequences, MAGI Homo sapiens cDNA
							601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
							hm58b05.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7748	20257	33153	4.44	1.0E-103	AI580071.1	EST_HUMAN	hm58003.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
8556	21085	34015	1.14	1.0E-103	AU140344.1	EST_HUMAN	Q13769 ANONYMOUS. ;
8556	21085	34016	1.14	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8637	21176	34085	1.13	1.0E-103	BF108244.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9038	21573	34502	2.82	1.0E-103	6005921	NT	718003.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525884 3' similar to SW:PTNF_HUMAN Q18825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9038	21573	34503	2.82	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9075	21812	34544	1.06	1.0E-103	AA581088.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9117	21853	34584	1.29	1.0E-103	AA774880.1	EST_HUMAN	nd13c02.x1 NCL CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800182 3' similar to gb:L02428 26S
9970	22465	35449	1.65	1.0E-103	Z37978.1	NT	PROTEASE SUBUNIT 4 (HUMAN);
10011	22508	35497	1.84	1.0E-103	AW983878.1	EST_HUMAN	ae94d12.e1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb:X03747_cds1 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
10137	22832	35621	9.08	1.0E-103	AI878958.1	EST_HUMAN	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10521	23059	36089	2.78	1.0E-103	BE549706.1	EST_HUMAN	EST375749 MAGI resequences, MAGI Homo sapiens cDNA
10812	23145	36156	3.48	1.0E-103	AI792759.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518328 5' similar to TR:O16046 O16048 KIAA0338 ;
10713	23241	36257	2.21	1.0E-103	11424081	NT	7b41f03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M89043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10713	23241	36258	2.21	1.0E-103	11424081	NT	cd02d08.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING ;
10724	23251	36266	3.66	1.0E-103	AF149773.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10724	23251	36267	3.66	1.0E-103	AF149773.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11253	23763	36839	2.51	1.0E-103	AU136283.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11320	23018	36027	5.38	1.0E-103	L43810.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11590	24033	37103	4.36	1.0E-103	BE644611.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11684	24101		2.23	1.0E-103	AF224699.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11717	24126		1.91	1.0E-103	11828281	NT	7668a10.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER20.t3 MER29 repetitive element ;
11816	24254	31010	2.89	1.0E-103	AB011398.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
254	12814	25398	4.81	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
254	12814	25399	4.81	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
							DKFZp564H1072_r1 584 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564H1072 5'
							DKFZp564H1072_r1 584 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564H1072 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1832	14516	27072	2.08	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2235	14810	27382	2.22	1.0E-104	AA132975.1	EST_HUMAN	z02200.s1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:587628 3' similar to gb:Z14116_maf CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2245	14819	27394	1.47	1.0E-104	BE744828.1	EST_HUMAN	601577480F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928438 5'
2407	14975	27548	0.89	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-214-f12 CT0249 Homo sapiens cDNA
2407	14975	27548	0.89	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-214-f12 CT0249 Homo sapiens cDNA
2481	15047	27816	1.28	1.0E-104	5031670	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2898	15513	27893	8.17	1.0E-104	M34871.1	NT	Human lymphocyte antigen CD58/MEIM43 mRNA, complete cds
2941	15537		3.21	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3438	16046		1.77	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3681	16263	28736	0.63	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3681	16263	28736	0.63	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4015	16813	28088	1.2	1.0E-104	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4210	16789	28248	0.82	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31e07
4488	17052	28488	6.67	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4715	17288	29740	1.28	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4715	17288	29741	1.28	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5330	17891	30305	1.84	1.0E-104	4502162	NT	Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB) mRNA
6095	18711	31459	1.18	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6095	18711	31480	1.18	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6139	18753	31511	0.98	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/pil1-related kinase 3, complete cds
6593	19190	31893	8.25	1.0E-104	A1768797.1	EST_HUMAN	w03b12.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6593	19190	31894	8.25	1.0E-104	A1768797.1	EST_HUMAN	w03b12.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6756	19349	32158	1.07	1.0E-104	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6895	19829	32485	1.48	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6895	19829	32488	1.48	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7278	19804	32893	2.22	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8533	21072	33882	0.71	1.0E-104	BF509244.1	EST_HUMAN	U1-H-B14-sow-b-09-0-J1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088178 3'
9094	21630	34598	2.59	1.0E-104	BF448230.1	EST_HUMAN	ncd16g11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:33365948 3'
9187	21704	34848	0.6	1.0E-104	AA882308.1	EST_HUMAN	z98b05.s1 Soares_fetal_liver脾_1NFLS S1 Homo sapiens cDNA clone IMAGE:482897 3'
9208	21726		1.62	1.0E-104	174218.1	EST_HUMAN	y83f02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:22440 5'
9238	21764	34710	4.74	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9238	21764	34711	4.74	1.0E-104	AF091395.1	NT	Homo sapiens Tric isoform mRNA, complete cds
9302	20301	33201	4.8	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0819-080800-249-F07 HT0819 Homo sapiens cDNA
9392	20301	33202	4.8	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0819-080800-249-F07 HT0819 Homo sapiens cDNA
9698	22167	35142	0.69	1.0E-104	AW103848.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9698	22167	35143	0.69	1.0E-104	AW103848.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9859	22356	35336	0.54	1.0E-104	AF113514.1	NT	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10005	22500	35490	3.88	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10005	22500	35491	3.88	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10289	22783	36783	1.05	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10338	22832	35827	4.98	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001388 5'
10445	22839	35949	3.94	1.0E-104	U88535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
10457	22851		1.04	1.0E-104	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11176	23683	36728	2.44	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11176	23683	36728	2.44	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11208	23712	36766	5.34	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302507 5'
12538	24848		2.58	1.0E-104	BE393892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658876 5'
300	16384	25446	2.78	1.0E-105	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nepril-in, Alzheimer disease) (APP), mRNA
450	12878	25135	15.84	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
620	13247	25720	5.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
620	13247	25721	5.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1718	14311		1.84	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1859	14447	27094	1.35	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1970	14554	27110	1.24	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2231	14808	27379	1.38	1.0E-105	AA318389.1	EST_HUMAN	EST20609 Spleen I Homo sapiens cDNA 5' end similar to subunit Ku, p70/p80 subunit
2747	15302		1.43	1.0E-105	AA594808.1	EST_HUMAN	no10005.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1109285 3'
3039	15855		3.35	1.0E-105	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3394	16002	28482	0.72	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ28), mRNA
3394	16002	28483	0.72	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ28), mRNA
4173	16764	29212	2.65	1.0E-105	AW061688.1	EST_HUMAN	EST373761 MAGG resequenced, MAGG Homo sapiens cDNA
4833	17431	29881	0.65	1.0E-105	BE989881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4833	17431	29882	0.65	1.0E-105	BE989881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4874	17449	26600	1.08	1.0E-105	AJ698335.1	EST_HUMAN	z144g02.s1 Soares fetal_liver_spleen_TNFSF_S1 Homo sapiens cDNA clone IMAGE:433682 3'
5073	17648		4.94	1.0E-105	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5533	18165	30578	0.97	1.0E-105	AF016704.1	NT	Homo sapiens E8-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5594	18224		1.12	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6985	19483	32303	1.68	1.0E-105	BF314302.1	EST_HUMAN	601801028F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4130334 5'
6985	19483	32304	1.68	1.0E-105	BF314302.1	EST_HUMAN	601801028F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4130334 5'
7058	18077	30430	3.85	1.0E-105	11419188	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7058	18077	30431	3.85	1.0E-105	11419188	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7328	19855	32718	1.09	1.0E-105	BE602816.1	EST_HUMAN	601877278F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:38680019 5'
7800	20343	33252	0.87	1.0E-105	X12558.1	NT	Human mRNA for cdi proto-oncogene
7971	20513	33420	5.88	1.0E-105	T05087.1	EST_HUMAN	EST02878 Fetal brain, Striatum gene (cathepsin B206) Homo sapiens cDNA clone HFBOR32
8337	20878	33789	1.43	1.0E-105	AW007194.1	EST_HUMAN	w550c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500628 3' similar to SW/ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
8858	21397	34320	0.75	1.0E-105	AW840817.1	EST_HUMAN	RC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
8980	21618	34444	2.82	1.0E-105	AW016879.1	EST_HUMAN	U1-H-B10p-ab1-b-12-Q-J1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9131	21668	34606	0.87	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
9131	21668	34607	0.87	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
9487	21944	34891	1.07	1.0E-105	BE897793.1	EST_HUMAN	601443755F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3847884 5'
9487	21944	34892	1.07	1.0E-105	BE897793.1	EST_HUMAN	601443755F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3847884 5'
10812	23334	36347	6.07	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11109	23818	36660	2.15	1.0E-105	D83548.1	NT	Homo sapiens COL4A6 gene for $\alpha 1(V)$ collagen, exon 31
11101	23868	36713	2.07	1.0E-105	7705938	NT	Homo sapiens Ran binding protein 11 (LOC51184), mRNA
11467	23907	36974	2.58	1.0E-105	AW027554.1	EST_HUMAN	ww74f07.x1 Soares thymus_NHIFth Homo sapiens cDNA clone IMAGE:2635301 3' similar to TR:P87892 P87892 PROTEASE ;
11624	23972	37042	1.82	1.0E-105	BF430921.1	EST_HUMAN	T018c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680 RIN1 ;
13	12892	25148	2.29	1.0E-108	AB04483.1	EST_HUMAN	IL-BT057-281198-001 BT057 Homo sapiens cDNA
162	12825		1.55	1.0E-106	AW503208.1	EST_HUMAN	U1-HIF-BNO-akt-g-07-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
219	12880	25386	1.75	1.0E-108	AB650965.1	EST_HUMAN	tg78c001.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2215008 3'
567	13198	25678	1.82	1.0E-108	AW085558.1	EST_HUMAN	EST377829 MAGE resequences, MAGI Homo sapiens cDNA
633	13258	25733	2.3	1.0E-108	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
634	13258	25733	3.03	1.0E-108	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1572	14165	26696	1.57	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1739	14326	26873	4.72	1.0E-108	U49724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1757	14347	26892	0.89	1.0E-108	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1838	14427	26978	5.32	1.0E-108	AA527448.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element:
1839	14427	26979	5.32	1.0E-108	AA527448.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element:
2187	14744	27313	2.48	1.0E-108	BE144289.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2356	14927	27501	3.35	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2636	15196	27769	1.49	1.0E-108	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502481 5'
2768	15339	27910	0.69	1.0E-108	AJ276528.1	EST_HUMAN	q78h10.x1 Source NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2852	14071	26609	1.52	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2852	14071	26610	1.52	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2899	15516	27685	0.68	1.0E-108	BE384296.1	EST_HUMAN	60127676F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613618 5'
2968	15583	28063	6.37	1.0E-105	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
2968	15583	28064	6.37	1.0E-108	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3214	16826	28303	2.04	1.0E-108	8922868	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3214	15826	28304	2.04	1.0E-108	8922868	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3420	16028	28509	0.72	1.0E-108	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3488	16093	28585	1.14	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3488	16093	28586	1.14	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4111	16705	29158	9.08	1.0E-108	AW974850.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4111	16706	29159	9.08	1.0E-108	AW974850.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4706	17288	29732	1.47	1.0E-108	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5438	17993	30399	8.6	1.0E-108	S87479.1	NT	(GC)S=Vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomix, 2128 nt, segment 6 of 9]
5572	18203	30683	2.78	1.0E-108	AA781155.1	EST_HUMAN	q24b09.s1 Source testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
6017	18636	31375	0.67	1.0E-108	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6017	18636	31376	0.67	1.0E-108	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6145	18759	31517	0.82	1.0E-108	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6145	18759	31518	0.82	1.0E-108	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6250	18859	31631	13.06	1.0E-108	BF679574.1	EST_HUMAN	602164012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'
6355	18880	31738	0.68	1.0E-108	BE5897112.1	EST_HUMAN	601438870F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6551	19149	31945	19.14	1.0E-108	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6551	19149	31946	19.14	1.0E-108	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7408	19931	32795	5.83	1.0E-108	AA683779.1	EST_HUMAN	ae72e07.a1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:989732 3' similar to gb:X63873
7453	19977	32842	4.92	1.0E-108	11428817	NT	KINESIN HEAVY CHAIN (HUMAN);
7614	20035	32901	1.23	1.0E-108	BE292722.1	EST_HUMAN	Homo sapiens XPMG2 protein (LOC37109), mRNA
7608	20119	32995	8.75	1.0E-108	11425503	NT	601105738F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7608	20119	32996	8.75	1.0E-108	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7769	20277	33176	0.72	1.0E-108	AW163047.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
7928	20468	33379	5.97	1.0E-108	BE741408.1	EST_HUMAN	au9105.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783849 5' similar to TR:075834
7928	20468	33377	5.97	1.0E-108	BE741408.1	EST_HUMAN	O75834 CJLLIN-4A ;
8115	20858	33585	13.85	1.0E-108	AE23088.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
8564	21103	34022	0.74	1.0E-108	BE387850.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
8564	21103	34023	0.74	1.0E-108	BE387850.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
8640	21179	34096	3.9	1.0E-108	AE54123.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
8646	21184	34103	0.54	1.0E-108	AE54123.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
8882	21820	34448	0.58	1.0E-108	AV838831.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9074	21811	34542	2	1.0E-108	AA825307.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9074	21811	34543	2	1.0E-108	AA825307.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9210	21727	34870	2.03	1.0E-108	AE750447.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9350	21864	34814	1.46	1.0E-108	AE750447.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9350	21864	34815	1.46	1.0E-108	AE750447.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9913	22409	35385	1.35	1.0E-108	BE389234.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9988	22491	35479	1.47	1.0E-108	BF027310.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
9988	22491	35480	1.47	1.0E-108	BF027310.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
10139	22834	35624	8.16	1.0E-108	AA604417.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
10139	22834	35625	8.16	1.0E-108	AA604417.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
10185	22880	35672	1.56	1.0E-108	AW363269.1	EST_HUMAN	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
10180	22885	35677	0.77	1.0E-108	11438432	NT	601694331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10190	22685	35678	0.77	1.0E-108	11438432	NT	Homo sapiens multimilin (MMRN), mRNA
10358	22852	35848	0.45	1.0E-108	AL039888.1	EST_HUMAN	DKFZp434F0712_1 434 (synonym: hhs3) Homo sapiens cDNA clone DKFZp434F0712 5'
10472	22868	35978	3.31	1.0E-108	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10776	23288	38304	8.85	1.0E-108	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857388 5'
10776	23288	38305	8.85	1.0E-108	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857388 5'
10941	23457	38480	2.93	1.0E-108	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
10941	23457	38481	2.93	1.0E-108	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11288	23739	38785	1.87	1.0E-108	BE267385.1	EST_HUMAN	601108219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3348887 5'
11418	23869	38929	1.83	1.0E-108	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-802 BN0192 Homo sapiens cDNA
11418	23869	38930	1.83	1.0E-108	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-802 BN0192 Homo sapiens cDNA
11782	24887		6.89	1.0E-108	AW410405.1	EST_HUMAN	60108111.xt NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2881644 5'
11891	24301	30888	4.03	1.0E-108	BE884488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
11891	24301	30887	4.03	1.0E-108	BE884488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12218	24439		3.44	1.0E-108	BE895005.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
255	12915		2.78	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
288	12842		1.25	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
658	13281	25761	1.82	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
848	13482	25970	1.45	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
919	13532	28050	2.27	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
1004	13615	28129	8.14	1.0E-107	AF164121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1321	13915	28437	1.33	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1615	14208	26741	2.81	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120500-358-q05 HT0540 Homo sapiens cDNA
1788	14378	26922	2.7	1.0E-107	AF138276.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1880	14468	27023	0.89	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1880	14468	27024	0.89	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2248	14823	27399	1.17	1.0E-107	U13728.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2400	14888	27541	0.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2400	14888	27542	0.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2572	15135	27708	5.5	1.0E-107	BE732460.1	EST_HUMAN	601587619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2572	15135	27707	5.5	1.0E-107	BE732460.1	EST_HUMAN	601587619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
3040	15658	28135	3.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3040	15658	28136	3.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3134	15748	28217	3.02	1.0E-107	5902087	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homologue 2 (SMT3H2), mRNA

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Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3898	16497	28959	4.68	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
3972	16570	26039	1.69	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
3972	16570	26040	1.69	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
6026	18644	31388	4.74	1.0E-107	BE887469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'
7398	18824	32788	1.4	1.0E-107	AW603913.1	EST_HUMAN	U1-HF-BNO-alf-c-08-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076310 5'
7398	18824	32789	1.4	1.0E-107	AW603913.1	EST_HUMAN	U1-HF-BNO-alf-c-08-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076310 5'
7536	20056	32930	1.28	1.0E-107	A1765078.1	EST_HUMAN	w158n04.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2384791 3'
8308	21908	34858	0.88	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10533	23070	36083	2.05	1.0E-107	BE169726.1	EST_HUMAN	QV1-HT0516-140300-107-c10 HT0516 Homo sapiens cDNA
10583	23116	36133	3.35	1.0E-107	A1982850.1	EST_HUMAN	t910d08.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
10825	23346	36362	2.16	1.0E-107	L49141.1	NT	P068096 ALPHA-ACTININ 3, NON MUSCULAR
10839	23360	36375	2.39	1.0E-107	BF686511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11203	23708	36760	4.35	1.0E-107	BE540550.1	EST_HUMAN	602123063F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281039 5'
11271	23009	36016	4.67	1.0E-107	11419701	NT	60106688F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452828 5'
11271	23009	36017	4.67	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11577	24023	37082	3.77	1.0E-107	4507823	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11830	26014		7.41	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
189	12850		1.3	1.0E-108	AA341934.1	EST_HUMAN	z945a01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
990	13802	26116	1.84	1.0E-108	BE286042.1	EST_HUMAN	EST147363 Fetal muscle Homo sapiens cDNA 5' end
1308	13902	26421	4.68	1.0E-108	Y18000.1	NT	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2123	14701	27271	0.95	1.0E-108	BF028728.1	EST_HUMAN	Homo sapiens NF2 gene
2368	14839	27511	1.91	1.0E-108	A1686040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954839 5'
2368	14839	27512	1.91	1.0E-108	A1686040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954839 5'
2472	15039	27607	7.53	1.0E-108	BE206694.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
3392	16000	28478	0.73	1.0E-108	AF032897.1	NT	1691610.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
3392	16000	28479	0.73	1.0E-108	AF032897.1	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
4237	16825	28275	1.43	1.0E-108	AW684438.1	EST_HUMAN	1691610.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963889 3' similar to gb:X53777 60S
							RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							h12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2072060 3' similar to SW:3BP1_MOUSE
							P55194 SH3-BINDING PROTEIN 3BP-1.;

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4824	17207	28656	1.92	1.0E-108	U72861.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4824	17207	28657	1.92	1.0E-108	U72861.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4926	17501	28948	2.66	1.0E-108	7661978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5044	17617	30082	0.93	1.0E-108	AW604799.1	EST_HUMAN	UI-HF-BNO-ah-e-04-0-UI.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3080168 5'
5094	17657	30088	2.16	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5318	17880	30289	0.81	1.0E-108	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5870	18207	30777	1.2	1.0E-108	AW384094.1	EST_HUMAN	RCO-HT0372-241199-031-c03 HT0372 Homo sapiens cDNA
5718	18344	30851	2.96	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848980 5'
5718	18344	30852	2.96	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848980 5'
6084	18701		0.83	1.0E-108	AF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6163	18766	31528	0.88	1.0E-108	BF334861.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6288	18896	31696				NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6288	18896	31697	5.83	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6409	19012	31795	1.16	1.0E-108	AJ133289.1	NT	Homo sapiens carvedin-1/-2 locus, Contig1, DTS522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6489	18766	31528	1.01	1.0E-108	BF334861.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6732	18328	32130	0.85	1.0E-108	AF016708.1	NT	Homo sapiens E8-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6732	18328	32131	0.85	1.0E-108	AF016708.1	NT	Homo sapiens E8-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7211	19742	32598	5.04	1.0E-108	11431887	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7485	19887	32852	3.44	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7492	20015	32881	1.67	1.0E-108	BE252807.1	EST_HUMAN	601113471F1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:3354064 5'
7516	20036	32803	1.06	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
7516	20036	32804	1.06	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8008	20550		1.77	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8058	20600	33509	1.47	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3082878 5'
8058	20600	33510	1.47	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3082878 5'
8977	21515	34439	1.08	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
9016	21662	34480	0.52	1.0E-108	N44974.1	EST_HUMAN	y33h10.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
10501	22895	36004	0.49	1.0E-108		NT	A45773 ketch protein, long form - fruit fly;
10547	20278	33178	1.87	1.0E-108	BE538227.1	EST_HUMAN	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83448), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10707	18037	30497	2.08	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
11151	23659	36703	4.23	1.0E-108	AW968185.1	EST_HUMAN	EST1378258 MAGE resequences, MAGI Homo sapiens cDNA
11204	23709	36761	1.81	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11204	23709	36762	1.81	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11248	23778		2.91	1.0E-108	11441466	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11306	23798	36857	1.72	1.0E-108	D83539.1	NT	Homo sapiens COL4A8 gene for α (IV) collagen, exon 23
12005	24308	30991	5.17	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12414	24597		7.56	1.0E-108	BF346358.1	EST_HUMAN	602018571F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4184297 5'
46	12725	25186	2.13	1.0E-109	AW803116.1	EST_HUMAN	IL2-JM0077-260-000-079-D08 UM0077 Homo sapiens cDNA
68	12747	25225	3.04	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
235	12895	25378	4.41	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11318 (FLJ11318), mRNA
246	12905	25388	2.89	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
492	13125	25610	4.89	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
624	13251	25726	19.67	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
624	13251	25726	19.67	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1050	13657	26166	0.72	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1244	13842	26356	24.19	1.0E-109	M26699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1245	13842	26359	15.82	1.0E-109	M26699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1589	14182	26714	0.88	1.0E-109	BE283673.1	EST_HUMAN	60118692F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959638 5'
1589	14182	26715	0.88	1.0E-109	BE283673.1	EST_HUMAN	60118692F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959638 5'
1915	14500	27055	3.28	1.0E-109	D13843.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2263	14857	27434	1.19	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2292	14898	27441	2.08	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2652	15211	27763	2.86	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1854538 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;
2652	15211	27764	2.86	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1854538 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;
2653	15212	27765	2.01	1.0E-108	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3094	15709	28180	1.68	1.0E-109	N85190.1	EST_HUMAN	J2818F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2818 5' similar to ZINC FINGER PROTEIN ZNF43
3435	16043	28524	1.34	1.0E-108	AW893182.1	EST_HUMAN	CM3-NN0008-180400-150-110 NN0008 Homo sapiens cDNA
3435	16043	28525	1.34	1.0E-108	AW893182.1	EST_HUMAN	CM3-NN0008-180400-150-110 NN0008 Homo sapiens cDNA
3569	16173	28655	0.9	1.0E-109	AF240698.1	NT	Homo sapiens retinal dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3609	16508		0.83	1.0E-108	BE146144.1	EST_HUMAN	MRO-HT0208-110400-108-404 HT0208 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	16816	28264	4.43	1.0E-109	AI655417.1	EST_HUMAN	ts9608.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2289330 3' similar to WP.F83A2.8
4493	17078	28528	2.7	1.0E-109	4504208	NT	CE16100 ;
4705	17287	29731	1.18	1.0E-109	7682083	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
5051	17824	30069	1.14	1.0E-109	R15400.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5485	18100	30418	0.78	1.0E-109	BF673718.1	EST_HUMAN	ye48e08.r1 Soenke infant brain 1N1B Homo sapiens cDNA clone IMAGE:53057 5'
5516	18148	30560	2.8	1.0E-109	5174822	NT	602138448F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272822 5'
6762	18417		1.24	1.0E-109	BE178386.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6085	24758	31448	1.02	1.0E-109	BF379688.1	EST_HUMAN	RC1-HT0816-200400-022-404 HT0816 Homo sapiens cDNA
8147	18417		1.3	1.0E-109	BE178386.1	EST_HUMAN	CM1-UT0038-060900-389-h07 UT0038 Homo sapiens cDNA
8491	19082	31876	0.8	1.0E-109	M23442.1	NT	RC1-HT0815-200400-022-404 HT0815 Homo sapiens cDNA
8491	19082	31876	0.8	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
8491	19082	31876	0.8	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
7289	19817	32876	0.95	1.0E-109	AB048811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7668	20083	32969	4.08	1.0E-109	11432674	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7568	20085	32861	5.84	1.0E-109	BF182707.1	EST_HUMAN	601809485F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7668	20085	32862	5.94	1.0E-109	BF182707.1	EST_HUMAN	601809485F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8114	20855	33564	1.17	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
8227	20768	33687	1.27	1.0E-109	AW748130.1	EST_HUMAN	PMC-BT0340-081289-002-e05 BT0340 Homo sapiens cDNA
8591	21130		2.85	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8669	21208	34125	14.1	1.0E-109	BE787640.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8669	21208	34126	14.1	1.0E-109	BE787640.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8908	21448	34368	0.57	1.0E-109	BE145872.1	EST_HUMAN	ILG-HT0205-071189-142-g01 HT0205 Homo sapiens cDNA
9163	21688	34642	1.82	1.0E-109	HB4860.1	EST_HUMAN	ye80g08.r1 Soenke retina N265HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP.A53491
9272	21768	34747	0.54	1.0E-109	BE397098.1	EST_HUMAN	A63491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINY ;
9272	21768	34748	0.54	1.0E-109	BE397098.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3920030 5'
9405	21814	34863	3.55	1.0E-109	F06604.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3920030 5'
10653	23185	36200	2.73	1.0E-109	BE540808.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-16012
10653	23185	36201	2.73	1.0E-109	BE540808.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449589 5'
10653	23185	36201	2.73	1.0E-109	BE540808.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449589 5'
10687	23217	36228	35.63	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246341 5'
10847	23368	36386	2	1.0E-109	7682278	NT	Homo sapiens KIAA0744 gene product, histone deacetylase 7 (KIAA0744), mRNA
10847	23368	36387	2	1.0E-109	7682278	NT	Homo sapiens KIAA0744 gene product, histone deacetylase 7 (KIAA0744), mRNA
11004	23518	36553	1.85	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002680 5'
11248	23778	36835	2.84	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11285	23738	36764	6.81	1.0E-109	W16510.1	EST_HUMAN	z008b12.r1 Soares fetal lung NIH.L19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
12131	14866	27441	1.6	1.0E-109	Y17123.1	NT	PIR:S43959 S43959 p54-beta stress-activated protein kinases - rat;
12252	24483	30981	15.45	1.0E-109	AB011366.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	12683	25139	1.19	1.0E-110	7549804	NT	Homo sapiens gene for AF-8, complete cds
40	12719	25178	4.61	1.0E-110	5803073	NT	Homo sapiens deloidinase, iodotyrosine, type II (DIO2), transcript variant 2, mRNA
40	12719	25180	4.61	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
114	12683	25139	0.83	1.0E-110	7549804	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
316	12970	25438	1	1.0E-110	D87291.1	NT	Homo sapiens deloidinase, iodotyrosine, type II (DIO2), transcript variant 2, mRNA
553	13184	25662	0.93	1.0E-110	U84550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1222	13822	26337	0.97	1.0E-110	6031820	NT	Human dyshidrotic (DTN) gene, exon 20
1322	13916	26438	1.28	1.0E-110	AB032253.1	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1965	14549	27105	1.48	1.0E-110	BE379477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2103	14882		1.66	1.0E-110	BF508898.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608883 5'
2868	15484		0.95	1.0E-110	4503098	NT	U14-B14-acc-b-05-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086784 3'
3066	13916	26438	0.85	1.0E-110	AB032253.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3123	15737		1.2	1.0E-110	U78027.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3228	15840	28319	6.37	1.0E-110	11436041	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3228	15840	28320	6.37	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4128	16720	29175	0.92	1.0E-110	BE018556.1	EST_HUMAN	Homo sapiens pregnancy-zone protein (PZP), mRNA
4261	16867	29314	1.06	1.0E-110	M15918.1	NT	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048948 5' similar to TR:O60312 O60312
4740	17321	29781	2.32	1.0E-110	A017213.1	EST_HUMAN	KIAA0586 PROTEIN ;
4758	17339	29785	3.28	1.0E-110	AU117812.1	EST_HUMAN	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene
5109	17681		1.8	1.0E-110	7682441	NT	cu32b10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627863 3' similar to
5498	18132	30540	2.18	1.0E-110	BE289408.1	EST_HUMAN	SW.N121_RAT P62591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
5900	18522	31247	0.7	1.0E-110	BE621089.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5917	18539	31264	6.81	1.0E-110	11419323	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5917	18538	31265	6.81	1.0E-110	11419323	NT	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028638 5'
6818	24771	32226	3.2	1.0E-110	M55112.1	NT	601483977F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895785 5'
7169	19691	32536	0.83	1.0E-110	U08888.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7159	19691	32537	0.83	1.0E-110	U08888.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
							Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
							Human GS2 gene, exon 2
							Human GS2 gene, exon 2

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7364	19880	32763	0.74	1.0E-110	AI560289.1	EST_HUMAN	bt12d08.x1 NCI_CGAP_Bm28 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7454	19978	32843	11.26	1.0E-110	AV714276.1	EST_HUMAN	P50549 ETS TRANSLOCATION VARIANT 1;
7454	19978	32844	11.26	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7478	20000	32865	2.84	1.0E-110	AB020675.1	NT	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7571	20088	32884	1.08	1.0E-110	AU137923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0888 protein, partial cds
9258	21784	34737	0.64	1.0E-110	BE302594.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007611 5'
9497	21987	34853	2.81	1.0E-110	AW838394.1	EST_HUMAN	ba8861.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2005561 5' similar to TR:O77258 O77258
10228	22721	35712	3.91	1.0E-110	11432732	NT	EG.114D8.2 PROTEIN.;
10826	23168	36171	3.89	1.0E-110	Y12337.1	NT	QV2-LT0053-020400-118-e04 LT0053 Homo sapiens cDNA
10848	23367	36384	3.87	1.0E-110	BE734357.1	EST_HUMAN	Homo sapiens galactokinase 2 (GALK2), mRNA
10848	23367	36385	3.87	1.0E-110	BE734357.1	EST_HUMAN	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
11317	23015	36024	3.28	1.0E-110	AA446526.1	EST_HUMAN	601565504F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11719	24128		2.88	1.0E-110	BE697218.1	EST_HUMAN	601565504F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11849	24209	AW062258.1	11.88	1.0E-110	AW062258.1	EST_HUMAN	zxc67g02.r1 Soares_bedis_NHT Homo sapiens cDNA clone IMAGE:781288 5' similar to TR:G1145818
12082	24360		2.73	1.0E-110	AB011398.1	NT	G1145818 FKBP64;
12239	25027		8.39	1.0E-110	BF364546.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924948 5'
12537	14882		1.43	1.0E-110	BF508896.1	EST_HUMAN	IL0-BT0163-040309-084-q10 BT0163 Homo sapiens cDNA
186	12847		28.49	1.0E-111	U43701.1	NT	Homo sapiens gene for AF-6, complete cds
210	12871	25357	0.94	1.0E-111	4788807	NT	PM3-NN1082-140900-008-f12 NN1082 Homo sapiens cDNA
764	13383		1.84	1.0E-111	BF03327.1	EST_HUMAN	U1-H-BI4-acc-b-05-Q-U1.at NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
773	13392	26882	5.48	1.0E-111	8383082	NT	Human ribosomal protein L23a mRNA, complete cds
982	13573	26088	2.34	1.0E-111	M25142.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
1670	14263	26797	2.34	1.0E-111	7882177	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
4250	16838	29288	1.25	1.0E-111	7881669	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
4423	17008	29451	4.84	1.0E-111	K02268.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
5814	18438	31160	0.91	1.0E-111	BE687606.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
6183	18793	31562	1.58	1.0E-111	A1344678.1	EST_HUMAN	Homo sapiens DKFZP434D158 protein (DKFZP434D158), mRNA
6781	19372	32188	1	1.0E-111	AL040782.1	EST_HUMAN	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
6808	19632	32470	1.3	1.0E-111	AW204648.1	EST_HUMAN	601443890F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3847855 5'
7471	19993	32856	2.68	1.0E-111	BF366228.1	EST_HUMAN	qp09g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M28883 RAS-RELATED PROTEIN RAL-A (HUMAN);
							DKFZp34C1815_j1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp34C1815 5'
							U1-H-BW0-ail-4-03-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2726525 3'
							IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7540	20080	32834	3.47	1.0E-111	A1761228.1	EST_HUMAN	w188d01.x1 NCI CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIA5 (HUMAN);
7610	20123	33000	1.1	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) gene, complete cds
8038	20580	33486	0.77	1.0E-111	AA278868.1	EST_HUMAN	zs79g03.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8038	20580	33487	0.77	1.0E-111	AA278868.1	EST_HUMAN	zs79g03.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8128	20670	33580	0.89	1.0E-111	11431888	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8183	20724	33638	5.8	1.0E-111	U86533.1	NT	Human beta4-Integrin (ITGB4) gene, exon 13
8613	21152	34086	0.82	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8710	21249	34172	0.89	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00046 protein, partial cds
8743	21282		23.24	1.0E-111	BF214892.1	EST_HUMAN	601847132F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4078303 5'
8817	21356	34280	12.59	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
8817	21356	34281	12.59	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
9017	21654	34482	3.03	1.0E-111	AF091365.1	NT	Homo sapiens T10 isoform mRNA, complete cds
9241	21767	34716	0.58	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-e06 BT0817 Homo sapiens cDNA ae58g02.a1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826170 3' similar to gb:L09235
10056	22551	35546	2.03	1.0E-111	AA504180.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10082	22577		1.53	1.0E-111	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10173	22688	35683	5.78	1.0E-111	AA131248.1	EST_HUMAN	z31f01.r1 Soares_pregnant_uterus_NBRPU Homo sapiens cDNA clone IMAGE:503545 5'
10922	23441	36482	4.83	1.0E-111	U88159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
11674	24083	37146	4.3	1.0E-111	11417801	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (M1N1), mRNA
12234	24450	30954	2.23	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADOA0808 5'
12360	24816	30791	6.35	1.0E-111	W22562.1	EST_HUMAN	72C9 Human retina cDNA Tap5081-cleaved sublibrary Homo sapiens cDNA not directional
12507	18039	30488	1.31	1.0E-111	AB035356.1	NT	Homo sapiens mRNA for neurodin I-alpha protein, complete cds
836	13259	25734	1.69	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
838	13261	25736	5.94	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
638	13261	25737	5.94	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
660	13283	25763	1.42	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-act-g-04-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
680	13283	25784	1.42	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-act-g-04-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1039	13649	26161	3.88	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1100	13705	26213	2	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1722	14313	26853	4.44	1.0E-112	7682126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1722	14313	28854	4.44	1.0E-112	7882128	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1858	14444	27000	1.58	1.0E-112	AF248540.1	NT	Homo sapiens Interleukin 2 (SH3D1B) mRNA, complete cds
2550	15114	27684	1.81	1.0E-112	BE968959.1	EST_HUMAN	601442874F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3846858 5'
3114	18729		0.59	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3853	18551	29020	0.74	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-080300-113-709 BT0590 Homo sapiens cDNA
4709	17281	29735	0.65	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4884	17441	28881	5.1	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4884	17441	28892	5.1	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5848	18472	31198	38.42	1.0E-112	N46046.1	EST_HUMAN	Y93507.1 Scars melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273229 5'
6227	18836	31609	1.36	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6294	18802	31672	0.95	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0P-aje-g-08-0-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6294	18902	31673	0.85	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0P-aje-g-08-0-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6397	19000	31778	1.2	1.0E-112	BE741668.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6747	18340	32148	0.88	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6747	18340	32147	0.88	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6828	19587	32418	1.36	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7376	19801	32784	1.57	1.0E-112	11418777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC9A7), mRNA
7375	19801	32785	1.57	1.0E-112	11418777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC9A7), mRNA
8134	20876	33587	1.63	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
8887	21425	34350	2.49	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3847285 5'
8887	21425	34351	2.49	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3847285 5'
9807	22305	35289	2.08	1.0E-112	BF111413.1	EST_HUMAN	730g07.x1 Scars_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
10657	23189	36205	3.51	1.0E-112	AW863327.1	EST_HUMAN	TR-Q8VW35 Q8VW35 CG8743 PROTEIN ;
10743	23267	36283	1.85	1.0E-112	T63987.1	EST_HUMAN	MR3-SN0009-100400-108-b12 SN0009 Homo sapiens cDNA
10743	23267	36284	1.85	1.0E-112	T63987.1	EST_HUMAN	Yd56d10.a1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
10827	23348	36384	4.28	1.0E-112	AJ246800.1	NT	SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
10878	23491	36521	1.78	1.0E-112	BE280478.1	EST_HUMAN	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11051	23564	36599	2.08	1.0E-112	AJ904594.1	EST_HUMAN	601153323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3136889 5'
11082	23574	36611	4.71	1.0E-112	AW377870.1	EST_HUMAN	IL-BT081-311289-009 BT081 Homo sapiens cDNA
							PMO-CT0237-141099-001-02 CT0237 Homo sapiens cDNA

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	13391	25890	6.13	1.0E-113	A385588.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
772	13391	25891	6.13	1.0E-113	A385588.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
978	13590	26105	6.33	1.0E-113	M11985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1588	14181	26713	2.48	1.0E-113	A385588.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
1983	16396	27126	0.82	1.0E-113	AF240776.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2142	14720	27281	1.02	1.0E-113	BF513218.1	EST_HUMAN	U1-H-BW1-ent-4-03-Q-U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3164	15778	28249	2.08	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5484	24852		3.07	1.0E-113	BE780868.1	EST_HUMAN	801468465F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872536 5'
5684	18311	30808	6	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6080	18697	31444	3.89	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLAGE2000274 5'
6106	18722	31475	1	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6220	18830	31604	2.43	1.0E-113		NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 6 (GalNAc-T6) mRNA
6304	18911	31684	0.88	1.0E-113		NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6304	18911	31685	0.88	1.0E-113		NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6458	19059	31844	0.71	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7362	19898	32751	0.77	1.0E-113	BE262181.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7382	19888	32752	0.77	1.0E-113	BE262181.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
8024	21561	34488	3	1.0E-113	BE382842.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
9024	21561	34489	3	1.0E-113	BE382842.1	EST_HUMAN	601287708F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827654 5'
9322	21838		0.72	1.0E-113	BE772687.1	EST_HUMAN	601287708F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827654 5'
9745	22243	35224	1.2	1.0E-113	11426337	NT	RC1-F10134-280600-021-002 F10134 Homo sapiens cDNA
9843	22341	35323	0.56	1.0E-113	M21535.1	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
9863	22458	35441	0.81	1.0E-113	5453987	NT	Human erg protein (eto-related gene) mRNA, complete cds
9963	22458	35442	0.81	1.0E-113	5453987	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11002	23516	36551	1.71	1.0E-113	AW600519.1	EST_HUMAN	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11011	23525	36559	2.11	1.0E-113	AW603291.1	EST_HUMAN	U1-HF-BNO-ak-b-12-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077328 5'
11011	23525	36560	2.11	1.0E-113	AW630291.1	EST_HUMAN	h81a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868176 5' similar to TR:O60327 O60327
11097	19059	31844	1.58	1.0E-113	6006002	NT	KIAA0584 PROTEIN ;
							h81a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868176 5' similar to TR:O60327 O60327
							KIAA0584 PROTEIN ;
							h81a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868176 5' similar to TR:O60327 O60327
							KIAA0584 PROTEIN ;
							Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11097	18059	31846	1.58	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11141	23849	36891	3.51	1.0E-113	BE292988.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988868 5'
11370	23822	36884	2.53	1.0E-113	AA680720.1	EST_HUMAN	nc80b03.1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
11370	23822	36885	2.53	1.0E-113	AA590720.1	EST_HUMAN	nc80b03.1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
62	12741	25213	1.2	1.0E-114	Y17151.2	NT	P36748 FLAP ENDONUCLEASE-1;
62	12741	25214	1.2	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
62	12741	25215	1.2	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
673	13297	25779	22.22	1.0E-114	T70551.1	EST_HUMAN	y415c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108286 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element
1109	13713	26223	2.83	1.0E-114	8923037	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1386	13950	26476	3.57	1.0E-114	7867828	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
1684	14276	26809	1.26	1.0E-114	6831094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1711	14304	26841	7.13	1.0E-114	6876073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2830	12727	25189	2.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
2830	12727	25190	2.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3185	15778	28250	2.38	1.0E-114	X04088.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3207	15819	28295	1.02	1.0E-114	BF208374.1	EST_HUMAN	601869832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4088	16694	29142	1.81	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4480	17005	29515	0.82	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5324	17888	30302	0.89	1.0E-114	BE278324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346098 5'
5380	17920	30334	0.83	1.0E-114	AA184488.1	EST_HUMAN	zq05e05.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:628832 5' similar to contains MER22.13 MER22 repetitive element;
5587	18227	30874	1.36	1.0E-114	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5597	18227	30875	1.36	1.0E-114	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5781	18408	31122	1.35	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTOL1), transcript variant 2, mRNA
7137	18476		1.13	1.0E-114	AB041633.1	NT	Homo sapiens HOMOGT-1 mRNA for sperm antigen, complete cds
7288	19818	32874	1.2	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVAC1 Homo sapiens cDNA clone OVARC1001444 5'
7288	19818	32876	1.2	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVAC1 Homo sapiens cDNA clone OVARC1001444 5'
7328	19853	32715	7.05	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7328	19863	32716	7.05	1.0E-114	Y18030.1	NT	Homo sapiens NF2 gene
7832	20374	33280	1.88	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8108	20849	33557	1.81	1.0E-114	A1363139.1	EST_HUMAN	qy68d06.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017183 3'
8108	20849	33558	1.81	1.0E-114	A1363139.1	EST_HUMAN	qy68d06.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017183 3'
8835	21174	34083	4.12	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD58 mRNA, complete cds
8702	21241	34165	5.52	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
8702	21241	34166	5.52	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
9110	21648	34586	0.92	1.0E-114	BF108832.1	EST_HUMAN	7189p12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q8UHN8 Q8UHN8 TRANSMEMBRANE PROTEIN 2 ;
9335	21849		18.44	1.0E-114	AW327465.1	EST_HUMAN	dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9384	20322	33227	3.14	1.0E-114	AF077764.1	NT	Homo sapiens tyrosine kinase pp60-cro (SRC) gene, exon 12 and partial cds
9487	21892		6.13	1.0E-114	M13536.1	NT	Human ceruloplasmin mRNA
10045	22540	35537	0.94	1.0E-114	BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10086	22561	35556	1.32	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10434	22926	35935	0.71	1.0E-114	BE171884.1	EST_HUMAN	MRO-HT0556-250200-002-007 HT0556 Homo sapiens cDNA
							ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806086 5' similar to gb:X17208.40S
							RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
10866	23186		13.62	1.0E-114	BE302668.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11070	23582	36822	3.31	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11070	23582	36823	3.31	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
12137	25093		3.79	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12410	24585	30909	2.85	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12410	24585	30910	2.85	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
25	12704	25162	6.12	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D8S81E) mRNA
135	12800	25288	2.34	1.0E-115	4506938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
139	12804		6.73	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
314	12888	25456	3.77	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0084-300300-158-608 UM0084 Homo sapiens cDNA
561	13192	25670	0.95	1.0E-115	A1339208.1	EST_HUMAN	q06f01.x1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1846809 3' similar to TR:O00536 O00536
561	13192	25671	0.95	1.0E-115	A1339208.1	EST_HUMAN	q06f01.x1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1846809 3' similar to TR:O00536 O00536
819	13438	25942	1.28	1.0E-115	5174702	NT	TTF-1 INTERACTING PEPTIDE 5 ;
819	13438	25943	1.28	1.0E-115	5174702	NT	TTF-1 INTERACTING PEPTIDE 5 ;
821	13438	25945	180.74	1.0E-115	4503784	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
							Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
							Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA

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1608	14188	28730	1.2	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1608	14188	28731	1.2	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1881	14467	27025	1.19	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2125	14703	27273	1.11	1.0E-115	BE745488.1	EST_HUMAN	601578338F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2125	14703	27274	1.11	1.0E-115	BE745488.1	EST_HUMAN	601578338F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
3149	16763	28230	2.81	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3149	16763	28231	2.81	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3518	16124	28604	2.12	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4115	18709	29184	4.23	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4353	16940	28382	1.31	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4490	17075	28525	2.88	1.0E-115	6912859	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4528	17113	28557	4.4	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4783	17363	28813	2.89	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4783	17363	28814	2.89	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5032	17608	30050	3.79	1.0E-115	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
5032	17608	30051	3.79	1.0E-115	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
5550	18182	30597	2.42	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGC resequences, MAGK Homo sapiens cDNA
5617	18248	30697	1.07	1.0E-115	BF665387.1	EST_HUMAN	60219348F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278738 5'
6732	18358	31083	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
6732	18358	31084	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
5859	18491	31217	1.1	1.0E-115	AI928799.1	EST_HUMAN	au84901.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519558 3' similar to gbL07807
5859	18491	31218	1.1	1.0E-115	AI928799.1	EST_HUMAN	au84901.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519558 3' similar to gbL07807
6408	18011	31793	0.89	1.0E-115	11428786	NT	DYNAMIN-1 (HUMAN);
6408	18011	31794	0.89	1.0E-115	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6528	19128	31923	20.52	1.0E-115	11428038	NT	Homo sapiens sperm surface protein (HSS), mRNA
6648	19245	32047	1.74	1.0E-115	7881883	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC83439), mRNA
6648	19245	32048	1.74	1.0E-115	7881883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7014	19512	32333	0.89	1.0E-115	T88774.1	EST_HUMAN	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7322	19848	32708	1.16	1.0E-115	AI076598.1	EST_HUMAN	Y88508.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP:DPGG_YEAST P15801 DNA POLYMERASE GAMMA ;
7322	19848	32710	1.18	1.0E-115	AI076598.1	EST_HUMAN	alpha31a08.x1 Scores fetal spleen INFLS Homo sapiens cDNA clone IMAGE:1676814 3'
7322	19848	32710	1.18	1.0E-115	AI076598.1	EST_HUMAN	alpha31a08.x1 Scores fetal spleen INFLS Homo sapiens cDNA clone IMAGE:1676814 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7438	19682	32828	6.85	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
8101	20842	33553	12.93	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8101	20842	33554	12.93	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8747	21286	34207	4.14	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
9690	22189	35162	0.56	1.0E-115	BF382028.1	EST_HUMAN	601816352F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4055108 5'
8810	22407	35382	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
8910	22407	35383	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10414	22608	35608	1.08	1.0E-115	A1221878.1	EST_HUMAN	qg89e09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10414	22608	35607	1.08	1.0E-115	A1221878.1	EST_HUMAN	qg89e09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10420	22914	35914	0.68	1.0E-115	A1524687.1	EST_HUMAN	h12a07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2118036 3' similar to TR:O16129 O16129
10448	22842	35952	0.79	1.0E-115	BE886285.1	EST_HUMAN	PHENYLANALYL TRNA SYNTHETASE ;
10588	23130	38144	3.79	1.0E-115	AW571644.1	EST_HUMAN	60150879F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911610 5'
11140	23648	38689	1.84	1.0E-115	BE045880.1	EST_HUMAN	x032708.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE ;
11140	23648	38680	1.84	1.0E-115	BE045880.1	EST_HUMAN	h954c10.x1 NCI_CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378
11276	23729	38784	2.84	1.0E-115	4502628	NT	PRP4 PROTEIN KINASE HOMOLOG ;
11698	24111		1.48	1.0E-115	AF240788.1	NT	PRP4 PROTEIN KINASE HOMOLOG ;
598	13227	25701	2.19	1.0E-115	BE275502.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
833	13450	25957	1.23	1.0E-115	4507334	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
892	13508		0.9	1.0E-115	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2888375 5'
2040	14922	27190	3.39	1.0E-115	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2040	14922	27191	3.39	1.0E-115	5174478	NT	Homo sapiens perlecanin (PCNT) mRNA
2072	14852	27224	1.95	1.0E-115	AU133080.1	EST_HUMAN	Homo sapiens perlecanin (PCNT) mRNA
2145	14548	27293	2.87	1.0E-115	M16824.1	NT	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2145	14548	27284	2.87	1.0E-115	M16824.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 17 and 18
2348	14917	27491	1.87	1.0E-115	5453941	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2380	14849		0.97	1.0E-115	U78306.1	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2497	15081	27635	2.84	1.0E-115	AB018333.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
2762	15404	27883	2.18	1.0E-115	BE889256.1	EST_HUMAN	Homo sapiens mRNA for KIAA0790 protein, partial cds
							601513337E1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914870 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3209	15821	28298	4.18	1.0E-118	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric and
3209	15821	28297	4.18	1.0E-118	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric and
4487	17053	28497	2.11	1.0E-116	5031894	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4981	17555	29997	1.88	1.0E-118	A067098.1	EST_HUMAN	PM-BT135-070489-016 BT135 Homo sapiens cDNA
5383	17823	30337	0.88	1.0E-118	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5483	18117	30525	0.82	1.0E-118	AJ302082.1	EST_HUMAN	qnt18404.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1888895 3' similar to contains element MER25 repetitive element ;
6132	18746	31502	2.1	1.0E-116	W42822.1	EST_HUMAN	zz24407.1 Soares_sarcescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALLATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6359	18983	31740	1.81	1.0E-118	A0408856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
6359	18983	31741	1.81	1.0E-118	A0408856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
6423	19026	31809	1.14	1.0E-118	BE408097.1	EST_HUMAN	601302281F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638764 5'
6530	19130	31924	1.98	1.0E-118	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
6637	19233		1.82	1.0E-116	BE159133.1	EST_HUMAN	MR2-HT0378-210200-102-804 HT0378 Homo sapiens cDNA
7023	19557	32382	2.08	1.0E-118	C02944.1	EST_HUMAN	C02944 Human heart cDNA (Y Nakamura) Homo sapiens cDNA clone 3NHC0567
7254	19782	32638	7.18	1.0E-118	AV16314.1	EST_HUMAN	AV16314 DCB Homo sapiens cDNA clone DCB8CG08 6'
8310	20851	33775	1.4	1.0E-118	AA354256.1	EST_HUMAN	EST62885 Jurkat T-cell V Homo sapiens cDNA 5' end similar to similar to keratin 2
8310	20851	33775	1.4	1.0E-118	AA354256.1	EST_HUMAN	EST62885 Jurkat T-cell V Homo sapiens cDNA 5' end similar to similar to keratin 2
8416	20956	33873	1.49	1.0E-118	A1604151.1	EST_HUMAN	CM-BT043-080289-075 BT043 Homo sapiens cDNA
8888	21407	34331	1.16	1.0E-118	BE585507.1	EST_HUMAN	601338288F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3880880 5'
9028	21565	34494	2.75	1.0E-116	A1216932.1	EST_HUMAN	q08c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:X53741.mat FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
9582	22092	35056	1.38	1.0E-118	11418848	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
10171	22668	35681	0.67	1.0E-118	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10171	22668	35682	0.67	1.0E-118	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10250	22745	35733	0.82	1.0E-118	BE158913.1	EST_HUMAN	QV4-HT0401-281289-063-c08 HT0401 Homo sapiens cDNA
10587	23103	36117	3.89	1.0E-118	BF339949.1	EST_HUMAN	CM2-CT0482-300800-349-e08 CT0482 Homo sapiens cDNA
11015	23520	36585	3.83	1.0E-118	A1367140.1	EST_HUMAN	qq41e04.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:80495.7 CE01766 ;
12456	24948		3.82	1.0E-118	AL134888.1	EST_HUMAN	DKFZp762L1110_r1 762 (synonym: hml2) Homo sapiens cDNA clone DKFZp762L1110 5'
584	13214	25681	1.88	1.0E-117	4826836	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1116	15433	26231	1.46	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1288	13885	26382	0.81	1.0E-117	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1780	14379	26923	1.28	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1871	14457	27014	5.27	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2252	14826	27402	1.15	1.0E-117	AW937689.1	EST_HUMAN	EST369769 MAGe resequences, MAGe Homo sapiens cDNA
3308	15917	28304	1.53	1.0E-117	AA078114.1	EST_HUMAN	cp32c11.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1678548 3'
4082	16659	29122	8.83	1.0E-117	AA318723.1	EST_HUMAN	EST189414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L28
4436	17022	29482	2.27	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4677	17256	29710	2.1	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4833	17508	29855	10.14	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4833	17508	29856	10.14	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5074	17847	30086	3.29	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0898 protein, complete cds
5551	18183	30598	3.8	1.0E-117	BE730508.1	EST_HUMAN	601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
7473	18995	32859	5.22	1.0E-117	L78571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7473	19095	32860	5.22	1.0E-117	L78571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7550	20089	32844	4.48	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7550	20089	32846	4.48	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7919	20461	33387	3.77	1.0E-117	A1890145.1	EST_HUMAN	wp86807.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2468628 3' similar to TR:076065
8253	20764	33711	1.07	1.0E-117	10834889	NT	O76065 KIAA0477 PROTEIN, ;
8253	20764	33712	1.07	1.0E-117	10834889	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8350	20891	33811	1.32	1.0E-117	A1804151.1	EST_HUMAN	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8350	20891	33812	1.32	1.0E-117	A1804151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
9223	21739	34682	1.73	1.0E-117	D16534.1	NT	CM-BT043-090289-075 BT043 Homo sapiens cDNA
9701	22200	36172	1.71	1.0E-117	BE733922.1	EST_HUMAN	Human gene for very low density lipoprotein receptor, exon 11
9857	24798	35339	0.63	1.0E-117	AF080033.1	NT	601568317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
10482	22856	35987	1.88	1.0E-117	11420222	NT	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2) mRNA, complete cds
10737	23262	36277	1.89	1.0E-117	D83776.1	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10801	23421	36439	1.81	1.0E-117	W80606.1	EST_HUMAN	Human mRNA for KIAA0191 gene, partial cds
10917	23436	36456	1.85	1.0E-117	11424836	NT	Human mRNA for KIAA0191 gene, partial cds
10917	23436	36457	1.85	1.0E-117	11424836	NT	gdM14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11153	23660	36704	3.48	1.0E-117	AB011541.1	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11153	23660	36705	3.46	1.0E-117	AB011541.1	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11272	23725		31.65	1.0E-117	BE28856.1	EST_HUMAN	Homo sapiens mRNA for MEGF8, partial cds
							Homo sapiens mRNA for MEGF8, partial cds
							601188203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544286 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11484	23914	36881	2.04	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11484	23914	36882	2.04	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11938	25028		1.7	1.0E-117	AF224688.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12662	15433	26231	1.81	1.0E-117	AF124383.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
74	12792	25231	8.91	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
99	12775	25257	0.88	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434058_r1 434 (synonym: hhas3) Homo sapiens cDNA clone DKFZp434058 5'
843	13174	25654	6.79	1.0E-118	7657018	NT	Homo sapiens hypothetical protein (DJ328E19.G1.1), mRNA
947	15428	26073	1.3	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2275	14849	27425	1.93	1.0E-118	BE388705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2275	14849	27426	1.93	1.0E-118	BE388705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2275	14849	27427	1.93	1.0E-118	BE388705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2367	14938		0.98	1.0E-118	AW951729.1	EST_HUMAN	EST363798 IMAGE resequencing, MAGB Homo sapiens cDNA
2768	15322	27888	2.82	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2768	15322	27889	2.82	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3138	15752		4.01	1.0E-118	Y13632.1	NT	Homo sapiens PRKY exon 7
3229	15841	28321	8.49	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3229	15841	28322	8.49	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
4162	16753	28204	9.89	1.0E-118	D23880.1	NT	Human mRNA for ribosomal protein, complete cds
4817	17395	29848	1.45	1.0E-118	11425783	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5616	18245	30695	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5616	18245	30698	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5813	18437	31158	1.01	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5813	18437	31159	1.01	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5880	18513	31238	0.77	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5890	18513	31240	0.77	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5944	18564	31284	0.92	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
6023	18642	31383	1.2	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6023	18642	31384	1.2	1.0E-118	11426900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6098	18714	31484	1.4	1.0E-118	11420784	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6793	18384	32198	1.58	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6793	18384	32200	1.58	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7164	18868	32528	1.03	1.0E-118	AL043781.1	EST_HUMAN	DKFZp43400127_r1 434 (synonym: hhas3) Homo sapiens cDNA clone DKFZp43400127 5'
7194	18886	32528	1.03	1.0E-118	AL043781.1	EST_HUMAN	DKFZp43400127_r1 434 (synonym: hhas3) Homo sapiens cDNA clone DKFZp43400127 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7697	20111	32898	4.89	1.0E-118	11431060	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7609	20122	32899	0.7	1.0E-118	L48590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
7913	20455	33381	2.75	1.0E-118	BE781223.1	EST_HUMAN	601489159F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872247 5'
8323	20884	33788	6.08	1.0E-118	BE082856.1	EST_HUMAN	QV0-BT0263-080200-087-h03 BT0263 Homo sapiens cDNA
8323	20884	33789	6.08	1.0E-118	BE082856.1	EST_HUMAN	QV0-BT0263-080200-087-h03 BT0263 Homo sapiens cDNA
8328	20889	33792	1.44	1.0E-118	AA443024.1	EST_HUMAN	Z98d07.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8328	20889	33793	1.44	1.0E-118	AA443024.1	EST_HUMAN	Z98d07.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8607	21146	34081	0.89	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8607	21146	34082	0.89	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8655	21194	34112	1.61	1.0E-118	4587792	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8655	21194	34113	1.61	1.0E-118	4587792	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8905	21903	34425	5.31	1.0E-118	BE283134.1	EST_HUMAN	601144963F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
8908	21634	34484	0.52	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586K1824
9512	22012	34971	1.62	1.0E-118	7657016	NT	Homo sapiens hypothetical protein [QJ328E19.C1.1], mRNA
9637	22394	35370	0.62	1.0E-118	AL138321.1	EST_HUMAN	DKFZp5470017_r1 547 (synonym: hbrt1) Homo sapiens cDNA clone DKFZp5470017 5'
10237	22732	35723	0.98	1.0E-118	BE738213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10237	22732	35724	0.98	1.0E-118	BE738213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10277	22772	35761	1.6	1.0E-118	BF195407.1	EST_HUMAN	7n1709.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785.3' similar to SW:ZP3A_HUMAN
10425	22919	35921	0.52	1.0E-118	AW298351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
11187	23684	36710	4.87	1.0E-118	AA315007.1	EST_HUMAN	U1H-BW0-alo-a-07-Q.U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729772 3'
11433	23883	36946	1.94	1.0E-118	BE908878.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11433	23883	36950	1.94	1.0E-118	BE908878.1	EST_HUMAN	601489514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11436	23886	36953	1.69	1.0E-118	BF093687.1	EST_HUMAN	601489514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11438	23888	36954	1.69	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
11606	24049	37115	1.58	1.0E-118	BE218235.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
788	13408	25911	2.89	1.0E-119	AF170492.1	NT	h38a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176474 3' similar to TR:Q9Z2H4
1076	15432	26169	1.82	1.0E-119	7705607	NT	Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGR4 ;
1977	14560	27118	2.24	1.0E-119	AB023147.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3136	15760	28218	1.04	1.0E-119	8922205	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
							Homo sapiens mRNA for KIAA0630 protein, partial cds
							Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
							on10b05.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558241 3' similar to WP:ED4F8.2
3277	15988		0.79	1.0E-119	AA819780.1	EST_HUMAN	CE01214 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	18824	28098	1.09	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5540	18172	30587	3.45	1.0E-119	AU133399.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001891 5'
5553	18185	30600	15.55	1.0E-119	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5557	18189	30605	3.01	1.0E-119	BE036121.1	EST_HUMAN	RC1-NN0073-260800-018-q08 NN0073 Homo sapiens cDNA
5626	18264	30723	1.62	1.0E-119	AV683731.1	EST_HUMAN	AV683731 GKC Homo sapiens cDNA clone GKCDH03 5'
6276	18884	31652	5.78	1.0E-119	AI150703.1	EST_HUMAN	q577c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6426	19032	31815	0.68	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6429	19032	31816	0.68	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6473	19074	31857	1.08	1.0E-119	AI476732.1	EST_HUMAN	bm23110.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
8588	19185	31987	2.82	1.0E-119	X08292.1	NT	Human c-fos proto-oncogene
8598	19185	32000	4.9	1.0E-119	AW974193.1	EST_HUMAN	EST388298 IMAGE resequencing, MAGM Homo sapiens cDNA
7440	18984	32830	1.27	1.0E-119	BE786814.1	EST_HUMAN	601592005F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3946081 5'
8586	21135	34050	0.94	1.0E-119	BE616150.1	EST_HUMAN	601280564F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3622628 5'
8670	22189	35145	0.55	1.0E-119	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
8821	22319	35303	1.04	1.0E-119	11036843	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10145	22840	35630	2.78	1.0E-119	AA465124.1	EST_HUMAN	es3205.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814077 5'
10398	22892	35896	0.82	1.0E-119	AJ287701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10438	22932	35939	0.66	1.0E-119	11428837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10438	22932	35940	0.68	1.0E-119	11428837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10502	22986	36005	3.99	1.0E-119	AB032281.1	NT	Homo sapiens Sod mRNA for stearyl-CoA desaturase, complete cds
11082	23584		10.54	1.0E-119	BF568571.1	EST_HUMAN	602186072F1 NIH_MGC 45 Homo sapiens cDNA clone IMAGE:4310633 5'
11997	25012		3.05	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240898-011-f03 CT0212 Homo sapiens cDNA
288	12917	25404	0.65	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
323	12977	25465	0.77	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
1079	13884	26195	2.62	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1079	13884	26196	2.82	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1471	14083	26598	3.24	1.0E-120	N44873.1	EST_HUMAN	yy40g12.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:273768 5'
1845	14237	26772	2.49	1.0E-120	AF18708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1842	14430	26883	1.64	1.0E-120	4557260	NT	Homo sapiens diaphanin and metalloproteinase domain 10 (ADAM10) mRNA
3348	12977	25465	1.04	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
4449	17035	29478	1.88	1.0E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4449	17035	29479	1.68	1.0E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4768	17350	29801	2.82	1.0E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4768	17360	26802	2.82	1.0E-120	AF098483.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5150	17720	30181	1.11	1.0E-120	AF054821.1	NT	Homo sapiens cytochrome P-450 mRNA, complete cds
5442	17697		0.95	1.0E-120	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5911	18533	31258	13.5	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC 42 Homo sapiens cDNA clone IMAGE:4300174 5'
5911	18533	31259	13.5	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC 42 Homo sapiens cDNA clone IMAGE:4300174 5'
7573	20089	32885	1.78	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
7835	20377	33282	1.81	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
7835	20377	33283	1.81	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8274	20816	33737	2.9	1.0E-120	BF337596.1	EST_HUMAN	60203532F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183333 5'
8343	20884	33805	0.8	1.0E-120	AB033067.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8343	20884	33806	0.8	1.0E-120	AB033067.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8347	20888	33808	2.83	1.0E-120	AB007664.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8347	20888	33809	2.83	1.0E-120	AB007664.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8390	20930	33850	1.13	1.0E-120	AB007634.1	NT	Homo sapiens mRNA for KIAA0495 protein, partial cds
9421	21930	34877	4.8	1.0E-120	BE382102.1	EST_HUMAN	601307739F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3825544 5'
9421	21930	34878	4.8	1.0E-120	BE382102.1	EST_HUMAN	601307739F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3825544 5'
9680	22169	35131	3.07	1.0E-120	BF308541.1	EST_HUMAN	60188895F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4122876 5'
9675	22174	35150	8.09	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9682	22191	35185	0.89	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
9688	22483	35488	2.88	1.0E-120	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11006	23520	36555	14.73	1.0E-120	BE296387.1	EST_HUMAN	60117672F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3632015 5'
11222	23753	36810	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC 89 Homo sapiens cDNA clone IMAGE:3847281 5'
11222	23753	36811	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC 89 Homo sapiens cDNA clone IMAGE:3847281 5'
11504	23853	37021	1.55	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
12153	24395	30975	1.31	1.0E-120	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
77	12784	26236	0.92	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
401	13045	25536	1.88	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
753	15423	25887	1.19	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
2008	14580	27150	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate 4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2008	14590	27151	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate 4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2150	14727	27300	1.74	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2686	15612	28092	1.03	1.0E-121	AF111198.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3117	16731	28201	3.63	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3117	16731	28202	3.63	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3589	16183	28677	0.94	1.0E-121	AB037768.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3589	16183	28678	0.94	1.0E-121	AB037768.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3741	16342	28810	6.78	1.0E-121	AF165166.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4424	17009	28452	1.42	1.0E-121	AI283284.1	EST_HUMAN	q57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
5112	17684	30120	3.64	1.0E-121	X91837.1	NT	H. sapiens ECE-1 gene (exon 17)
5472	18108	30425	1.02	1.0E-121	BE22250.1	EST_HUMAN	h0908.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3186119 3'
5750	18378	31086	0.89	1.0E-121	BE271424.1	EST_HUMAN	801140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6988	18845		1.08	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudocentromeric region, segment 2/2
7042	18062	30451	0.76	1.0E-121	AW688088.1	EST_HUMAN	RC3-NN0068-270400-011-402 NN0068 Homo sapiens cDNA
7042	18062	30452	0.76	1.0E-121	AW688088.1	EST_HUMAN	RC3-NN0068-270400-011-402 NN0068 Homo sapiens cDNA
7878	20420	33328	1.88	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
7882	20424	33332	2.19	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
7882	20424	33333	2.19	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
9772	22270	35254	0.9	1.0E-121	AW593858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
9772	22270	35255	0.9	1.0E-121	AW593858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
10655	23187	36203	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
10682	23184	36208	4.2	1.0E-121	AF084200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UG12B4*E458 allele, complete cds
10848	23369	36368	3.51	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
10875	23396	36412	2.11	1.0E-121	N59824.1	EST_HUMAN	y74c01.s1 Scars fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248448 3'
289	12845	25430	1.68	1.0E-122	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
358	13007	25480	3.01	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
380	13027	25515	1.61	1.0E-122	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
915	13528	26047	5.29	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1262	13858	26376	4.63	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1731	14322	26884	1.08	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14340	26887	1.8	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1780	14340	26888	1.8	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1850	14438	26895	6.15	1.0E-122	BE908024.1	EST_HUMAN	801497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3689358 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2533	15097	27689	6.48	1.0E-122	BF316170.1	EST_HUMAN	601868173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2533	15097	27670	5.48	1.0E-122	BF316170.1	EST_HUMAN	601868173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2864	15483	27857	1.11	1.0E-122	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4972	17546	28988	1.23	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5127	17699		1.26	1.0E-122	AW504645.1	EST_HUMAN	U1-HF-BN0-ali-e-03-0-UI1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
6752	18378	31089	1.36	1.0E-122	BE256038.1	EST_HUMAN	601113667F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6833	18378	31089	6.98	1.0E-122	BE256038.1	EST_HUMAN	601113667F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7268	19794	32650	0.88	1.0E-122	A4888871.1	EST_HUMAN	ek48908.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8731	21270	34189	0.55	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
8988	21498	34419	1.37	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LGL2), mRNA
9247	21773	34723	0.9	1.0E-122	A1358818.1	EST_HUMAN	q32h07.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
9247	21773	34724	0.9	1.0E-122	A1358818.1	EST_HUMAN	q32h07.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
10040	22535	35531	0.71	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dcl (proto-oncogene)
10866	23387	38402	1.55	1.0E-122	AW955834.1	EST_HUMAN	EST387804 MAGE resequences, MAGO Homo sapiens cDNA
11738	24141		3.98	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
202	12863	25347	19.89	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
800	13417	25921	2.06	1.0E-123	BF345274.1	EST_HUMAN	802018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153870 5'
800	13417	25922	2.06	1.0E-123	BF345274.1	EST_HUMAN	802018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153870 5'
1051	13658	26169	5.07	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1060	13666	26176	6.63	1.0E-123	58031114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1281	13876	26397	4.2	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1281	13876	26398	4.2	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2147	14724	27286	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2147	14724	27287	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2147	14724	27288	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2364	14925		5.59	1.0E-123	7706982	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3288	15899	28378	0.67	1.0E-123	6912817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5638	18267	30739	1.8	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6638	18287	30740	1.6	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
6789	18399	31109	1.33	1.0E-123	BE79748.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6595	19192	31697	2.14	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7076	19848	32488	0.71	1.0E-123	H53198.1	EST_HUMAN	Y484603.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14880 PROTEIN KINASE YAK1;
7084	19855	32494	1.22	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7245	19774	32831	0.68	1.0E-123	U55258.1	NT	Human hBRAVONIN-CAM precursor (hBRAVONIN-CAM) gene, complete cds
7433	19987	32822	0.73	1.0E-123	11625833	NT	Homo sapiens heparan sulfates (glucosaminide) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7638	20160	33034	1.31	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7847	20159	33046	1.79	1.0E-123	BE283001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509182 5'
7764	20272	33170	0.8	1.0E-123	N35841.1	EST_HUMAN	y484111.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49811
7764	20272	33171	0.8	1.0E-123	N35841.1	EST_HUMAN	S49811 protein kinase PkA - Phycomyces blakesleeanus;
8472	21012	34838	2.25	1.0E-123	AW371924.1	EST_HUMAN	y484111.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49811
9291	21891	34838	2.04	1.0E-123	AB007823.1	NT	RC4-BT0311-251199-012-e07 BT0311 Homo sapiens cDNA Homo sapiens mRNA for KIAA0454 protein, partial cds
9424	21933	34882	39.78	1.0E-123	U08923.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabelfa2) mRNA, complete cds
11587	24014	37083	5.42	1.0E-123	BF677292.1	EST_HUMAN	602088791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
11587	24014	37084	5.42	1.0E-123	BF677292.1	EST_HUMAN	602088791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
290	12946	25431	0.93	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
290	12946	25432	0.93	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
298	12952		1.2	1.0E-124	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
511	13144	26630	2.28	1.0E-124	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
720	13340	25828	4	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
720	13340	25830	4	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
789	13407	25912	4.88	1.0E-124	AF155654.1	NT	z81b04.r1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
841	13457	25968	1.18	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
837	13550	26066	5.09	1.0E-124	7705448	NT	Human putative ribosomal protein S1 mRNA
1358	13932	26479	0.62	1.0E-124	11419092	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1381	13985	26511	6.15	1.0E-124	AF274892.1	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1391	13985	26512	6.15	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
							Homo sapiens glucose transporter 3 gene, exons 8, 10, and complete cds

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1861	14439	28988	3.16	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (no-H61 gene)
2107	14685	27263	1.73	1.0E-124	BE879524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3537	16142	28824	0.72	1.0E-124	S78884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/IR1) gene, exon
3537	16142	28826	0.72	1.0E-124	S78884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/IR1) gene, exon
3987	16585	28034	0.68	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4150	16742	29196	0.8	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4855	17433	28884	2.18	1.0E-124	AB024080.1	NT	Homo sapiens gene for B120, exon 11
5088	17641		1.29	1.0E-124	M19178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5256	17819	30244	0.87	1.0E-124	AW963390.1	EST_HUMAN	EST375463 MAGE resequences, MAGH Homo sapiens cDNA
5501	18135	30545	10.59	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5852	18478	31189	1.05	1.0E-124	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6048	18697	31406	6.57	1.0E-124	BF688138.1	EST_HUMAN	602124844F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4281635 5'
6317	18924	31701	0.88	1.0E-124	AV711283.1	EST_HUMAN	AV711283 Cu Homo sapiens cDNA clone CUAADF07 5'
6563	19181	31959	0.9	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7083	19654	32493	3.45	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
7191	19723	32571	1.23	1.0E-124	BE271296.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2868585 5'
7191	19723	32572	1.23	1.0E-124	BE271296.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2868585 5'
7555	20074	32850	1.15	1.0E-124	AA630331.1	EST_HUMAN	ac08105.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'
8201	20742	33655	18.99	1.0E-124	4508854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8399	20939	33861	1.45	1.0E-124	AW612108.1	EST_HUMAN	hg94409.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853240 3' similar to TR:O95182
8399	20939	33862	1.45	1.0E-124	AW612108.1	EST_HUMAN	O95182 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
8088	21625	34560	1.42	1.0E-124	AI788884.1	EST_HUMAN	hg94409.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853240 3' similar to TR:O95182
9089	21625	34561	1.42	1.0E-124	AI788884.1	EST_HUMAN	hg94409.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853240 3' similar to TR:O95182
9411	21920	34868	2.52	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9411	21920	34869	2.52	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9498	21998	34954	1.14	1.0E-124	AF022655.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCAGE04 3'
9498	21998	34955	1.14	1.0E-124	AF022655.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCAGE04 3'
9529	22028	34984	8.22	1.0E-124	AI797133.1	EST_HUMAN	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9526	22028	34985	8.22	1.0E-124	AI797133.1	EST_HUMAN	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9785	22283	35289	1.66	1.0E-124	AW503755.1	EST_HUMAN	wic302.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
11213	23716	36770	3.81	1.0E-124	AW68583.1	EST_HUMAN	wic302.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
							UI-HF-BN0-ekz-b-04-0-J11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078848 5'
							h105c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980908 3'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11347	23045	36058	2.28	1.0E-124	AI448455.1	EST_HUMAN	if19c03.x1 NCI_CGAP_Gap4 Homo sapiens cDNA clone IMAGE:2141880 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
11347	23045	36057	2.28	1.0E-124	AI448455.1	EST_HUMAN	if19c03.x1 NCI_CGAP_Gap4 Homo sapiens cDNA clone IMAGE:2141880 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
11818	13340	25829	6.1	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
11818	13340	25830	6.1	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12284	24474	30934	1.28	1.0E-124	AB028016.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
12542	24980	30632	2.42	1.0E-124	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12542	24980	30633	2.42	1.0E-124	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
341	12893		8.05	1.0E-125	AB032888.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
451	12890	25136	3.95	1.0E-125	BE743922.1	EST_HUMAN	601677881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
672	13296	25777	23.21	1.0E-125	AI110886.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
672	13296	25778	23.21	1.0E-125	AI110886.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
757	13376	25871	1.7	1.0E-125	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
893	13507	28025	2.68	1.0E-125	AA042813.1	EST_HUMAN	z63c07.g1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:488540 3' similar to gb:X65957_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1036	13848	26158	2.18	1.0E-125	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1193	13794	26303	1.9	1.0E-125	7682279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1712	15448	28842	1.66	1.0E-125	7681887	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1836	14424	26975	0.86	1.0E-125	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1847	14435	26991	2.28	1.0E-125	AF015450.1	NT	Homo sapiens Ueupin-alpha mRNA, complete cds
1847	14435	26992	2.28	1.0E-125	AF015450.1	NT	Homo sapiens Ueupin-alpha mRNA, complete cds
2397	14985	27536	1.03	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2832	15193	27764	1.08	1.0E-125	4504898	NT	Homo sapiens inhibin, alpha (INH) mRNA
2832	15193	27765	1.06	1.0E-125	4504898	NT	Homo sapiens inhibin, alpha (INH) mRNA
3925	16523	28991	1.59	1.0E-125	AA042813.1	EST_HUMAN	z63c07.g1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:488540 3' similar to gb:X65957_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4848	17230	29686	2.78	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4848	17230	29687	2.78	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4724	17305	29749	1.54	1.0E-125	BE315412.1	EST_HUMAN	60114152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140798 5'
5832	18584	31281	0.69	1.0E-128	BF683645.1	EST_HUMAN	602138874F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4300770 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6033	18652	31394	1.55	1.0E-126	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6032	18870	31409	1.18	1.0E-125	BE176189.1	EST_HUMAN	QV2-HT0577-010500-105-508 HT0577 Homo sapiens cDNA
6089	18705	31453	3.2	1.0E-125	BE892860.1	EST_HUMAN	601493472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6129	18744	31497	0.75	1.0E-125	AI078904.1	EST_HUMAN	tu87607.x1 NCI_CGAP_Gene4 Homo sapiens cDNA clone IMAGE:2258108 3' similar to WP:Q46G9.2
6095	18291	32094	1.55	1.0E-125	BE562526.1	EST_HUMAN	CE01854;
6095	19291	32095	1.55	1.0E-125	BE662526.1	EST_HUMAN	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3889760 5'
7121	18481	32277	65.83	1.0E-128	X03427.1	NT	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3889760 5'
7121	18481	32278	65.83	1.0E-128	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7538	20058	32832	0.75	1.0E-125	BE278823.1	EST_HUMAN	Homo sapiens IGF-II gene, exon 5
8483	21022	33838	1	1.0E-125	U60288.1	NT	601158076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
8483	21022	33839	1	1.0E-125	U60288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8048	21583	34512	9.65	1.0E-125	BE181640.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8048	21583	34513	9.65	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-412 HT0638 Homo sapiens cDNA
9303	21903	34852	1.05	1.0E-125	AI685896.1	EST_HUMAN	QV1-HT0638-070500-191-412 HT0638 Homo sapiens cDNA
10350	22844	35839	0.53	1.0E-125	BE794576.1	EST_HUMAN	h52503.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171081 3' similar to TR:Q14089 Q14089
10388	22842	35878	0.73	1.0E-125	AB002298.1	NT	HYPOTHETICAL PROTEIN;
10562	23098	36112	3.78	1.0E-125	AF043458.1	NT	601560345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39444531 5'
11016	23530	36568	4.05	1.0E-125	AB014587.1	NT	Human mRNA for KIAA0300 gene, partial cds
11169	23878	36722	1.56	1.0E-125	7689505	NT	Homo sapiens I-REL gene, exon 5
11174	23881	36727	6.41	1.0E-125	AF026029.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11278	23732	36787	2.88	1.0E-125	AW812898.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11375	23827	36888	6.08	1.0E-125	BE074287.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11375	23827	36889	6.08	1.0E-125	BE074287.1	EST_HUMAN	RC9-ST0188-260200-018-c11 ST0188 Homo sapiens cDNA
808	13423	25929	3.44	1.0E-126	4758007	NT	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
808	13426	25832	1.92	1.0E-126	M61838.1	NT	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
952	13564	26076	295	1.0E-126	X88735.1	NT	Homo sapiens CDC-like kinase (CLK) mRNA
3108	15723	28194	9.08	1.0E-128	AA180709.1	EST_HUMAN	Human laminin B1 chain gene, exon 20
3108	15723	28195	9.08	1.0E-128	AA180709.1	EST_HUMAN	H. sapiens gene for alpha1-antichymotrypsin, exon 3
3691	16292	28781	0.98	1.0E-126	X53941.1	NT	z072003.r1 Stratiogene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3718	16317	28785	2.02	1.0E-128	7657038	NT	z072003.r1 Stratiogene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
							H. sapiens DNA for liver cytochrome b5 pseudogene
							Homo sapiens death receptor 8 (DR8), mRNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4802	17477	28833	1.03	1.0E-128	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4802	17477	28834	1.03	1.0E-128	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4881	17538	28978	1.31	1.0E-128	N34078.1	EST_HUMAN	YK78C08.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:287850 5'
6380	18984	31764	3.48	1.0E-128	AA460078.1	EST_HUMAN	z88603.r1 Soares_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788444 5' similar to
6432	18035	31820	4.2	1.0E-128	AB040958.1	NT	TR:G1145880 G1145880 TTIN ;
6432	18035	31821	4.2	1.0E-128	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7511	20032	32897	0.85	1.0E-128	AF257737.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7511	20032	32898	0.85	1.0E-128	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7819	20381	33287	0.92	1.0E-128	AB037715.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7819	20381	33288	0.92	1.0E-128	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
7828	20471	33380	5.78	1.0E-128	X16809.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
						NT	Human mRNA for ankryrin (variant 2.1)
8124	20665	33575	0.85	1.0E-128	AA483368.1	EST_HUMAN	ne74b1.2.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TS98_HUMAN
9711	22209	35181	0.52	1.0E-128	4505424	NT	P88068 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;
10872	23204	36217	1.73	1.0E-128	M63198.1	NT	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
10738	23263	36278	3.69	1.0E-128	BF693175.1	EST_HUMAN	Human macrophage mannose receptor (MRC1) gene, exon 5
11392	23844	36808	2.32	1.0E-128	BE281680.1	EST_HUMAN	602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4288240 5'
11638	18292	28781	2.82	1.0E-128	X53941.1	NT	601148404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602129 5'
12304	18038	30496	6.78	1.0E-128	BE743922.1	EST_HUMAN	H. sapiens DNA for liver cytochrome b5 pseudogene
183	12845	25330	4.5	1.0E-127	AB024597.1	NT	601577881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
183	12845	25331	4.5	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
184	12845	25331	2.76	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
184	12845	25331	2.76	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
285	12951	26439	1.3	1.0E-127	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
285	12951	26440	1.3	1.0E-127	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
814	13527	26048	2.22	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
848	13581	26075	1.37	1.0E-127	U72821.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1728	14320	26882	1.33	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2111	14689	27256	2.81	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2111	14689	27257	2.81	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2241	14816	27388	6.62	1.0E-127	4506820	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2381	14950	27523	3.29	1.0E-127	AF248505.1	NT	Homo sapiens ediclin mRNA, complete cds
2840	15198	27773	6.29	1.0E-127	X12881.1	NT	Human mRNA for cyclostatin 18
3753	16354	28822	1.02	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (TSN) mRNA, complete cds
3884	16482	28944	0.75	1.0E-127	AW181297.1	EST_HUMAN	au80408.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
4194	16783	29232	0.68	1.0E-127	AF135186.1	NT	Homo sapiens delayed rectifier potassium channel subunit IaK mRNA, complete cds
4303	16889	29332	0.61	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4340	16927	29387	21.24	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4340	16927	29388	21.24	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4595	17178	29825	0.68	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4708	17290	29734	5.02	1.0E-127	4506394	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4738	17318	29734	2.84	1.0E-127	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4780	17361	29811	1.04	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5894	18506	31232	2.37	1.0E-127	W03547.1	EST_HUMAN	z601a10.1 Sources melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:P196_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 ;
5912	18534	31260	0.86	1.0E-127	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5970	18591	31326	4.61	1.0E-127	X85764.1	NT	H. sapiens NOS2 gene, exon 6
6310	18917	31691	2.21	1.0E-127	X94090.1	NT	H. sapiens TCF11 gene, exon 3-5
6463	19064	31849	5.89	1.0E-127	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6764	19357	32196	0.93	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7122	19462	32279	0.85	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7760	20268	33165	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7760	20268	33166	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7763	20271	33169	0.67	1.0E-127	BF971355.1	EST_HUMAN	602161232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4282575 5'
8820	21359	34285	0.7	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8820	21359	34286	0.7	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9558	22058	35018	4.96	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9558	22058	35020	4.96	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9787	22285	35270	0.68	1.0E-127	A1288932.1	EST_HUMAN	qm94h09.xt NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'

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10245	22740	35730	2.25	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11037	23551	36565	6.54	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11037	23551	36566	6.54	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11490	23639	37009	1.9	1.0E-127	BE895416.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916917 5'
11490	23639	37010	1.9	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916917 5'
12046	12845	25330	1.43	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12046	12845	25331	1.43	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12263	24464	30982	1.7	1.0E-127	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
12620	24967		2.23	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
485	13118	25605	2.44	1.0E-128	BE385817.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
1185	13768	26305	1	1.0E-128	4768081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1185	13768	26306	1	1.0E-128	4768081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2115	14893	27260	4.14	1.0E-128	U02523.1	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2115	14893	27261	4.14	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2250	14824	27400	18.53	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3441	16048	28527	1.14	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4771	17352	29804	5.43	1.0E-128	11426873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5734	18360	31066	6.97	1.0E-128	X69639.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6550	18148	31944	2.08	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7010	18508	32328	8.01	1.0E-128	BF224345.1	EST_HUMAN	7q85b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3'
8208	20747	33659	0.75	1.0E-128	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
8208	20747	33660	0.75	1.0E-128	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10043	22838	35635	1.82	1.0E-128	AA689188.1	EST_HUMAN	hs04a11.1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182820 similar to TR:G951338 G951338
10388	23123	36137	5.48	1.0E-128	11425254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
10687	23131	36145	5.15	1.0E-128	AA928959.1	EST_HUMAN	om68h08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCJN-
11805	24244		4.37	1.0E-128	AW955290.1	EST_HUMAN	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
127	13071	25568	12.08	1.0E-129	SA7722.1	NT	EST3367350 MAGC resequences, MAGC Homo sapiens cDNA
438	13071	25568	14.84	1.0E-129	SA7722.1	NT	Insulin-like growth factor binding protein-2 (human, placenta, Genomic, 1019 nt, segment 2 of 4)
1756	14346	26891	2.48	1.0E-129	AL096980.1	NT	Insulin-like growth factor binding protein-2 (human, placenta, Genomic, 1019 nt, segment 2 of 4)
1761	14351	26898	1.62	1.0E-129	AF240786.1	NT	Novel human mRNA containing zinc finger C2H2 type domains
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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1761	14351	26887	1.82	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1898	14471	27028	2.2	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3162	15776	28244	1.41	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3162	15776	28245	1.41	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3162	15776	28246	1.41	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4244	16832	29283	1.95	1.0E-129	AB040882.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4397	16954	29384	2.57	1.0E-129	AW755264.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
4397	16954	29385	2.57	1.0E-129	AW755264.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
6241	18850	31620	4.78	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
7181	19713	32561	4.38	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
7241	19770	32828	14.44	1.0E-129	AF041056.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
7535	20055	32828	0.78	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7535	20055	32828	0.78	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8260	20801		3.93	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
8991	22486	35473	1.16	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9991	22486	35474	1.18	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11102	23812	36652	3.34	1.0E-129	AA825528.1	EST_HUMAN	af7207.r1 Scores_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'
11177	19770	32826	11.7	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
11892	24235		2.32	1.0E-129	H83155.1	EST_HUMAN	X4905.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:189112 5' similar to SP:BA8150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
12287	24484		2.07	1.0E-129	AL120739.1	EST_HUMAN	DKFZp782K171.1 762 (synonym: hmal2) Homo sapiens cDNA clone DKFZp782K171 5'
80	12757	25239	1.85	1.0E-130	7705530	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1212	13812	26326	1.23	1.0E-130	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1708	14289	26836	8.62	1.0E-130	BE276192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
1708	14289	26837	8.62	1.0E-130	BE276192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
2027	14609		4.8	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2127	14705		1.69	1.0E-130	8394394	NT	Homo sapiens candidate taste receptor T2R16 (T2R16), mRNA
2798	15351		7.47	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2803	15520	27989	1.17	1.0E-130	BE584219.1	EST_HUMAN	601343018F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
2803	15520	27990	1.17	1.0E-130	BE584219.1	EST_HUMAN	601343018F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
3637	16240	28716	0.96	1.0E-130	AF240696.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds

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3831	16520	27889	5.82	1.0E-130	BE684219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885488 5'
3831	15520	27900	5.82	1.0E-130	BE684219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885488 5'
4010	16608	28081	1.56	1.0E-130	AW503580.1	EST_HUMAN	U1HF-BNO-aky-g-08-Q-J1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4147	16739	28192	1.18	1.0E-130	M97710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
4636	17219	28672	9	1.0E-130	AW843893.1	EST_HUMAN	GM4-CN0045-180200-611-02 CN0045 Homo sapiens cDNA
5258	17821	30246	1.11	1.0E-130	AW363289.1	EST_HUMAN	RC0-CT0318-201199-031-011 CT0318 Homo sapiens cDNA
5258	17821	30247	1.11	1.0E-130	AW363289.1	EST_HUMAN	RC0-CT0318-201199-031-011 CT0318 Homo sapiens cDNA
6910	16599	32398	0.74	1.0E-130	AW843876.1	EST_HUMAN	GM0-CN0045-170200-225-003 CN0045 Homo sapiens cDNA
6910	16599	32397	0.74	1.0E-130	AW843876.1	EST_HUMAN	GM0-CN0045-170200-225-003 CN0045 Homo sapiens cDNA
6923	19582	32411	0.7	1.0E-130	11428448	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7301	19829	32687	2.1	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8616	21155		0.98	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
8763	21292	34212	4.06	1.0E-130	AW968242.1	EST_HUMAN	EST388312 MAGC resequenced, MAGD Homo sapiens cDNA
8141	21676	34619	1.87	1.0E-130	AB037766.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
9846	22344		0.78	1.0E-130	AW103454.1	EST_HUMAN	x338609.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2585874 3'
4	12694	25140	2.27	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667560 5' similar to TR:G222811
4	12694	25141	2.27	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	12697	25145	1.56	0.0E+00	4885136	NT	Homo sapiens checkpoint suppressor 1 (CHEST), mRNA
17	12696	25152	2.85	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
17	12696	25153	2.85	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
24	12703	25160	4.29	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
24	12703	25161	4.29	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
29	12708	25165	30.44	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
37	12716	25175	38.88	0.0E+00	6802967	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
39	12718	25178	23.21	0.0E+00	M59600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 6
42	12721	25182	7.78	0.0E+00	M59600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
44	12723	25184	4.41	0.0E+00	6867826	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
61	12740	25211	8.23	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	12740	25212	8.23	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
63	12742	25216	1	0.0E+00	D78804.1	EST_HUMAN	HUM516H088 Human placenta polyA+ (TFujilwara) Homo sapiens cDNA clone GEN-516H08 5'
63	12742	25217	1	0.0E+00	D78804.1	EST_HUMAN	HUM516H088 Human placenta polyA+ (TFujilwara) Homo sapiens cDNA clone GEN-516H08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
64	12743	26218	28.22	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
66	12745	26221	11.83	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
68	12746	26222	11.83	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
70	12748	26226	0.8	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
71	12749		0.85	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
78	12766	25237	3.66	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
79	12768	25238	3.68	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	12768	25237	1.9	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	12768	25238	1.9	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
86	12761	26244	0.85	0.0E+00			Homo sapiens ariloid binding protein 1 (amine oxidase (copper-containing))(ABP1), nuclear gene encoding mitochondrial protein, mRNA
88	12762		38.11	0.0E+00	4501890	NT	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
98	12771	25263	37.48	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
98	12774	25266	28.23	0.0E+00	U99277.1	NT	Human polyomavirus 1 homolog (HPV1) mRNA, partial cds
105	12781	25263	2.29	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
108	12782	25284	2.19	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1393 protein, partial cds
112	12786	25288	0.64	0.0E+00	X91213.1	NT	H. sapiens nct1 gene (exon 2)
121	12792	25274	1.98	0.0E+00	A1823701.1	EST_HUMAN	ts3b05.x1 NCJ CGAP U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551
122	12792	25274	2.44	0.0E+00	A1823701.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
123	15383	25275	2.64	0.0E+00	N35040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
123	15383	25276	2.64	0.0E+00	N35040.1	EST_HUMAN	y01h09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017 5'
126	12796	25281	1.12	0.0E+00			y01h09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017 5'
136	12801	25289	3.85	0.0E+00	4505938	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
136	12801	25290	3.85	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
144	13060	25552	0.8	0.0E+00	4503680	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
146	12809	25297	0.85	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens IgG Fc binding protein (FCGAMMA)BP mRNA
148	12809	25298	0.85	0.0E+00	T56945.1	EST_HUMAN	y83g04.r2 Strategene fetal spleen (H937205) Homo sapiens cDNA clone IMAGE:68310 5'
164	12827		35.47	0.0E+00	4504444	NT	y83g04.r2 Strategene fetal spleen (H937205) Homo sapiens cDNA clone IMAGE:68310 5'
168	12831	26317	2.64	0.0E+00	BF038881.1	EST_HUMAN	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
170	12833		92.51	0.0E+00	4504444	NT	601480375F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3863303 5'
173	12836	26320	0.75	0.0E+00	AF111168.2	NT	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
176	12836	26321	1.22	0.0E+00	BE284973.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes

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176	12838	25321	0.84	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528954 5'
177	12839	25322	2.37	0.0E+00	W73973.1	EST_HUMAN	z662805.r1 Soares fetal heart_NH-H19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X18282_cds1 ZINC FINGER PROTEIN CLONE 847 (HUMAN);
178	12840	25323	0.77	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
178	12840	25324	0.77	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
178	12841	25325	1.97	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
182	12844	25328	24.46	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
182	12844	25328	24.45	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
183	12853	25336	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y67A10A.Z
183	12853	25337	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y67A10A.Z
188	12858	25340	2.9	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	12858	25341	2.9	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	12858	25342	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	12858	25343	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
208	12859	25355	92.14	0.0E+00	D50689.1	NT	Human gamma-xyloplasmic actin (ACTGP9) pseudogene
213	12874	25380	4.7	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen ssa14-3 mRNA, complete cds
213	12874	25381	4.7	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen ssa14-3 mRNA, complete cds
215	12876	25383	8.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
215	12876	25384	8.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
225	15410	25371	33.35	0.0E+00	AI597308.1	EST_HUMAN	lq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
225	15410	25372	33.35	0.0E+00	AI597308.1	EST_HUMAN	lq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
227	12887	25374	1.91	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
231	12891		44.28	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
232	12892		8.88	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
239	12898	25382	2.84	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
240	12899	25382	1.99	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
241	12900	25383	3.13	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tapy), mRNA
248	12908	25397	0.78	0.0E+00	BE246780.1	EST_HUMAN	TC8AP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TC8AP4468

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248	12808	25388	0.78	0.0E+00	BE248780.1	EST_HUMAN	TCBAP1E4488 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project:TCBA Homo sapiens cDNA clone TCBAP4488
248	12808	25388	0.78	0.0E+00	BE248780.1	EST_HUMAN	TCBAP1E4488 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project:TCBA Homo sapiens cDNA clone TCBAP4488
256	12918	25400	0.97	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
256	12918	25401	0.97	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
259	12918	25405	9.57	0.0E+00	5463805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
261	12920		11.18	0.0E+00	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
268	12925	25411	4.83	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
270	12927	25414	1.82	0.0E+00	X99772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
278	12935		7.37	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
281	12947	25433	1.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
291	12947	25434	1.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
293	12949	25436	1.98	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
304	12959		2.01	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
305	12960	25449	2.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
305	12960	25450	2.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
308	12981		1.14	0.0E+00	AW845263.1	EST_HUMAN	IL2-CT0031-181198-020-803 CT0031 Homo sapiens cDNA
315	12989	25457	6.39	0.0E+00	4557020	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	12989	25458	6.39	0.0E+00	4557020	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
326	12980	25466	8.1	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
327	12981	25469	4.44	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
328	15413		23.15	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
328	12982	25470	0.99	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylmethylidazole synthetase (GART) mRNA
330	12983		2.5	0.0E+00	AA480002.1	EST_HUMAN	zv18c08.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:753894 5'
331	12984	25471	18.8	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
332	12984	25471	19.33	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
336	12988	25475	3.18	0.0E+00	AF114488.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
348	13000	25484	1.84	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
348	13000	25485	1.84	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
350	13001	25486	3.83	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
351	13001	25486	1.41	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

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366	13015	25488	5.41	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
367	13016	25489	1.14	0.0E+00	4506256	NT	Homo sapiens moesin (MSN), mRNA
370	13018	25503	20.33	0.0E+00	4827087	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
373	13022	25508	1.49	0.0E+00	U71900.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
378	13028	25512	2.59	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
378	13028	25513	2.59	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
379	15414	25514	2.88	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
381	13028	25516	0.74	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
384	13031	25520	1.3	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
385	13032	25521	1.87	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
388	13032	25521	1.52	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
388	13034	25523	0.83	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
389	13043	25534	3.85	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
410	13085	25578	8.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
411	13088	25579	2.03	0.0E+00	A193014.1	EST_HUMAN	q81H05.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54189
418	13051	25541	2.38	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
419	13053	25544	1.95	0.0E+00	4503880	NT	RC2-CT0320-300100-018-a09 CT0320 Homo sapiens cDNA
420	13054	25545	2.21	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
420	13054	25546	2.21	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
421	13055	25547	1.1	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
422	13056	25548	1.46	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
422	13056	25549	1.46	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
423	13057	25550	0.95	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
424	13058	25551	2.9	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
425	13059	25552	1.17	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
426	13060	25553	1.66	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
426	13060	25554	1.66	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
427	13060	25553	2.78	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
427	13060	25554	2.78	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
431	13064		98.04	0.0E+00	4506808	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
445	12874	25130	1.11	0.0E+00	R17795.1	EST_HUMAN	y909e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'

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453	13087	25580	1.82	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
454	13088		20.68	0.0E+00	4506728	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
455	13089	25581	5.49	0.0E+00	A8028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
456	13090	25582	10.07	0.0E+00	4507182	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
456	13090	25583	10.07	0.0E+00	4507192	NT	Homo sapiens SON DNA binding protein (SON) mRNA
457	13091	25584	6.34	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
458	13102		0.81	0.0E+00	AL163201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
476	13104	25597	2.98	0.0E+00	4557879	NT	Homo sapiens chromosome 21 segment HS21C901
477	13109		0.92	0.0E+00	AA324282.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
477	13110		1.1	0.0E+00	BE25447.1	EST_HUMAN	EST27054 Carabellum II Homo sapiens cDNA 5' end
483	13126	25611	4.29	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
483	13126	25612	4.29	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
486	13131	25620	11.34	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
489	13131	25621	11.34	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
509	13142	25627	2.62	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C946
510	13143	25628	5.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C948
510	13143	25629	5.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C948
519	13151	25634	6.04	0.0E+00	AB033036.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
521	13163	25636	2.12	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
528	13161	25642	6.27	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3615758 5'
530	15417	25643	1.89	0.0E+00	AW908825.1	EST_HUMAN	PMO-DT0065-130400-002-008 DT0065 Homo sapiens cDNA
533	13164	25645	1.33	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
534	13165	25646	1.42	0.0E+00	8923386	NT	Homo sapiens PC328 protein (PC328), mRNA
538	13168		0.72	0.0E+00	BF373403.1	EST_HUMAN	IL2-F10169-070800-120-F07 F10159 Homo sapiens cDNA
545	13176	25656	4.88	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C910
552	15418	25660	1.31	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
556	13187	25665	1.27	0.0E+00	BF028005.1	EST_HUMAN	601764658F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3686988 5'
562	13193	25672	1.12	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
565	13196	25675	14.24	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
566	13197	25676	4.05	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13197	25677	4.05	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13199	25678	1.38	0.0E+00	8923831	NT	Homo sapiens anillin (LOC644443), mRNA
568	13200	25680	0.96	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA

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569	13200	25681	0.88	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
574	13204		4.55	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arthralgia ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
582	13212	25680	1.45	0.0E+00	AW135324.1	EST_HUMAN	UHH-B11-acb-h-04-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
592	13222		8.6	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
612	13240	25715	4.68	0.0E+00	6174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
626	13252		6.05	0.0E+00	J04086.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
628	13255	25729	2.19	0.0E+00	BF104898.1	EST_HUMAN	601822827F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
630	13257	25731	1.8	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
630	13257	25732	1.8	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
631	13257	25731	1.74	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
631	13257	25732	1.74	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13257	25731	1.81	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13257	25732	1.81	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
637	13260	25735	0.88	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
642	13265	25741	0.94	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
642	13265	25742	0.94	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
650	13273	25750	3.63	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
652	13275	25763	0.89	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
654	13277	25764	1.8	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
655	13278	25765	2.31	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
655	13278	25766	2.31	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
656	13278	25767	0.73	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
656	13279	25768	0.73	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
663	13287	25768	1.2	0.0E+00	AA390486.1	EST_HUMAN	z80c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728732 5'
667	13291	25772	8.55	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
671	13295	25775	48.91	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415667 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
671	13295	25776	48.91	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415667 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
674	13298		3.09	0.0E+00	4885528	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
681	13305	25788	2.88	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
683	13307	25781	1.7	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
688	13310	25795	1.77	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
689	13314	25798	0.9	0.0E+00	AF103889.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
690	13314	25799	0.9	0.0E+00	AF103890.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
696	13319	25804	4.78	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
696	13319	25805	4.78	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
702	13421		1.23	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
711	13332	25819	21.02	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
716	13337	25823	5.36	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
726	13346	25836	7.22	0.0E+00	7657488	NT	Homo sapiens similar to ret integral membrane glycoprotein POM121 (POM121L1), mRNA
736	13356	25852	87.91	0.0E+00	AA914537.1	EST_HUMAN	np48d01.s1 NCI_CGAP_Brt.1 Homo sapiens cDNA clone IMAGE:1128633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-BJ (HUMAN);
742	13362	25856	4.31	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
742	13362	25857	4.31	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
752	13372	25866	1.46	0.0E+00	9032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
756	13372	25872	4.75	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
756	13377	25873	4.75	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
760	13379	25876	11.52	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
766	13385	25884	2.52	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HGSC project TCAA Homo sapiens cDNA clone TCAAP0779
766	13404	25908	1.47	0.0E+00	AF228990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
766	13404	25908	1.47	0.0E+00	AF228990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
767	13405	25910	0.72	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
780	13408	25913	19.87	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
790	13408	25914	19.87	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
793	13411	25915	1.08	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
794	13412	25916	1.82	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
798	13425	25918	2.4	0.0E+00	D30812.1	NT	Homo sapiens mRNA for repressor protein, partial cds
797	13414	25919	3.29	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849803 5'
801	13418	25923	2.87	0.0E+00	R48915.1	EST_HUMAN	y66908.r1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154048 5'
802	13418	25924	4.63	0.0E+00	5032088	NT	Homo sapiens aplicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
811	13428	25933	1.72	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
814	13432	25937	3.26	0.0E+00	7661968	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
826	13442	25948	1.15	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
825	13442	25950	1.15	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
830	13447	25954	2.88	0.0E+00	X68772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
834	13451	25958	2.77	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
834	13451	25959	2.77	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
839	13455	25985	9.17	0.0E+00	6174478.1	NT	Homo sapiens pericentriin (PCNT) mRNA
840	13456		8.31	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
857	13473	25988	1.71	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated new tumor-associated kinase (HUNK), mRNA
858	13474	25987	2.61	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated new tumor-associated kinase (HUNK), mRNA
860	13476	25989	2.3	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNIE1) mRNA
868	13481	25995	1.58	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBBH) mRNA, complete cds
868	13481	25996	1.58	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBBH) mRNA, complete cds
887	13482	25997	0.95	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBBH) mRNA, complete cds
872	13487	26002	2.8	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (80KD) (GABPA), mRNA
876	13490	26007	1.98	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
876	13490	26008	1.98	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
883	13497		1.72	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
887	13501	26019	6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
887	13501	26020	6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
888	13502	26021	12.88	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
889	13503	26022	8.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
890	13504	26023	15.65	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S6 (RPS6) mRNA
894	13508	26026	1.84	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
894	13508	26027	1.64	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
895	13509	26028	2.12	0.0E+00	AA53272.1	EST_HUMAN	U66407.81 NCI CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
895	13509	26029	2.12	0.0E+00	AA53272.1	EST_HUMAN	U66407.81 NCI CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
886	13510		6.29	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248915 5'
900	13514	26030	1.67	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated new tumor-associated kinase (HUNK), mRNA
900	13514	26031	1.67	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated new tumor-associated kinase (HUNK), mRNA
901	13515	26032	2.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated new tumor-associated kinase (HUNK), mRNA
901	13515	26033	2.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated new tumor-associated kinase (HUNK), mRNA
924	13537	26058	0.95	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
931	13544	26061	1.84	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
931	13544	26062	1.84	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
941	13554	26071	2.92	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
951	13563		32.18	0.0E+00	4504868	NT	Homo sapiens laminitin receptor 1 (87kD, ribosomal protein SA) (LAMR1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
954	13568	26076	6.19	0.0E+00	U35484.1	NT	Human protein C inhibitor (PCH-B) mRNA, complete cds
954	13568	26080	6.19	0.0E+00	U35484.1	NT	Human protein C inhibitor (PCH-B) mRNA, complete cds
956	13563		27.9	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (LR1D, ribosomal protein SA) (LAMR1), mRNA
957	13568	26082	269.29	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
958	13568	26083	16.83	0.0E+00	S69384.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
958	13568	26084	16.83	0.0E+00	S69384.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
958	13568	26085	16.83	0.0E+00	S69384.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
959	13570	26086	12.58	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (Pl4) gene, exons 1-4, complete cds
986	13568	26111	0.9	0.0E+00	M37190.1	NT	Human res inhibitor mRNA, 3' end
987	13569	26112	8.4	0.0E+00	M37190.1	NT	Human res inhibitor mRNA, 3' end
988	13600	26113	0.8	0.0E+00	M37190.1	NT	Human res inhibitor mRNA, 3' end
989	13601	26114	1.28	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
989	13601	26115	1.28	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
987	15430	26122	6.65	0.0E+00	A1001948.1	EST_HUMAN	cs988d3.s1 NCJ CGAP GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
987	15430	26123	6.65	0.0E+00	A1001948.1	EST_HUMAN	cs988d3.s1 NCJ CGAP GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
998	13610	26125	8.95	0.0E+00	7687266	NT	Homo sapiens KIAA0929 protein Mas2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1010	13620	26135	2.35	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
1019	13628	26142	1.58	0.0E+00	BF386974.1	EST_HUMAN	PM2-GN0014-050900-001-r02 GN0014 Homo sapiens cDNA
1019	13628	26143	1.58	0.0E+00	BF386974.1	EST_HUMAN	PM2-GN0014-050900-001-r02 GN0014 Homo sapiens cDNA
1019	13628	26144	1.56	0.0E+00	BF386974.1	EST_HUMAN	PM2-GN0014-050900-001-r02 GN0014 Homo sapiens cDNA
1021	13631	26147	2.54	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1021	13631	26148	2.54	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1030	13640	26155	2.14	0.0E+00	4757869	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1042	13651	26163	1.60	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1043	13652	26164	31.87	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1044	13652	26164	15.2	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1047	13655		5.72	0.0E+00	AF189490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1048	13655		7.76	0.0E+00	AF189490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1052	13659	26170	1.8	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1053	13659	26170	2.85	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1054	13659	26170	2.84	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1055	13660	26171	2.87	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1058	13663	26174	1.89	0.0E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1062	13667	26178	3.66	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (MIMP), mRNA
1063	13668		2.66	0.0E+00	AA459880.1	EST_HUMAN	aa8907.61 Stratiotes fetal retina 937202 Homo sapiens cDNA clone IMAGE:839236 3' similar to SW:PR38_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8:
1066	13671	26182	0.94	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1068	13671	26183	0.94	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1067	13672	26184	2.11	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1067	13672	26185	2.11	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1071	13676		2.06	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1085	13690	26200	5.51	0.0E+00	4759568	NT	Homo sapiens heat shock 70kD protein 98 (mortalin-2) (HSPA98), mRNA
1103	13707	26215	2.09	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6), mRNA
1103	13707	26216	2.09	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6), mRNA
1107	13711	26220	3.31	0.0E+00	8923924	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1107	13711	26221	3.31	0.0E+00	8923924	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1108	13712	26222	72.04	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1110	13714		1.08	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1112	13716	26226	4.16	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1121	13724	26237	4.89	0.0E+00	4768117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1135	13738	26247	2.88	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1158	13761	26271	4.25	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1158	13761	26272	4.25	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1171	13773	26282	1.29	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1171	13773	26283	1.29	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1172	13774	26284	23.49	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1174	13776	26288	1.24	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1177	13778	26289	15.95	0.0E+00	AB002056.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1179	13781	26290	37.33	0.0E+00	AB002056.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1180	13782	26291	6.32	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1180	13782	26292	6.32	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1184	13785	26296	2.19	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51728), mRNA
1185	13788	26298	1.92	0.0E+00	X95926.1	NT	H. sapiens ART4 gene
1185	13788	26297	1.92	0.0E+00	X95926.1	NT	H. sapiens ART4 gene
1186	13787	26298	2.18	0.0E+00	AI147850.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1188	13788	26300	1.59	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1197	13788	26309	0.7	0.0E+00	4756081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1197	13788	26310	0.7	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1198	13789	26311	1	0.0E+00	9988844	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
1210	13810	26323	3.09	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1210	13810	26324	3.09	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1213	13813	26327	1.78	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1220	13820	26336	8.63	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1261	13848		0.85	0.0E+00	7657336	NT	Homo sapiens muL (E. coli) homolog 3 (MLH3), mRNA
1265	13862	26379	0.63	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1289	13866	26383	2.13	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1289	13866	26384	2.13	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1270	13887	26385	2.51	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1271	16438	26386	2.03	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1289	13884	26409	6.85	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1290	13885	26410	1.33	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1300	13884	26416	0.83	0.0E+00	4508740	NT	Homo sapiens prefoldin 4 (PF4N4) mRNA
1309	13903		2.3	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1317	13911	26431	180.44	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1324	13918	26440	3.35	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
1331	13925	26445	1.6	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1331	13925	26446	1.6	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1343	13938	26459	2.38	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1343	13938	26460	2.38	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1343	13938	26461	2.38	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1344	13939		2.61	0.0E+00	AF088156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1354	15438	26473	2.05	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1354	15438	26474	2.05	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1360	13954	26480	4.79	0.0E+00	5803148	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1361	13955	26481	1.2	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1363	13957	26482	0.87	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1364	13958	26483	4.9	0.0E+00	5803148	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1365	13959	26484	1.23	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1367	13981	26486	3.51	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1388	13982	26487	2.78	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1389	13983	26488	4.87	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1370	13984	26489	4.11	0.0E+00	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1370	13984	26490	4.11	0.0E+00	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1382	13975	26503	1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1442	14035	26563	0.98	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350471 5'
1442	14035	26564	0.98	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350471 5'
1454	14046	26576	0.82	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1462	14054	26587	1.2	0.0E+00	AJ208758.1	EST_HUMAN	qg38b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.6 CE14213 ;
1463	14055	26588	11.41	0.0E+00	6042208	NT	RAN, member RAS oncogene familyHomo sapiens RAN, member RAS oncogene family (RAN), mRNA
1472	14064	26598	1	0.0E+00	4505948	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1472	14064	26600	1	0.0E+00	4505948	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1474	14066	26603	3.26	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1474	14066	26604	3.26	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1477	14069	26606	7.19	0.0E+00	AJ238003.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1488	14081	26620	3.54	0.0E+00	AF038290.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1510	14102	26638	3.27	0.0E+00	AL132898.1	NT	Novel human gene on chromosome 20
1512	14104	26639	1.4	0.0E+00	AL137784.1	NT	Novel human gene mapping to chromosome 1
1516	14108	26644	1.45	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1518	14111	26647	9.88	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1521	14113	26648	2.74	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1521	14113	26649	2.74	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1521	14113	26650	2.74	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1558	14150	26682	1.8	0.0E+00	7705434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51888), mRNA
1573	14166	26697	1.48	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815118 6'
1579	14172	26701	23.67	0.0E+00	AF023860.1	NT	Carophilus aethiops cyclophilin A mRNA, complete cds
1579	14172	26702	23.67	0.0E+00	AF023860.1	NT	Carophilus aethiops cyclophilin A mRNA, complete cds
1581	14174	26705	1.2	0.0E+00	AW978097.1	EST_HUMAN	EST1388208 MAGI resequences, MAGN Homo sapiens cDNA
1581	14174	26706	1.2	0.0E+00	AW978097.1	EST_HUMAN	EST1388208 MAGI resequences, MAGN Homo sapiens cDNA
1582	14175	26707	1.02	0.0E+00	D10884.1	NT	Boxine mRNA for neurocalcin
1584	14177		3.89	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1585	14178	26710	1.89	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1585	14178	28711	1.89	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB), mRNA
1586	14179	28712	3.3	0.0E+00	7682405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1587	14180		8.59	0.0E+00	7659972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1593	14188	28718	8.98	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1596	15445		25.62	0.0E+00	4508654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1597	14189	28720	28.95	0.0E+00	M14189.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1609	14202	28735	11.52	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1617	14210		1.58	0.0E+00	D00335.1	NT	human c-yes-2 gene
1624	14217	28749	10.11	0.0E+00	Z83738.1	NT	H. sapiens NH2B/e gene
1625	14218	28750	2.24	0.0E+00	5921480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1626	14219	28751	2.24	0.0E+00	5921480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1628	14219	28752	7.83	0.0E+00	AV680831.1	EST_HUMAN	AV680831 GKC Homo sapiens cDNA clone GKCB0F02 5'
1628	14219	28753	7.83	0.0E+00	AV680831.1	EST_HUMAN	AV680831 GKC Homo sapiens cDNA clone GKCB0F02 5'
1628	15448	28754	2.78	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1632	14224	28755	1.01	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1634	14226	28758	3.22	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1634	14226	28759	3.22	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1636	14228	28760	37.34	0.0E+00	5728876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1636	14228	28761	37.34	0.0E+00	5728876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1638	14230	28763	0.87	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1652	14244	28778	7.35	0.0E+00	H28973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b-HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1661	14254	28789	1.48	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1661	14254	28790	1.48	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1680	14272	28805	0.9	0.0E+00	AW444637.1	EST_HUMAN	UIH-B13-gw-c-04-U1.s1 NCJ CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1708	14301	28838	0.91	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN, ;
1709	14302	28839	2.5	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1713	14305	28843	1.38	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1713	14305	28844	1.38	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1715	14307	28846	6.78	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1716	14308	28847	0.85	0.0E+00	7657066	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1720	14312	28850	0.85	0.0E+00	BE222374.1	EST_HUMAN	hu11605.x1 NCJ CGAP Lu23 Homo sapiens cDNA clone IMAGE:3168281 3' similar to TR:Q85147 Q85147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	14312	26851	0.85	0.0E+00	BE22374.1	EST_HUMAN	hU11605.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168281 3' similar to TR:085147 085147
1723	14314	26855	3.69	0.0E+00	H30132.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE
1723	14314	26856	3.69	0.0E+00	H30132.1	EST_HUMAN	y550e03.r1 Soares breast 3NHBTst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M84089
1725	14316	26858	6.58	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1726	14316	26859	6.58	0.0E+00	Z80780.1	NT	y550e03.r1 Soares breast 3NHBTst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M84089
1728	14318		20.47	0.0E+00		NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 6 PRECURSOR (HUMAN);
1737	14327	26871	4.36	0.0E+00	5031748	NT	H. sapiens H2B/h gene
1742	14332	26877	0.82	0.0E+00	8923841	NT	H. sapiens H2B/h gene
1742	14332	26878	0.82	0.0E+00	8923841	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1746	14335	26882	1.17	0.0E+00	M75980.1	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1751	14341	26888	3.79	0.0E+00	4826973	NT	Human hepatocyte growth factor gene, exon 15
1753	14343		3.16	0.0E+00	A8028542.1	NT	Human hepatocyte growth factor gene, exon 15
1762	14352	26898	1.05	0.0E+00	S94400.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1781	14371	26916	2.35	0.0E+00	AF273841.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1820	14450		35.11	0.0E+00	4557658	NT	TCR zeta (human, Genomic)mRNA, 365 nt, segment 1 of 8]
1825	14414	26900	1.31	0.0E+00	4557658	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
1825	14414	26901	1.31	0.0E+00	4557658	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1828	14417	26905	1.47	0.0E+00	U63963.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1831	15451	26909	5.45	0.0E+00	4505332	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1843	14431	26904	13.62	0.0E+00	U14967.1	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1845	14433	26907	7.44	0.0E+00	AB002331.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1848	14434	26908	9.59	0.0E+00	4502264	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1848	14434	26909	9.59	0.0E+00	4502264	NT	Human ribosomal protein L21 mRNA, complete cds
1848	14434	26909	9.59	0.0E+00	4502264	NT	Human mRNA for KIAA0333 gene, partial cds
1848	14434	26909	9.59	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1848	14434	26909	9.59	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1857	14445	27001	1.57	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1863	14450	27009	1.98	0.0E+00	4504628	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
1863	14450	27010	1.38	0.0E+00	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1874	14460	27016	7.82	0.0E+00	6003955	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1874	14460	27016	7.82	0.0E+00	6003955	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

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1874	14460	27017	7.62	0.0E+00	8006866	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1884	14470	27027	0.93	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1162 protein, partial cds
1884	14470	27028	0.93	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1162 protein, partial cds
1888	14473	27030	5	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1888	14473	27031	5	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1889	14474	27032	8.6	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1889	14474	27033	8.6	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1892	14477	27036	1.32	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-4-07-Q-U1.a1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1892	14477	27037	1.32	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-4-07-Q-U1.a1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1916	14501	27056	3.38	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1916	14501	27057	3.38	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1939	14523	27070	1.77	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0128-200300-012-504 BN0128 Homo sapiens cDNA
1967	14551	27106	2.82	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1967	14551	27107	2.92	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1975	14559		1.84	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1976	15455	27116	2.72	0.0E+00	M89478.1	NT	Human transglutaminase mRNA, complete cds
1976	15455	27117	2.72	0.0E+00	M89478.1	NT	Human transglutaminase mRNA, complete cds
1981	14584	27124	1.69	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1981	14584	27125	1.69	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1985	14587		5.88	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1990	14572		5.14	0.0E+00	M56632.1	NT	Human topoisomerase I pseudogene 1
1998	14581	27139	3.45	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1999	14581	27140	3.45	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2009	14581		0.89	0.0E+00	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C062
2011	14593	27153	1.13	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2011	14593	27154	1.13	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2012	14594	27155	2.07	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2012	14594	27156	2.07	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2024	14608	27171	1.03	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2024	14608	27172	1.03	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2030	14612	27176	1.43	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2030	14812	27177	1.43	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2032	14814	27178	0.89	0.0E+00	AW183024.1	EST_HUMAN	X68501.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2875913 3'
2032	14814	27179	0.89	0.0E+00	AW183024.1	EST_HUMAN	X68501.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2875913 3'
2033	14815	27180	7.64	0.0E+00	6812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2033	14815	27181	7.64	0.0E+00	6812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2035	14817	27183	0.88	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2038	14818	27184	0.82	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
2038	14818	27185	0.82	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
2043	14825	27194	2.25	0.0E+00	AB040948.1	NT	Homo sapiens mRNA for KIAA1813 protein, partial cds
2097	14876	27245	0.94	0.0E+00	7708742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2102	14881	27249	2.71	0.0E+00	BE743215.1	EST_HUMAN	601673895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
2102	14881	27250	2.71	0.0E+00	BE743215.1	EST_HUMAN	601673895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
2104	14883	27251	1.39	0.0E+00	4503848	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2105	14884	27252	3.79	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2106	14086	26803	1.97	0.0E+00	7705585	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2108	14086	26804	1.97	0.0E+00	7705585	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2108	14886	27254	1.59	0.0E+00	AA077589.1	EST_HUMAN	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10
2108	14886	27255	1.59	0.0E+00	AA077589.1	EST_HUMAN	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10
2110	14888		1.76	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2112	14690		1.76	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2114	14692		2.2	0.0E+00	AJ244247.1	EST_HUMAN	q96f08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1888871 3' similar to contains Alu repetitive element
2119	14697	27266	2.72	0.0E+00	BE877225.1	EST_HUMAN	601485148F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3887747 5'
2121	14699	27268	1.8	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2121	14699	27269	1.8	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2126	14704	27275	2.31	0.0E+00	BE697126.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2126	14704	27276	2.31	0.0E+00	BE697126.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2133	14711	27283	2.79	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2133	14711	27284	2.79	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2134	14712	27285	1.61	0.0E+00	AJ297708.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2139	14717	27289	1.28	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2143	14721	27292	34.67	0.0E+00	BE600985.1	EST_HUMAN	7834002.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2160	14737		2.08	0.0E+00	BE767884.1	EST_HUMAN	QV1-GN0085-140800-318-310 GN0086 Homo sapiens cDNA
2161	14738		1.8	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2163	14740	27310	3.84	0.0E+00	BF027582.1	EST_HUMAN	601872066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2165	14742	27311	0.68	0.0E+00	AF240768.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2166	14743	27312	1.35	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-310 CT0219 Homo sapiens cDNA
2168	14745	27314	6.51	0.0E+00	A1904840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2168	14745	27315	6.51	0.0E+00	A1904840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2202	14778		0.97	0.0E+00	7657262	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2224	14798		1.37	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3'end
2230	14805	27377	10.57	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2230	14805	27378	10.57	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2232	14807	27380	1.12	0.0E+00	AA931691.1	EST_HUMAN	cc32601.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1667888 3'
2234	14809		7.75	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 28
2236	14811	27383	10.88	0.0E+00	BF344434.1	EST_HUMAN	602014828F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150734 5'
2237	14812	27384	20.34	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2240	14816	27387	2.59	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2240	14815	27388	2.59	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2244	15481	27393	2.04	0.0E+00	BF313817.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126822 5'
2247	14821	27396	1.58	0.0E+00	BE018760.1	EST_HUMAN	bb84602.Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
2248	14822	27397	0.84	0.0E+00	AA042813.1	EST_HUMAN	z453c07.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2248	14822	27398	0.94	0.0E+00	AA042813.1	EST_HUMAN	z453c07.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2256	14830	27406	2.87	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2256	14830	27407	2.87	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2257	14831	27408	0.98	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2257	14831	27409	0.98	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2262	14836		1.58	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2263	14837	27414	0.91	0.0E+00	AA282281.1	EST_HUMAN	z121610.t1 NCI_CGAP_GC8T Homo sapiens cDNA clone IMAGE:712891 5'
2270	14844	27420	0.92	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2271	14845		4.79	0.0E+00	M20803.1	NT	Human apolipoprotein C-I pseudogene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2282	14856	27433	6.28	0.0E+00	4557658	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2288	14882	27437	1.15	0.0E+00	7862401	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
2295	14869	27445	1.05	0.0E+00	BE889281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2299	14872	27448	1.28	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2339	14910	27482	3.84	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2339	14910	27483	3.84	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2340	14911	27484	2.08	0.0E+00	AI078404.1	EST_HUMAN	cd09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2342	14913	27488	1.81	0.0E+00	AA428001.1	EST_HUMAN	zv78a11.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:159740 5'
2342	14913	27487	1.81	0.0E+00	AA428001.1	EST_HUMAN	zv78a11.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:159740 5'
2344	14916	27489	1.98	0.0E+00	AA680387.1	EST_HUMAN	zv11e12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430510 3'
2346	14916	27490	3.85	0.0E+00	BF347039.1	EST_HUMAN	802021946F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157339 5'
2350	14921	27498	3.07	0.0E+00	LO2840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2351	14922	27497	1.6	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2358	14928	27503	1.17	0.0E+00	BE576095.1	EST_HUMAN	7722a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3285370 3' similar to TR:O94839 O94839 KIAA0857 PROTEIN ;
2360	14931	27504	5.89	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHKA2) gene, exon 32
2361	14932	27505	2.94	0.0E+00	AB25542.1	EST_HUMAN	ly67c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2366	14937	27509	1.72	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2368	14937	27510	1.72	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2371	14946	27520	0.99	0.0E+00	D83778.1	NT	Human mRNA for KIAA0184 gene, partial cds
2377	14948	27521	0.99	0.0E+00	D83778.1	NT	Human mRNA for KIAA0184 gene, partial cds
2378	14947		1.07	0.0E+00	4557521	NT	Homo sapiens deloninase, lisdithionine, type I (DIO1) mRNA
2387	14956	27527	2.83	0.0E+00	5174878	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2391	14959	27531	1.95	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002094 5'
2392	14960		8.95	0.0E+00	BE784026.1	EST_HUMAN	601386843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2393	14961	27532	0.98	0.0E+00	AW867076.1	EST_HUMAN	MRI1-SN0033-120400-002-404 SN0033 Homo sapiens cDNA
2394	14962	27533	6.08	0.0E+00	7682017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2395	14963	27534	1.69	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2396	14963	27535	1.69	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2398	14964		3.28	0.0E+00	AF280107.1	NT	
2398	14968	27537	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2398	14968	27538	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'

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2398	14968	27639	10.18	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 6'
2458	15025	27595	4.3	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2459	15026		3.3	0.0E+00	AJ042035.1	EST_HUMAN	oxd002.x1 Soares NIH-MPQ S1 Homo sapiens cDNA clone IMAGE:1690683 3' similar to TR:008662
2460	15027	27598	1.08	0.0E+00	8923820	NT	008682 230KDA PHOSPHATIDYLINOSITOL 4-KINASE. ; Homo sapiens hypothetical protein FLJ20683 (FLJ20683), mRNA
2463	15030	27598	1.3	0.0E+00	AW303088.1	EST_HUMAN	xv1507.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:064924
2465	15032		1.28	0.0E+00	BE895605.1	EST_HUMAN	O54924 EXO84. ; 801432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2476	15043		1.17	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HcLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2480	15048	27615	8.35	0.0E+00	8008002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2484	15049	27619	1.94	0.0E+00	D86608.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
2484	15049	27620	1.94	0.0E+00	D86608.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
2491	15056	27629	3.24	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2498	15063	27638	3.07	0.0E+00	572977	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2507	15071	27644	4.18	0.0E+00	BF669144.1	EST_HUMAN	802184558F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2518	15082	27655	2.85	0.0E+00	AW466922.1	EST_HUMAN	h04040.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2520	15084	27656	2.91	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-ale-c-07-0JL1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2528	15093		1.39	0.0E+00	AJ287878.1	EST_HUMAN	q23f00.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
2537	15101	27674	1.64	0.0E+00	5453986	NT	MIR repetitive element ; Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2537	15101	27675	1.54	0.0E+00	5453986	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2548	15112		1.81	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2552	15116	27686	0.72	0.0E+00	BE794542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3948518 5'
2553	15117	27687	1.32	0.0E+00	BF509482.1	EST_HUMAN	UI-HB14-eoz-b-08-Q-U1.s1 NCI_CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086555 3'
2555	15119	27689	1.52	0.0E+00	Z32894.2	NT	Homo sapiens mRNA for membrane transport protein (XX gene)
2557	15121		3.57	0.0E+00	8453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2559	15123	27692	0.89	0.0E+00	BE010378.1	EST_HUMAN	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2560	15124	27693	3.1	0.0E+00	7657468	NT	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2561	15125	27694	3.58	0.0E+00	BE150885.1	EST_HUMAN	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2562	15126	27695	1.24	0.0E+00	8923340	NT	RC4-H10276-160200-013-d05 HT0278 Homo sapiens cDNA
2563	15127	27698	3	0.0E+00	U92339.1	NT	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2568	15132	27700	1.34	0.0E+00	BE886490.1	EST_HUMAN	Human Sec62 (Sec62) mRNA, complete cds
2571	15134	27704	4.84	0.0E+00	BE76511.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908868 5'
2571	15134	27704	4.84	0.0E+00	BE76511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2571	15134	27705	4.84	0.0E+00	BE76511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2587	15150	27714	0.9	0.0E+00	BE538921.1	EST_HUMAN	601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2582	15154	27721	8.34	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1001673 5'
2582	15154	27722	9.34	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1001673 5'
2583	15155	27723	0.9	0.0E+00	BE282898.1	EST_HUMAN	601106312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887855 5'
2583	15155	27724	0.9	0.0E+00	BE282898.1	EST_HUMAN	601106312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887855 5'
2588	15158	27726	8.82	0.0E+00	AF245505.1	NT	Homo sapiens edican mRNA, complete cds
2633	15402	27766	1.78	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2633	15402	27767	1.78	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2634	15194		3.12	0.0E+00	BF513835.1	EST_HUMAN	UI-HBW1-amp1-12-0-UI.at NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070831 3'
2643	15202	27775	1.24	0.0E+00	AI671737.1	EST_HUMAN	In18608.x1 NCI CGAP Brn28 Homo sapiens cDNA clone IMAGE:2188055 3' similar to gb:L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2644	15203	27776	2.08	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21) mRNA
2647	15206	27778	6.91	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2648	15207	27780	0.89	0.0E+00	BE785445.1	EST_HUMAN	601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2648	15207	27781	0.99	0.0E+00	BE785445.1	EST_HUMAN	601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2651	15210	27782	1.18	0.0E+00	BE289328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2655	15214		6.88	0.0E+00	BE782472.1	EST_HUMAN	601584830F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2653	15221	27793	1.73	0.0E+00	4504688	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2671	15228		1.85	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2672	15230	27800	6.98	0.0E+00	AF13227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2676	15234	27801	2.15	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
2680	15238	27803	1.01	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2680	15238	27806	1.01	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2682	15240	27808	1.22	0.0E+00	AW887016.1	EST_HUMAN	RC1-OT0088-220303-011-407 OT0088 Homo sapiens cDNA
2685	15243	27811	3.43	0.0E+00	BE383185.1	EST_HUMAN	601288714F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3828923 5'
2686	15244		2.17	0.0E+00	BE531283.1	EST_HUMAN	601278373F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3610267 5'
2712	15289	27837	1.4	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2748	15303		9.58	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2749	15304	27868	12.57	0.0E+00	BE784884.1	EST_HUMAN	60158925F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2755	15310	27876	2.37	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2757	15312	27878	0.97	0.0E+00	7688517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2768	15313	27679	1.42	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2769	15315	27681	1.23	0.0E+00	AB051828.1	NT	Homo sapiens hG2AK mRNA for GTP-binding protein like 1, complete cds
2766	15319	27688	20.41	0.0E+00	BE786378.1	EST_HUMAN	601591981F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945993 5'
2768	15320	27686	2.11	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2768	15476	27690	14.33	0.0E+00	BE680433.1	EST_HUMAN	601335465F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689594 5'
2770	15323		1.77	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE08 5'
2772	15325	27693	2.47	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2772	15325	27694	2.47	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2773	15326	27695	1.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477). mRNA
2773	15326	27696	1.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477). mRNA
2774	15327	27697	2.27	0.0E+00	AF280195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2775	15328		131.05	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCOLD07 3'
2776	15329	27698	4.94	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2776	15329	27699	4.94	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2780	15333	27692	7.42	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2780	15333	27693	7.42	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2784	15337	27698	3.11	0.0E+00	BE747169.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2786	15349		0.98	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2797	15350	27919	2.78	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-armw-e-07-UJ.e1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2804	15356		0.88	0.0E+00	4503068	NT	Homo sapiens chondrinin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2808	15361	27828	1.76	0.0E+00	7703275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2809	15361	27828	1.76	0.0E+00	7703275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2810	15362	27830	4.3	0.0E+00	BF677694.1	EST_HUMAN	602085578F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248816 5'
2814	15366	27836	1.1	0.0E+00	7427822	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2817	15369	27838	17.28	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTGCCA03 5'
2817	15369	27838	17.28	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTGCCA03 5'
2819	15371		9.44	0.0E+00	AI876183.1	EST_HUMAN	au55404.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40428 60S RIBOSOMAL PROTEIN L13A ;
2822	15374	27944	1.69	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCL_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4214879 5'
2823	15375	27945	7.68	0.0E+00	BE972768.1	EST_HUMAN	601460912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854842 5'
2825	15377	27946	1.55	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2825	15377	27947	1.55	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2826	15378	27948	34.11	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2826	15378	27949	34.11	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2832	12861	26345	7.88	0.0E+00	S78830.1	NT	glycoprotein D=Duffy group antigen (human, blood, Genomic DNA, 3088 nt)
2833	13385		1.75	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2841	13382	25881	1.88	0.0E+00	AF284750.1	NT	Homo sapiens ALR-III protein mRNA, partial cds
2841	13382	26882	1.88	0.0E+00	AF284750.1	NT	Homo sapiens ALR-III protein mRNA, partial cds
2846	13682	28192	3.33	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2846	13682	28193	3.33	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2861	15480	27956	4.7	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2862	15481		2.28	0.0E+00	AF068824.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2863	15482		1.63	0.0E+00	AB040980.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2870	15488		1.06	0.0E+00	AJ239852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2871	15489	27960	2.43	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2875	15493	27963	1.55	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2877	15495	27985	1.25	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281269-003-402 HT0343 Homo sapiens cDNA
2877	15495	27988	1.26	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281269-003-402 HT0343 Homo sapiens cDNA
2879	15497		1	0.0E+00	X73428.1	NT	H. sapiens lds gene for LH type transcription factor
2881	15499		2.78	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
2882	15500	27969	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2882	15500	27970	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2882	15500	27971	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2884	15502	27972	2.39	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
2886	15505	27975	15.68	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGIP3) pseudogene
2888	15505	27976	15.68	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGIP3) pseudogene
2891	15508	27979	1.95	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2892	15509		7.43	0.0E+00	Y10858.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2893	15510		1.17	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2894	15511	27980	112.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2894	15511	27981	112.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2894	15521	27981	2.68	0.0E+00	4507280	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2907	15524	27995	1.03	0.0E+00	AL047699.1	EST_HUMAN	DKFZp586G0821.1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp586G0821
2908	15525	27986	1.64	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2908	15525	27997	1.64	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2909	15526		2.8	0.0E+00	4503098	NT	Homo sapiens chondroclitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2912	15529	27999	6.04	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0638-130400-138-H03 BT0638 Homo sapiens cDNA
2912	15529	28000	6.04	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0638-130400-138-H03 BT0638 Homo sapiens cDNA
2918	15535	28008	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2918	15535	28009	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2921	15538	28013	2.25	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2921	15538	28014	2.25	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2922	15539	28015	1.29	0.0E+00	AA218579.1	EST_HUMAN	z98b11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683617 3' similar to contains Alu repetitive element
2929	15545	28024	4.1	0.0E+00	Y19210.1	NT	Homo sapiens HHb5 gene for hair keratin, exons 1 to 9
2932	15548	28024	1.24	0.0E+00	4768279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2934	15550	28027	41.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2936	15552	28028	1.85	0.0E+00	P62740	SWISSPROT	ZINC FINGER PROTEIN 132
2937	15553	28030	1.25	0.0E+00	AF152338.1	NT	Homo sapiens proteodielphin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2946	15562	28037	0.92	0.0E+00	AI209084.1	EST_HUMAN	q94904.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838527 3' similar to
2954	15570	28045	1.78	0.0E+00	AB033083.1	NT	SW_C820_HUMAN P62298 20 KD NUCLEAR CAP BINDING PROTEIN
2954	15570	28046	1.78	0.0E+00	AB033083.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2955	15571	28047	6.84	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2955	15571	28048	6.84	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2958	15574	28051	3.14	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2958	15574	28052	3.14	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2959	15575	28053	3.48	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2959	15575	28054	3.48	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2964	15578	28059	1.12	0.0E+00	BF110702.1	EST_HUMAN	7n4d003.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
2964	15579	28059	1.12	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17293 PROTEIN ;
2972	15588	28070	2.98	0.0E+00	4505084	NT	7n4d003.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
2972	15588	28071	2.98	0.0E+00	4505084	NT	Q9VLN1 CG17293 PROTEIN ;
2981	15597	28077	1.82	0.0E+00	4768827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2981	15597	28077	1.82	0.0E+00	4768827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2985	15601	28080	1.33	0.0E+00	X15309.1	NT	Homo sapiens neurath III (NRXN3) mRNA
2985	15601	28080	1.33	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4

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2986	15601	28081	1.33	0.0E+00	X16309.1	NT	H.sapiens NF-H gene, exon 4
2987	15603	28083	9.26	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (LT1c) gene, exon 6
3001	15617		1.26	0.0E+00	A1148890.1	EST_HUMAN	qf43f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3009	15625	28103	0.72	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3009	15625	28104	0.72	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3010	15626	28105	1.24	0.0E+00	4508118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3011	15627	28106	2.29	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3023	15639	28116	1.93	0.0E+00	7682273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3025	15641	28118	2.52	0.0E+00	5728755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3026	15641	28119	2.52	0.0E+00	5728755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3036	15652	28130	1.45	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3036	15652	28131	1.45	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3060	15678		0.73	0.0E+00	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
3062	15678	28162	1.4	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3072	15687	28166	0.72	0.0E+00	4506882	NT	Homo sapiens semenogelin 1 (SEMG1) mRNA
3076	15690	28163	0.68	0.0E+00	AW978268.1	EST_HUMAN	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3080	15695		3.06	0.0E+00	AF108963.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3083	15698	28171	20.17	0.0E+00	5579499	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3083	15698	28172	20.17	0.0E+00	5579499	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3085	16700		7.12	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3089	15704	28176	2.79	0.0E+00	AF017493.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3092	15707						Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3112	15727	28198	2.39	0.0E+00	AF198779.1	NT	Human germ-line gene 16.1 for Ig lambda L-chain C region (Ig-LC16.1)
3118	15732		3.45	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3118	15732		1.69	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3122	15738	28205	1.74	0.0E+00	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3140	15754	28221	3.56	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3141	15755	28222	5.25	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3146	15760	28226	4.35	0.0E+00	7682139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3147	15761	28227	1.46	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3176	15768	28260	3.49	0.0E+00			Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3189	15767	28266	48.14	0.0E+00	L20841.1	NT	Human ferritin heavy chain mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3188	15800	28272	2.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3188	15800	28273	2.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3188	15808	28281	18.48	0.0E+00	T94970.1	EST_HUMAN	ye3703 s1 Stratiopene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S20639 S20639 BASIC PROTEIN, 23K -;
3210	15822	28288	1.23	0.0E+00	BF243398.1	EST_HUMAN	60187507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3211	15823	28298	1.28	0.0E+00	AI880886.1	EST_HUMAN	wu12h10x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2810803 3'
3216	15828	28308	4.68	0.0E+00	X98022.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3216	15828	28307	4.68	0.0E+00	X98022.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3218	15830	28309	0.83	0.0E+00	AI88950.1	EST_HUMAN	U33509.X1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2283376 3' similar to SW:RASD_DICD1
3226	15838	28317	1.87	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3226	15838	28318	1.57	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3233	15845	28325	10.76	0.0E+00	4604658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3234	15848	28328	0.82	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3234	15848	28327	0.82	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3245	15857	28340	1	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
3253	15865	28348	2.88	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3257	15869	28349	2.27	0.0E+00	4602088	NT	Homo sapiens solute carrier family 28 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3263	15875	28367	0.86	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3263	15876	28358	0.86	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3265	15877	28359	4.57	0.0E+00	AA774783.1	EST_HUMAN	ae87b11.s1 Stratiopene schizo brain S11 Homo sapiens cDNA clone IMAGE:871133 3'
3273	15885	28367	4.14	0.0E+00	AF288598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3273	15885	28368	4.14	0.0E+00	AF288598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3285	15888	28374	1.44	0.0E+00	4657590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3282	15803	28383	1.09	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3300	15911		0.86	0.0E+00	M85189.1	NT	Human connexin 43 processed pseudogene
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3301	15912	28380	1.7	0.0E+00	AF018413.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3303	15914	28392	4.47	0.0E+00	AF055084.1	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3313	18001	28400	2.26	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3313	18001	28401	2.26	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3328	15839	28415	2.87	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds

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3330	15940	28416	1.86	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20698 (FLJ20698), mRNA
3355	15963	28440	1.02	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3366	15974	28461	6.6	0.0E+00	AI88284.1	EST_HUMAN	U58108.X2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222635 3' similar to SW:RL11_RAT
3369	15977	28464	1.4	0.0E+00	AW055400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11; contains Alu repetitive element
3374	15983	28460	2.28	0.0E+00	AF128893.1	NT	EST387470 MAGE sequences, MAGE Homo sapiens cDNA
3374	15983	28461	2.28	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3376	15984	28462	0.91	0.0E+00	7667213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3375	15984	28463	0.91	0.0E+00	7667213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3376	15987	28466	1.23	0.0E+00	4502592	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3378	15987	28466	1.23	0.0E+00	4502592	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3382	15991	28469	13.03	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFY) gene, complete cds
3384	15993	28471	0.89	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3403	16012	28491	1.08	0.0E+00	AI632569.1	EST_HUMAN	wb10704.x1 NCL CGAP_QG8 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929
3443	16051	28526	3.18	0.0E+00	AU123684.1	EST_HUMAN	ZINC FINGER PROTEIN, :
3450	16057	28532	0.94	0.0E+00	7363436	NT	AU123684 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3450	16057	28533	0.94	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3453	16060	28535	1.88	0.0E+00	7708239	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3454	16061	28536	1.04	0.0E+00	AF211189.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3458	16065	28550	1.03	0.0E+00	AW867015.1	EST_HUMAN	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-1 isoform (CACNA1I) mRNA, complete cds
3471	16077	28551	1.28	0.0E+00	7662401	NT	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3471	16077	28551	1.28	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3472	16078	28552	1.05	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3475	16081	28554	1.72	0.0E+00	5803087	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3484	15313	27879	1.56	0.0E+00	AF110763.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3486	16094	28567	2.36	0.0E+00	7657038	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3490	16095	28568	0.97	0.0E+00	5453965	NT	Homo sapiens death receptor 6 (DR6), mRNA
3490	16095	28569	0.97	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3493	16098	28573	5.92	0.0E+00	K02380.1	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3495	16100	28575	1.2	0.0E+00	7427522	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC incompatibility determinants
							Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR), mRNA

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3497	16102	28577	1	0.0E+00	4657748	NT	Homo sapiens mist proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3501	16106	28581	3.89	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCL_CQAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73834 O73834 NEURAL CELL ADHESION MOLECULE ;
3501	16106	28582	3.89	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCL_CQAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73834 O73834 NEURAL CELL ADHESION MOLECULE ;
3503	16110	28587	2.13	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF-1)
3506	16111	28588	1.12	0.0E+00	7706378	NT	Homo sapiens ASB-4 protein (LOC51668), mRNA
3512	16117	28596	2.09	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3518	16123	28603	2.09	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3523	16128	28608	8.45	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3528	16133	28612	0.94	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDST fusion) mRNA, partial cds
3528	16133	28613	0.94	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3532	16137	28618	2.45	0.0E+00	AF048452.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3532	16137	28619	2.45	0.0E+00	AF048452.1	NT	Homo sapiens cell-line K51 transcriptional regulatory protein p54 mRNA, complete cds
3540	16145	28628	1.19	0.0E+00	AF231922.1	NT	Homo sapiens cell-line K51 transcriptional regulatory protein p54 mRNA, complete cds
3547	16151	28631	0.95	0.0E+00	AA626677.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3547	16151	28632	0.95	0.0E+00	AA626677.1	EST_HUMAN	eb51112.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844387 5'
3547	16151	28633	0.95	0.0E+00	AA626677.1	EST_HUMAN	ab51112.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844387 5'
3553	16157	28638	1.53	0.0E+00	BE304791.1	EST_HUMAN	eb51112.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844387 5'
3553	16157	28640	1.53	0.0E+00	BE304791.1	EST_HUMAN	801143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3559	16160	28643	2.51	0.0E+00	4503848	NT	801143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3567	16161	28644	1.08	0.0E+00	4828785	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
3560	16164	28647	1.58	0.0E+00	O14867	SWISSPROT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3565	16169	28651	0.93	0.0E+00	A1384007.1	EST_HUMAN	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3568	16172	28654	1.52	0.0E+00	M10976.1	NT	ts35g12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3585	16189	28672	0.74	0.0E+00	AA456282.1	EST_HUMAN	ts35g12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3585	16189	28673	0.74	0.0E+00	AA456282.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
3594	16198	28681	1	0.0E+00	AV701869.1	EST_HUMAN	z09h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:311927 5'
3595	16198	28682	0.73	0.0E+00	4506884	NT	z09h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:311927 5'
3607	16201		1.47	0.0E+00	AF078888.1	NT	AV701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3609	16210	28690	1.07	0.0E+00	AL193204.1	NT	Homo sapiens semaphorin II (SEMG2) mRNA
							Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
							Novel human gene mapping to chromosome X

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3610	16213	28693	0.88	0.0E+00	AB040908.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3622	16225	28703	1.1	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3633	16236	28711	1.16	0.0E+00	6897248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3633	16236	28712	1.16	0.0E+00	6897248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3634	16237		1.14	0.0E+00	AJ081907.1	EST_HUMAN	α77c11.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1862356 3' similar to WP:110B4.4 CE13742;
3636	16239	28715	1.26	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTNSA3), mRNA
3641	16244		5.41	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3649	16248	28724	1.06	0.0E+00	4504294	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3649	16262		1.74	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcystine synthetase (GLCCLC) gene, partial cds
3650	16253	28725	8.35	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5'
3653	16256		0.68	0.0E+00	AA9889715.1	EST_HUMAN	cc94h06.a1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER29.b2 MER29 repetitive element;
3653	16266	28737	0.9	0.0E+00	AW637977.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3675	16276	28743	0.8	0.0E+00	BF672054.1	EST_HUMAN	602152485F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283845 5'
3675	16276	28744	0.8	0.0E+00	BF672054.1	EST_HUMAN	602152485F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283845 5'
3676	16277		1.3	0.0E+00	4826987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3678	16278	28749	0.86	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3678	16278	28747	0.86	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3682	16283	28751	0.8	0.0E+00	4826783	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3684	16285	28754	0.91	0.0E+00	7662318	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3682	16283	28762	0.72	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3692	16293	28763	0.72	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3708	16310	28777	1.47	0.0E+00	D97327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3712	16313		20.4	0.0E+00	7869491	NT	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (GAPD), mRNA
3730	16331	28797	2.49	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3732	16333	28799	0.93	0.0E+00	AB007896.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3734	16335	28800	2.62	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
3734	16335	28801	2.62	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
3739	16340	28807	2.63	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g091 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3739	16340	28808	2.63	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g091 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3743	16344	28811	1.66	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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3743	16344	28812	1.68	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3746	16347	28815	1.08	0.0E+00	AW851714.1	EST_HUMAN	MR2-GT0222-281088-005-005 GT0222 Homo sapiens cDNA
3748	16349	28817	1.4	0.0E+00	6720928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3760	16361	28819	1.23	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
3762	16353	28821	1.56	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3764	16355	28823	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
3764	16355	28824	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
3767	16368	28833	4.72	0.0E+00	AW288134.1	EST_HUMAN	UI-H-BWO-gis-e-12-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:27330223
3767	16368	28834	4.72	0.0E+00	AW288134.1	EST_HUMAN	UI-H-BWO-gis-e-12-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:27330223
3792	16392	28857	1.06	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen $\alpha 1$ chain, exon 6
3793	16393	28858	0.87	0.0E+00	AA463659.1	EST_HUMAN	es06p01.1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3798	16398	28863	1.04	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3801	16401	28866	4.05	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3810	16409	28874	0.95	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3823	16423	28885	7.87	0.0E+00	7662183	NT	Homo sapiens KIAA0868 gene product (KIAA0868), mRNA
3826	16426	28888	23.27	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3834	16433	28894	1.04	0.0E+00	7657085	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3834	16433	28895	1.04	0.0E+00	7657085	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3873	16471	28935	0.92	0.0E+00	7661887	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3873	16471	28936	0.92	0.0E+00	7661887	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3892	16491	28951	2.65	0.0E+00	AF176733.1	NT	Pen troglodytes olfactory receptor (PTR208) gene, partial cds
3896	16495	28956	1.55	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3896	16495	28957	1.55	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3900	16498	28962	1.35	0.0E+00	A377699.1	EST_HUMAN	166210.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2081307 3'
3901	16500	28963	1.09	0.0E+00	AF152498.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3902	16501	28963	2.32	0.0E+00	4766189	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
3905	16504	28966	10.94	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, complete cds
3906	16505	28967	2.15	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3907	16506	28968	2.69	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3910	16508	28970	1.1	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3910	16508	28971	1.1	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3916	16514	28977	0.84	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3921	16519	28985	6.15	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3921	16519	28988	6.15	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3923	16521	28989	4.15	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3924	16522	28990	32.21	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3927	16525	28992	1.46	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3930	16528	28995	1.1	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3931	16529	28996	1.83	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP128), mRNA
3933	16531	28998	1.09	0.0E+00	AF089117.1	NT	Homo sapiens amphiphysin gene, partial cds
3944	16542	29009	2.45	0.0E+00	AI84727.1	EST_HUMAN	wk0170.1, NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:043340 O43340 R28830_2; contains element PTR7 repetitive element;
3947	16545	29013	16.56	0.0E+00	4500742	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3952	16550	29019	1.8	0.0E+00	AL040338.1	EST_HUMAN	DKFZp434N0413_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0413 5'
3957	16555	29025	1.03	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3957	16555	29026	1.03	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3958	16556	29027	2.86	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3960	16558		2.2	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3964	16562	29031	1.02	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3975	16573	29043	1.92	0.0E+00	4500768	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3979	16577	29047	1.81	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIA0412) mRNA
3986	16586	29057	1.88	0.0E+00	BF355285.1	EST_HUMAN	RC3-HT0860-170800-011-e12 HT0860 Homo sapiens cDNA
3990	16588	29059	1.04	0.0E+00	AW898221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1886728 similar to MXRA5 Matrix remodelling associated gene 5
3990	16588	29060	1.04	0.0E+00	AW898221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1886728 similar to MXRA5 Matrix remodelling associated gene 5
3998	16596	29068	2.64	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
4001	16599	29071	1.06	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4001	16599	29072	1.06	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4006	16604	29076	4.1	0.0E+00	BE378602.1	EST_HUMAN	601235960F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4014	16812	29085	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-L T0031-100100-003-H09 L T0031 Homo sapiens cDNA
4047	16844	29110	13.52	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4047	16844	29111	13.52	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4057	16854		4.5	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4059	16856		6.04	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4085	16682	28124	1.23	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
4086	16685	28126	3.49	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4077	16673	28134	2.12	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4090	16686		60.86	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4096	16683	28150	1.89	0.0E+00	U09386.1	NT	Human zinc finger protein ZNF133
4120	16713	28166	10.72	0.0E+00	AB019910.1	NT	Chlorococcus ethiops mRNA for ribosomal protein S4X, complete cds
4130	16722		3.27	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4140	16732	28185	1.61	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C093
4141	16733	28186	2.96	0.0E+00	AJ277278.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4141	16733	28187	2.96	0.0E+00	AJ277278.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4148	16740	28183	8.52	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4148	16740	28184	8.52	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4158	16750	28203	0.98	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
4164	16755	28207	7.55	0.0E+00	4885306	NT	phosphoribosylglycinamide synthetase (GART) mRNA
4165	16756	28208	4.94	0.0E+00	AB008625.1	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4168	16759	28209	0.66	0.0E+00	4768807	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4169	16760	28210	6.82	0.0E+00	11419287	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4170	16761	28211	2.88	0.0E+00	AL098857.1	NT	Homo sapiens IMP (inosine triphosphate) dehydrogenase 1 (IMPDH1), mRNA
4171	16762		1.11	0.0E+00	AA018975.1	EST_HUMAN	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4178	16769	28218	3.61	0.0E+00	AF165527.1	NT	zef5c09.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:362820 5' similar to contains Alu repetitive element
4189	13773	28282	0.76	0.0E+00	4826947	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4189	13773	28283	0.76	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4185	16765	28283	2.14	0.0E+00	5901905	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4186	16766	28284	1.21	0.0E+00	4503854	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4186	16766	28285	1.21	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4188	16768	28282	0.57	0.0E+00	4506884	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4188	16768	28283	1.35	0.0E+00	8922391	NT	Homo sapiens semaphorin II (SEMG2) mRNA
4200	16789	28237	1.35	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4206	16796	28242	0.59	0.0E+00	AB020702.1	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4213	16802	28251	18.39	0.0E+00	AB02597.1	EST_HUMAN	Homo sapiens mRNA for KIAA0395 protein, partial cds
4213	16802	28252	18.39	0.0E+00	AB02597.1	EST_HUMAN	wu04404.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4216	16804	28254	1.08	0.0E+00	BE184856.1	EST_HUMAN	wu04404.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4216	16804	26255	1.08	0.0E+00	BE184896.1	EST_HUMAN	MR1-HT0707-100500-001-e02 HT0707 Homo sapiens cDNA
4221	16808		3.97	0.0E+00	BE274217.1	EST_HUMAN	60112078F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2687600 5'
4227	16815	26262	1.12	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4227	16816	26263	1.12	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4228	16817	26265	2.51	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4236	16824		5.9	0.0E+00	AW675599.1	EST_HUMAN	be51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800086 3' similar to SW:TH12_BOVIN
4241	16826	26279	1.14	0.0E+00	AW408788.1	EST_HUMAN	Q65108 MITOCHONDRIAL THIOREDOXIN PRECURSOR;
4242	16830	26280	1.84	0.0E+00	8922468	NT	UI-HF-8M0-edx-c-02-Q-U1r NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083147 5'
4242	16830	26281	1.84	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4251	16839		2.08	0.0E+00	5174832	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4263	16846	26297	1.08	0.0E+00	AB037739.1	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4270	16856	26303	10.06	0.0E+00	AA401438.1	EST_HUMAN	Homo sapiens mRNA for KIAA1318 protein, partial cds
4270	16856		10.06	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743187 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;
4273	16859	26308	1.01	0.0E+00	AF157476.1	NT	zu68h07.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743187 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;
4286	16872	26319	1.02	0.0E+00	4507720	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4286	16872	26320	1.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4301	16887	26331	1.08	0.0E+00	7691989	NT	Homo sapiens titin (TTN) mRNA
4305	16891	26333	1.8	0.0E+00	4758199	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4305	16891	26334	1.8	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4314	16900		0.72	0.0E+00	AL168303.2	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4344	16931	26372	1.17	0.0E+00	AJ003145.1	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4346	16933	26374	0.96	0.0E+00	AJ010770.1	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4360	16947	26389	17.92	0.0E+00	J02610.1	NT	Homo sapiens chromosome 21 segment HS21G103
4375	16962	26408	0.84	0.0E+00	AW936889.1	EST_HUMAN	Homo sapiens mRNA for ciliary receptor protein, pseudogene
4375	16968	26415	0.59	0.0E+00	4826827	NT	Homo sapiens hyperion gene, exon 1-50
4381	16968	26416	0.59	0.0E+00	4826827	NT	Human apolipoprotein B-100 mRNA, complete cds
4393	16970	26418	4.39	0.0E+00	AF174590.1	NT	PM2-DT0023-080300-004-e08 DT0023 Homo sapiens cDNA
4391	16977		2.19	0.0E+00	A1189844.1	EST_HUMAN	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4395	16980		4.49	0.0E+00	U14920.1	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
							q023f06.x1 Soares_pilocenta_8to9weeks_2NBHP858W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20 b2 MER20 repetitive element;
							Human CBFA3 (Cbfa3) gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4399	16984	29429	0.84	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4418	17003	29446	0.9	0.0E+00	6563384	NT	Homo sapiens protein kinase C, η (PRKCN), mRNA
4418	17003	29447	0.9	0.0E+00	6563384	NT	Homo sapiens protein kinase C, η (PRKCN), mRNA
4426	17010	29453	1.16	0.0E+00	U10981.1	NT	Human G2 protein mRNA, partial cds
4426	17010	29454	1.16	0.0E+00	U10981.1	NT	Human G2 protein mRNA, partial cds
4433	17019	29459	11.1	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4451	17037		1.13	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-38 (CX38) gene, complete cds
4480	17048	29489	4.8	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4484	17050	29494	5.78	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4484	17050	29495	5.78	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4470	17058	29501	1.97	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4470	17058	29502	1.97	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4475	17060	29508	10.17	0.0E+00	7862091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4475	17060	29509	10.17	0.0E+00	7862091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4484	17069	29510	1.11	0.0E+00	X82338.1	NT	Homo sapiens Menkes disease gene, exon 4
4487	17072	29523	16.07	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4488	17073	29524	1.73	0.0E+00	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4491	17076	29528	1.14	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4526	17110	29554	1.43	0.0E+00	7018456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4537	17121		7.31	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4545	17129	29572	1.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4546	17129	29573	1.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4549	17132	29579	0.58	0.0E+00	W26179.1	EST_HUMAN	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4549	17132	29580	0.58	0.0E+00	W26179.1	EST_HUMAN	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4555	17136	29585	6.07	0.0E+00	4508782	NT	Homo sapiens sphococerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA
4555	17136	29586	6.07	0.0E+00	4508782	NT	Homo sapiens sphococerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA
4567	17150		2.3	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4565	17168	29611	0.59	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cc8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F1205 5'
4565	17168	29612	0.59	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cc8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F1205 5'
4586	17171		0.65	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4589	17172	29816	1.48	0.0E+00	AA228128.1	EST_HUMAN	z68c04.r1 Soares_NIHMPJ_S1 Homo sapiens cDNA clone IMAGE:687690 5' similar to TR:G222811
4589	17172	29817	1.48	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4599	17183	29830	6.46	0.0E+00	AW084984.1	EST_HUMAN	z68c04.r1 Soares_NIHMPJ_S1 Homo sapiens cDNA clone IMAGE:687690 5' similar to TR:G222811
4601	18007		2.1	0.0E+00	8051819	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4603	17186	29833	0.92	0.0E+00	AI686888.1	EST_HUMAN	z68c04.r1 Soares_NIHMPJ_S1 Homo sapiens cDNA clone IMAGE:687690 5' similar to TR:G222811
4607	17190		8.58	0.0E+00	AL183207.2	NT	Q09668 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK.;
4609	17192	29838	2.41	0.0E+00	AW381670.1	EST_HUMAN	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4615	17188	29845	1.43	0.0E+00	AJ278120.1	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4616	17198	29846	1.43	0.0E+00	AJ278120.1	NT	PTB8 repetitive element.;
4617	17200	29848	2.01	0.0E+00	4785487	NT	Homo sapiens chromosome 21 segment HS21C007
4618	17201	29849	3.28	0.0E+00	AF108930.1	NT	PM1-H70305-101186-002-003 H70305 Homo sapiens cDNA
4623	17206	29855	1.19	0.0E+00	4506952	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4628	17211	29861	1.18	0.0E+00	AF111163.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4628	17211	29862	1.18	0.0E+00	AF111163.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4637	18008	29873	2.92	0.0E+00	8005973	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4642	17224	29878	4.04	0.0E+00	AF208161.1	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminatase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4647	17229	29885	1.66	0.0E+00	AF152337.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4650	17232	29889	1.5	0.0E+00	5454175	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4662	17244	29898	32.8	0.0E+00	4503470	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4671	17253	29705	0.79	0.0E+00	4505016	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4676	17257	29708	1.02	0.0E+00	4503098	NT	Homo sapiens synovial precursor, mRNA, complete cds
4679	17261	29713	1.14	0.0E+00	4502596	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4684	17266		3.03	0.0E+00	L35485.1	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4686	17268	29716	6.76	0.0E+00	7682091	NT	Homo sapiens sulfarytic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4686	17268	29717	9.75	0.0E+00	7682091	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4707	17289	29733	3.17	0.0E+00	AF143314.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4710	17292	29736	11.37	0.0E+00	AJ245418.1	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4710	17292	29737	11.37	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4712	17294	29738	0.84	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0785 protein, partial cds
4718	17299		0.65	0.0E+00	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4730	17311		1.68	0.0E+00	AA174072.1	EST_HUMAN	2018g08.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4732	17313		1.97	0.0E+00	7857410	NT	Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4734	17315		2.45	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4735	17316	29756	1.69	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4738	17317	29759	5.45	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4737	17318		1.94	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4739	17320	29760	0.82	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4747	17328	29770	8.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4747	17328	29771	8.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4748	17328	29772	1.57	0.0E+00	AF187441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4757	17338	29783	1.13	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4757	17338	29784	1.13	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4763	17344	29792	12.17	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4772	17363	29805	1.21	0.0E+00	BE081627.1	EST_HUMAN	QV2-BT0635-160400-142-H03 BT0635 Homo sapiens cDNA
4773	17354	29806	1.04	0.0E+00	AA418249.1	EST_HUMAN	2068607.s1 Soares NIHMPy_S1 Homo sapiens cDNA clone IMAGE:767805 3'
4779	17360		2.04	0.0E+00	AF089641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4785	17365	29816	1.09	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4785	17365	29817	1.09	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4786	17366	29818	2.54	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4786	17366	29819	2.54	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4787	17367	29820	2.04	0.0E+00	M74098.1	NT	Human displacement protein (CCAAT) mRNA
4792	17371	29824	2	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4792	17371	29825	2	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4794	12809	25297	1.8	0.0E+00	T56946.1	EST_HUMAN	y883g04.72 Strategene fetal spleen (H837205) Homo sapiens cDNA clone IMAGE:68310 5'
4794	12809	25298	1.8	0.0E+00	T56945.1	EST_HUMAN	y883g04.72 Strategene fetal spleen (H837205) Homo sapiens cDNA clone IMAGE:68310 5'
4797	17375		1.1	0.0E+00	BE278730.1	EST_HUMAN	60115835F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4803	17381	29831	0.64	0.0E+00	BE360050.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'
4818	17398	29849	0.83	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4818	17398	29850	0.83	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4819	17397	28851	1.01	0.0E+00	U56851.1	NT	Mus myosin heavy chain 1 (N2ph1) gene, large exon and 3' end of the intron, and partial cds
4823	17401	28854	5.32	0.0E+00	M80602.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4826	17404	28857	133.49	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4828	17407	28858	133.49	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4829	17404	28861	1.32	0.0E+00	AF184110.1	NT	Human sapiens cyclophilin-related protein (NKTR) gene, complete cds
4832	17410	28863	1.28	0.0E+00	7682181	NT	Human sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17428		1.08	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D8
4861	17439	28868	0.83	0.0E+00	7304922	NT	Human sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4861	17439	28868	0.83	0.0E+00	7304922	NT	Human sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4873	17448	28869	1.3	0.0E+00	AF026801.1	NT	Human sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4878	17451	28892	0.91	0.0E+00	6877700	NT	Human sapiens G-protein coupled receptor (RE2), mRNA
4878	17451	28893	0.91	0.0E+00	6877700	NT	Human sapiens G-protein coupled receptor (RE2), mRNA
4879	17454	28908	0.83	0.0E+00	7019320	NT	Human sapiens protein 0008 (AD013), mRNA
4879	17454	28908	0.83	0.0E+00	7019320	NT	Human sapiens protein 0008 (AD013), mRNA
4900	17475	28931	1.61	0.0E+00	AW44537.1	EST_HUMAN	U1-H-B13-qlw-c-04-QJ.1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4907	17482	28940	1.36	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4910	17485		1.51	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-like mRNA, complete cds
4923	17488		0.59	0.0E+00	AW339233.1	EST_HUMAN	xz59d06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4968	17542		3.61	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4971	17545	28987	1.76	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4973	17547	28989	1.19	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 8 (WBSCR8) mRNA, complete cds
4974	17548	28990	1.36	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4975	17549	28991	4.69	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4977	17551	28993	12.25	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4978	17552	28994	1.19	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4980	17554	28996	1.7	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp782E1312 (DKFZp782E1312), mRNA
4983	17557	30000	5.09	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4987	17561	30004	1.8	0.0E+00	M84081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4987	17561	30005	1.8	0.0E+00	M84081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4989	17563	30007	1.78	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4989	17563	30008	1.78	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4892	17688	30011	2.79	0.0E+00	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4894	17688	30012	0.98	0.0E+00	7708604	NT	Homo sapiens MAGE-C2 (MAGEC2), mRNA
5006	17678	30022	0.95	0.0E+00	6032160	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2I) mRNA
5015	17589	30032	1.75	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412), mRNA
5016	17590	30033	0.84	0.0E+00	AB037894.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
5017	17591	30034	1.32	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5018	17592	30035	2.53	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
5019	17593	30036	2.01	0.0E+00	6174960	NT	Homo sapiens meningioma expressed antigen 8 (colled-coil proline-rich) (MGEA8), mRNA
5021	17596	30038	2.81	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
5023	17597	30040	0.98	0.0E+00	Y18723.1	NT	Homo sapiens gene encoding filensin, exon 8
5024	17598	30041	1.28	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 8 (colled-coil proline-rich) (MGEA8), mRNA
5024	17598	30042	1.26	0.0E+00	6174560	NT	Homo sapiens meningioma expressed antigen 8 (colled-coil proline-rich) (MGEA8), mRNA
5028	17600	30045	16.3	0.0E+00	AF085086.1	NT	Homo sapiens MHC class 1 region
5028	17602	30046	2.87	0.0E+00	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
5028	17603	30048	3.33	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5041	17614	30058	2.27	0.0E+00	4503484	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) mRNA
5043	17618	30060	3.9	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
5043	17618	30061	3.9	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
5058	17631	30076	0.59	0.0E+00	AB291129.1	EST_HUMAN	qin1503.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q01632 Q01632
5061	17634	30078	2.85	0.0E+00	AB006825.1	NT	EN-2/LACZ FUSION PROTEIN ;
5061	17634	30077	2.85	0.0E+00	AB006825.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5072	17645	30087	0.92	0.0E+00	AB026898.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5088	17661	30101	1.38	0.0E+00	AL163284.2	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5088	17661	30101	1.38	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5083	17668	30105	0.57	0.0E+00	7682319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
5103	17675	30115	2.12	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
5108	17680	30128	7.33	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
5118	17680	30128	1.25	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5121	17683	30133	2.86	0.0E+00	BE408893.1	EST_HUMAN	601303729F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638118 5'
5124	17698	30133	3.82	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
5135	17707	30139	1.19	0.0E+00	AB026896.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5162	17722	30162	1.89	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5182	17722	30163	1.89	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5170	17738	30165	1.07	0.0E+00	AA601248.1	EST_HUMAN	nc14q09.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5170	17738	30166	1.07	0.0E+00	AA601248.1	EST_HUMAN	nc14q09.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5170	17738	30167	1.07	0.0E+00	AA601248.1	EST_HUMAN	nc14q09.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5172	17739	30168	0.98	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5172	17739	30169	0.98	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5183	12897	26374	0.58	0.0E+00	AF189698.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5188	17763		1.72	0.0E+00	4788228	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5198	17764	30189	0.94	0.0E+00	AF018705.1	NT	Homo sapiens E8-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
5204	17768	30192	0.87	0.0E+00	US3588.1	NT	Homo sapiens MHC class 1 region
5211	17778		1.3	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5214	17779		29.82	0.0E+00	D50897.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG3) pseudogene
5245	17809	30231	3.38	0.0E+00	X62988.1	NT	Bacillus amyloquelic acid sacB gene for levansucrase (EC 2.4.1.10)
5266	17828	30252	1.23	0.0E+00	AF240636.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5267	17828	30253	1.23	0.0E+00	AF240636.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5267	17828	30254	0.98	0.0E+00	5484163	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5282	17844	30271	0.95	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5298	17860	30285	0.77	0.0E+00	5802055	NT	Homo sapiens ring finger protein (RNF), mRNA
5300	17862	30286	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5300	17862	30287	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5301	17863	30288	0.93	0.0E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5308	17870	30292	0.84	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5328	17888	30304	0.97	0.0E+00	5902091	NT	Homo sapiens solute carrier family 6 (hospital transporters), member 3 (SLC5A3), mRNA
5333	17894	30308	1.1	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5333	17894	30309	1.1	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5340	17901	30318	0.81	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5340	17901	30317	0.81	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5341	17902	30318	0.8	0.0E+00	7682421	NT	Homo sapiens KIAA0871 protein (KIAA0871), mRNA

Table 4

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5347	17907	30322	25.99	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
5355	17915	30330	0.88	0.0E+00	U71601.1	NT	Human zinc finger protein zfp47 (z47) mRNA, partial cds
5357	17917	30332	1.08	0.0E+00	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
5365	17925	30339	9.37	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
5373	17932	30346	11.28	0.0E+00	5360213	NT	Human sapiens glypican 3 (GPC3) mRNA
5374	17933	30347	1.1	0.0E+00	4826777	NT	Human sapiens Junonil (mouse) homolog (JMU) mRNA
5377	17936	30349	0.68	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5385	17944	30357	8.06	0.0E+00	4502192	NT	Human sapiens apolipoprotein B (Including Ag(x) antigen) (APOB) mRNA
5389	17957	30368	1.01	0.0E+00	4855474	NT	Human sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5430	17987	30391	1.58	0.0E+00	4826977	NT	Human sapiens reelin (RELN) mRNA
5451	18020		3.66	0.0E+00	AF093083.1	NT	Human sapiens acetylase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5469	18094	30411	2.26	0.0E+00	AF137285.1	NT	Human sapiens keratin 12 (KRT12) gene, complete cds
5459	18094	30412	2.26	0.0E+00	AF137288.1	NT	Human sapiens keratin 12 (KRT12) gene, complete cds
5478	18112	30521	1.27	0.0E+00	A0934954.1	EST_HUMAN	wp080808.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2484084 3'
5481	18115	30524	2.18	0.0E+00	8256379	NT	Human sapiens protocadherin alpha 13 (PCDHA13), mRNA
5485	18129	30537	3.75	0.0E+00	BE031080.1	EST_HUMAN	RC3-GN0078-310800-013-503 GN0078 Homo sapiens cDNA
5499	18133	30541	3.31	0.0E+00	AF182034.1	NT	Human sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5499	18133	30542	3.31	0.0E+00	AF182034.1	NT	Human sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5508	18139	30550	2.08	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5508	18139	30551	2.08	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5584	18215	30684	5.94	0.0E+00	BE576498.1	EST_HUMAN	7110008.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5585	18216	30685	1.67	0.0E+00	BE220763.1	EST_HUMAN	h89a02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3185184 3' similar to SW:Y054_HUMAN
5586	18217	30686	1.58	0.0E+00	BE794412.1	EST_HUMAN	P42894 HYPOTHETICAL PROTEIN KIA0054.1
5588	18217	30687	1.58	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5589	18220	30670	7.35	0.0E+00	M28908.1	NT	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5600	24746	30678	4.43	0.0E+00	11421038	NT	Human sapiens eosinophil peroxidase (EPP) gene, exon 7
5609	18238		1.58	0.0E+00	BF665962.1	EST_HUMAN	Human sapiens Sp4 transcription factor (SP4), mRNA
5614	18243	30684	0.8	0.0E+00	BE538857.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278254 5'
5622	18251	30719	1.49	0.0E+00	BE282784.1	EST_HUMAN	601081489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5626	18255	30724	2.8	0.0E+00	BF526328.1	EST_HUMAN	601108391F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988310 5'
5626	18255	30725	2.5	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4214272 5'
5645	18508	32326	2.91	0.0E+00	4657394	NT	602071372F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4214272 5'
5648	18278	30751	0.9	0.0E+00	AB007835.1	NT	Human sapiens Bloom syndrome (BLM) mRNA
							Human sapiens mRNA for KIAA0466 protein, partial cds

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5648	18278	30752	0.8	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5652	18278	30756	4.93	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5652	18279	30757	4.93	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5686	18282	30771	1.42	0.0E+00	D28535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
5665	18282	30772	1.42	0.0E+00	D28535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5680	18307	30803	1.98	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5688	18312	30809	0.88	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5704	18330	30833	0.88	0.0E+00	D61584.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-418D05
5704	18330	30834	0.88	0.0E+00	D61584.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-418D05
5707	18333	30838	5.12	0.0E+00	BF628931.1	EST_HUMAN	602042322F1 NCI CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4178988 5'
5707	18333	30839	5.12	0.0E+00	BF628931.1	EST_HUMAN	602042322F1 NCI CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4178988 5'
5712	18338	30843	2.7	0.0E+00	BF313139.1	EST_HUMAN	601897688F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128816 5'
5723	18349	31052	4.03	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5753	18379	31090	1.49	0.0E+00	BE260777.1	EST_HUMAN	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502809 5'
5762	18388	31090	4.98	0.0E+00	AW867316.1	EST_HUMAN	MRO-SN0037-030400-001-007 SN0037 Homo sapiens cDNA
5775	18400	31114	2.42	0.0E+00	BE262889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887803 5'
5775	18400	31115	2.42	0.0E+00	BE262889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887803 5'
5783	18418	31133	1.67	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5783	18418	31134	1.67	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5800	18425	31142	4.39	0.0E+00	AF084254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5800	18425	31143	4.39	0.0E+00	AF084254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5808	18431	31151	2.56	0.0E+00	AJ224639.1	NT	Homo sapiens Surt-5 and Surt-6 genes
5808	18431	31152	2.56	0.0E+00	AJ224639.1	NT	Homo sapiens Surt-5 and Surt-6 genes
5833	18457	31178	0.72	0.0E+00	A198515.1	EST_HUMAN	qf94g10.x1 Soares placentas 86c9weeks, 2NbpH8b9W Homo sapiens cDNA clone IMAGE:1757730 3'
5837	18461	31184	6.38	0.0E+00	M85719.1	EST_HUMAN	similar to SW:CADC.HUMAN P66288 BRAIN-CADHERIN PRECURSOR ;
5844	18468	31193	6.26	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Stratiogene (cat#838208) Homo sapiens cDNA clone HFBGM48
5858	18479	31202	1.35	0.0E+00	Z26269.1	NT	UI-HF-BLO-adj-d-02-0-UL17 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3081658 5'
5866	18483	31212	1.78	0.0E+00	AW361877.1	EST_HUMAN	H. sapiens isoform 1 gene for L-type calcium channel, exon 14 adnd 15
5866	18488	31213	1.78	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091288-007-n05 CT0263 Homo sapiens cDNA
5868	18488	31214	1.78	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091288-007-n05 CT0263 Homo sapiens cDNA
5870	18492	31219	1.91	0.0E+00	U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5897	18519	31244	1.02	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for KIAA1841 protein, partial cds
5891	18573	31305	1.46	0.0E+00	AJ00345.1	NT	Homo sapiens KVLQT1 gene
5891	18573	31306	1.46	0.0E+00	AJ00345.1	NT	Homo sapiens KVLQT1 gene
5898	18580	31316	1.29	0.0E+00	AJ207816.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5875	18595	31330	4.89	0.0E+00	11416801	NT	Homo sapiens proteodherin beta 2 (PCDH2), mRNA
5890	18600	31333	1.09	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938551 5'
5897	18607	31341	1.29	0.0E+00	6868943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5898	18608	31342	6.36	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3677843 5'
5899	18609	31343	1.48	0.0E+00	10048478	NT	Mus musculus acorin (Acz), mRNA
5890	18610	31344	3.25	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5890	18610	31345	3.25	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6008	18628	31363	2.23	0.0E+00	BF339835.1	EST_HUMAN	602038272F1 NCI_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4184321 5'
6010	18630	31365	0.88	0.0E+00	AF142821.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
6011	18631	31366	3.17	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC 14 Homo sapiens cDNA clone IMAGE:3347463 5'
6020	18639	31379	1.22	0.0E+00	BE503096.1	EST_HUMAN	h283d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING ;
6024	18643	31385	2.27	0.0E+00	BF569605.1	EST_HUMAN	602185852F1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:4310076 5'
6028	18647	31388	1.14	0.0E+00	AA454642.1	EST_HUMAN	z06d08.a1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6030	18677	31419	3.11	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6032	18679	31421	2.35	0.0E+00	BE528144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6036	18683	31425	1.25	0.0E+00	BE595836.1	EST_HUMAN	601645287F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3930463 5'
6033	18700	31447	0.9	0.0E+00	AW276760.1	EST_HUMAN	xp65f03.x1 NCI_CGAP_Oy39 Homo sapiens cDNA clone IMAGE:2748245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN ;
6033	18709	31457	0.98	0.0E+00	BF031742.1	EST_HUMAN	601580606F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827775 5'
6033	18709	31458	0.98	0.0E+00	BF031742.1	EST_HUMAN	601580606F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827775 5'
6104	18720	31473	1.03	0.0E+00	AW470846.1	EST_HUMAN	hs34d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3 Q9Z1N3 MYOSIN-RHO GAP PROTEIN, MYR 7 ;
6115	18731	31483	1.1	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-230900-399-a10 HT0894 Homo sapiens cDNA
6115	18731	31484	1.1	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-230900-399-a10 HT0894 Homo sapiens cDNA
6123	18738	31490	1.38	0.0E+00	W33069.1	EST_HUMAN	z03h08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6123	18738	31491	1.38	0.0E+00	W33069.1	EST_HUMAN	z03h08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6124	18739		2.2	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6127	18742	31495	3.14	0.0E+00	BE280197.1	EST_HUMAN	601158315F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:350323 5'
6133	18747	31503	1.88	0.0E+00	BE5889810.1	EST_HUMAN	601612303F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
6148	18761	31520	1.48	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6148	18761	31521	1.48	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6148	18762	31522	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6149	18762	31523	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6149	18762	31524	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6164	24768	31540	10.18	0.0E+00	9789998	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6167	18778	31543	1.38	0.0E+00	AA193508.1	EST_HUMAN	z40h01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665805 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6167	18778	31544	1.38	0.0E+00	AA193508.1	EST_HUMAN	z40h01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665805 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6169	18769	31568	12.83	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-8 mRNA, complete cds
6169	18769	31569	12.83	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-8 mRNA, complete cds
6229	18838	31811	1.35	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3365665 5'
6238	18847	31818	1.84	0.0E+00	BE166561.1	EST_HUMAN	QVQ-HT0368-090200-099-008 HT0368 Homo sapiens cDNA
6280	18898	31657	1.54	0.0E+00	BE378007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608480 5'
6288	18894	31683	1.23	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6308	18913	31687	3.42	0.0E+00	U46982.1	NT	Human G protein-coupled receptor GPR-6 gene, complete cds
6334	18940	31717	4.13	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6335	18941	31718	3.68	0.0E+00	11645913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6335	18941	31719	3.68	0.0E+00	11645913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6354	18959	31737	0.7	0.0E+00	U0723.1	NT	Human beta2-chimerin mRNA, complete cds
6371	18976	31753	1.87	0.0E+00	11426367	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6375	18979	31758	3.62	0.0E+00	BE257173.1	EST_HUMAN	601108532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6388	18981		0.94	0.0E+00	A1868048.1	EST_HUMAN	189110.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839 MI-2 PROTEIN. ;
6392	18995	31774	1.39	0.0E+00	L35830.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6401	19004	31792	1.03	0.0E+00	BE797385.1	EST_HUMAN	601158797F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6401	19004	31793	1.03	0.0E+00	BE797385.1	EST_HUMAN	601158797F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6411	19014	31798	0.86	0.0E+00	BF367123.1	EST_HUMAN	MRC-HT0923-220800-102-005 HT0923 Homo sapiens cDNA
6419	19022	31808	1.53	0.0E+00	11435830	NT	Homo sapiens peptide transporter 3 (LOC51286), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6428	19031	31814	0.98	0.0E+00	D66849.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6442	19044	31832	1.11	0.0E+00	AW178142.1	EST_HUMAN	IL3-H10082-010898-014-A04 HT0082 Homo sapiens cDNA
6462	19063	31848	0.78	0.0E+00	BE674544.1	EST_HUMAN	7602c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302.3' similar to SW:Y176_HUMAN
6468	19087	31853	0.98	0.0E+00	7682039	NT	Q14681 HYPOTHETICAL PROTEIN KIAA0176 ;
6480	19081		8.14	0.0E+00	AV650020.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6487	19088	31871	3.19	0.0E+00	AW675698.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09.3'
6490	19091	31874	5.28	0.0E+00	H01255.1	EST_HUMAN	UI-HF-BLO-aco-g-12-Q-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751.3'
6501	19101	31886	3.3	0.0E+00	X16377.1	NT	y27603.r1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:149833.5'
6503	19103	31888	1.02	0.0E+00	A1812841.1	EST_HUMAN	Human gene for the light and heavy chains of myeloperoxidase
6508	19109	31894	4.19	0.0E+00	BE733889.1	EST_HUMAN	ts57d08.x1 NCL CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2292687.3' similar to SW:NTCS_HUMAN
6509	19109	31895	4.19	0.0E+00	BE733890.1	EST_HUMAN	P53798 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6513	19113	31901	0.83	0.0E+00	AW748598.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639818.5'
6513	19113	31902	0.83	0.0E+00	AW748598.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639818.5'
6515	19115	31904	187.18	0.0E+00	AU119245.1	EST_HUMAN	MRO-BT0284-221189-002-f11 BT0284 Homo sapiens cDNA
6515	19115	31905	187.18	0.0E+00	AU119245.1	EST_HUMAN	MRO-BT0284-221189-002-f11 BT0284 Homo sapiens cDNA
6519	19119	31910	0.83	0.0E+00	BE780453.1	EST_HUMAN	AU119245 HEMBAT Homo sapiens cDNA clone HEMBA1005360.5'
6520	19120	31911	0.89	0.0E+00	X92217.1	NT	AU119245 HEMBAT Homo sapiens cDNA clone HEMBA1005360.5'
6531	19131	31925	1.98	0.0E+00	A1899483.1	EST_HUMAN	H.sapiens germ-line immunoglobulin heavy chain, variable region, (13-2)
6543	19142	31934	2.84	0.0E+00	BE2893153.1	EST_HUMAN	wa25c07.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2498220.3'
6543	19142	31935	2.84	0.0E+00	BE2893153.1	EST_HUMAN	601105344F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:2887983.5'
6608	19203	32009	1.05	0.0E+00	AW406348.1	EST_HUMAN	601105344F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:2887983.5'
6609	19203	32010	1.05	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BLO-aco-h-02-Q-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058931.5'
6634	19230	32034	5.38	0.0E+00	AV719444.1	EST_HUMAN	UI-HF-BLO-aco-h-02-Q-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058931.5'
6642	19238	32040	1.02	0.0E+00	BE898340.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLCEHC08.5'
6642	19238	32041	1.02	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301.5'
6645	19241	32044	2.18	0.0E+00	AF190860.1	NT	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301.5'
6648	19244	32046	1.05	0.0E+00	11420858	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6655	19251	32053	3.35	0.0E+00	AW163940.1	EST_HUMAN	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA
6655	19251	32054	3.35	0.0E+00	AW163940.1	EST_HUMAN	au88h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159.5' similar to TR:O15390 GT24. [3] TR:O43840 TR:O43208 ;
6655	19251	32054	3.35	0.0E+00	AW163940.1	EST_HUMAN	au88h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159.5' similar to TR:O15390 GT24. [3] TR:O43840 TR:O43208 ;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6859	19255	32057	0.97	0.0E+00	W37163.1	EST_HUMAN	zb20c08.r1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW:ZN45_HUMAN Q02388 ZINC FINGER PROTEIN 45;
6859	19255	32058	0.97	0.0E+00	W37163.1	EST_HUMAN	zb20c08.r1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW:ZN45_HUMAN Q02388 ZINC FINGER PROTEIN 45;
6871	19267	32071	1.08	0.0E+00	BE79483.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6878	19274	32078	4.45	0.0E+00	BE799873.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6882	19278	32081	7.35	0.0E+00	BE888813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6882	19278	32082	7.35	0.0E+00	BE888813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6888	19285	32088	3.81	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6894	19290	32092	2.03	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6894	19290	32093	2.03	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6700	19298	32100	3.54	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6703	19298	32102	3.88	0.0E+00	AI638412.1	EST_HUMAN	131111.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR;
6704	19298	32103	1.36	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-4) mRNA, complete cds
6714	19308	32112	0.78	0.0E+00	AW905430.1	EST_HUMAN	UI-HF-BNO-ama-c-01-q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6716	19310	32113	3.78	0.0E+00	AA434584.1	EST_HUMAN	zb52c03.r1 Soares fetal_lung_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773688 5'
6730	19324	32113	1.08	0.0E+00	BF217200.1	EST_HUMAN	601585317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103683 5'
6734	19328	32133	1.72	0.0E+00	BE928875.1	EST_HUMAN	QV3-BN0047-300800-278-c08 BN0047 Homo sapiens cDNA
6774	19366	32178	1.88	0.0E+00	AU125928.1	EST_HUMAN	AU125928 NT261M4 Homo sapiens cDNA clone NT2RM4002430 5'
6778	19368	32180	0.73	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6778	19368	32181	0.73	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6795	19386	32202	1.26	0.0E+00	BE142383.1	EST_HUMAN	CMG-HT0143-270868-082-d08 HT0143 Homo sapiens cDNA
6815	19408	32222	0.91	0.0E+00	BE008012.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6815	19408	32223	0.91	0.0E+00	BE008012.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6835	19425	32241	7.25	0.0E+00	BE168131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6837	19427	32243	1.62	0.0E+00	BF065667.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6873	19507	32441	3.11	0.0E+00	AA190765.1	EST_HUMAN	zb99a03.r1 Streptococcus Hela cell s3 837218 Homo sapiens cDNA clone IMAGE:627282 5'
6882	19617	32452	0.99	0.0E+00	U38873.1	NT	Human salivary peroxidase mRNA, complete cds
6885	19620	32454	0.72	0.0E+00	BE671987.1	EST_HUMAN	7e49b07.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285 TEKTN;
6892	19628	32462	6.2	0.0E+00	AI640821.1	EST_HUMAN	IL3-ST0024-230789-001-B01 ST0024 Homo sapiens cDNA
6892	19628	32463	6.2	0.0E+00	AI640821.1	EST_HUMAN	IL3-ST0024-230789-001-B01 ST0024 Homo sapiens cDNA
6892	19636	32474	2.67	0.0E+00	11435828	NT	Homo sapiens CD8 antigen (CD8), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6913	19572	32401	0.94	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434D2021 5'
6916	19575	32404	0.84	0.0E+00	AI188270.1	EST_HUMAN	cc10401.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1585761 3' similar to TR:Q28823 Q28823 TEKIN C1.;
6921	19580	32409	0.89	0.0E+00	BE734087.1	EST_HUMAN	801567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6936	18044	30468	1.22	0.0E+00	BE568381.1	EST_HUMAN	801339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3882287 5'
6943	18051	30473	13.34	0.0E+00	BE897889.1	EST_HUMAN	801443867F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847687 5'
6943	18051	30474	13.34	0.0E+00	BE887889.1	EST_HUMAN	801443867F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847687 5'
6948	19525	32347	1.75	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-85.;
6948	19525	32348	1.75	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-85.;
6970	19547	32371	2.55	0.0E+00	BF088376.1	EST_HUMAN	GM1-H10877-080800-397-g11 H10877 Homo sapiens cDNA Z34g03.r1 Soares_NHRMPu_S1 Homo sapiens cDNA clone IMAGE:685332 5'
6977	19553	32376	2.01	0.0E+00	AA185108.1	EST_HUMAN	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
6984	19482		10.79	0.0E+00	11034810	NT	
6986	19484	32305	1.11	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7001	19499	32318	2.35	0.0E+00	BF569905.1	EST_HUMAN	802185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7008	19508	32325	0.75	0.0E+00	4657364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7018	19514		2.49	0.0E+00	J03089.1	NT	Human MYCL2 gene, complete cds
7024	19558	32383	4.16	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7024	19558	32384	4.16	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7025	19559	32385	1	0.0E+00	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x8
7036	18056	30479	2.94	0.0E+00	11420778	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7036	18059	30481	0.69	0.0E+00	BE268708.1	EST_HUMAN	801115516F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3366330 5'
7057	18076	30429	1.11	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003979 5'
7059	18078	30432	4.93	0.0E+00	BE262841.1	EST_HUMAN	801148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501828 5'
7080	18079	30433	2.1	0.0E+00	Z37076.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7080	18079	30434	2.1	0.0E+00	Z37076.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7081	18080	30435	2.68	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7081	18080	30436	2.68	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7089	18085	30441	1.44	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7071	19843	32480	0.68	0.0E+00	BE782770.1	EST_HUMAN	QV3-NT10022-140800-223-01 NT0022 Homo sapiens cDNA
7076	19847	32485	2.69	0.0E+00	BF569905.1	EST_HUMAN	802185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7076	19851	32480	3.92	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7089	18680	32498	0.82	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7089	18680	32500	0.82	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7095	18688	32505	8.1	0.0E+00	BF306898.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7100	18670	32509	2.1	0.0E+00	U41302.1	NT	Human chromosome 18 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7132	19472	32282	1.1	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7167	18688	32548	0.89	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7167	18688	32547	0.89	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7173	19705	32553	1.43	0.0E+00	AW954808.1	EST_HUMAN	EST366876 IMAGE resequences, MAGC Homo sapiens cDNA
7174	19708	32554	1.08	0.0E+00	BE284103.1	EST_HUMAN	601113958F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3354568 5'
7187	19719	32568	1.23	0.0E+00	L01973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7195	19728	32576	0.71	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7196	19728	32577	0.71	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7201	19732	32584	1.97	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001666 5'
7216	19747	32603	0.88	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7221	19752	32608	2.39	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y78AA1 Homo sapiens cDNA clone Y78AA1002365 5'
7222	19753	32608	1.2	0.0E+00	4758839	NT	Homo sapiens netrin 1 (NTN1), mRNA
7231	19762	32617	1.83	0.0E+00	BE891286.1	EST_HUMAN	601431818F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7231	19762	32618	1.83	0.0E+00	BE891286.1	EST_HUMAN	601431818F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7252	18084	30411	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7252	18084	30412	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7263	19791	32646	0.78	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7263	19791	32647	0.78	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7274	18802	32659	4.67	0.0E+00	11436689	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7274	18802	32660	4.67	0.0E+00	11436689	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7302	18830	32688	28.85	0.0E+00	A1128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:1714844 3'
7302	18830	32689	28.85	0.0E+00	A1128344.1	EST_HUMAN	similar to SW-ARSD_HUMAN P51689 ARYL-SULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7304	18832	32691	4.05	0.0E+00	11428392	NT	qc67a07.x1 Soares_placenta_8to9weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:1714844 3'
7304	18832	32692	4.05	0.0E+00	11428392	NT	similar to SW-ARSD_HUMAN P51689 ARYL-SULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7307	18835		14.08	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4182839 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7309	19837	32895	3.39	0.0E+00	AA128453.1	EST_HUMAN	zn6f08.r1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G808562
7314	19841	32701	0.9	0.0E+00	AL079497.1	EST_HUMAN	G808562 NEBULIN.;
7314	19841	32702	0.9	0.0E+00	AL079497.1	EST_HUMAN	DKFZp43480228_r1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp43480228 5'
7349	19875	32741	1.2	0.0E+00	BE295499.1	EST_HUMAN	DKFZp43480228_r1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp43480228 5'
7351	19877	32742	0.86	0.0E+00	11427893	NT	601174878F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7354	19880		2.37	0.0E+00	AU118607.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20261), mRNA
7355	19881	32745	1.77	0.0E+00	AF005213.1	NT	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7355	19881	32746	1.77	0.0E+00	AF005213.1	NT	Homo sapiens ankryth 1 (ANK1) mRNA, complete cds
7355	19881	32764	0.99	0.0E+00	AF245605.1	NT	Homo sapiens ankryth 1 (ANK1) mRNA, complete cds
7371	19897	32758	8.87	0.0E+00	X70172.1	NT	Homo sapiens edican mRNA, complete cds
7373	19899	32760	8.18	0.0E+00	U45448.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7373	19899	32761	8.18	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7385	19911	32776	0.98	0.0E+00	AW958603.1	EST_HUMAN	Human P2x1 receptor mRNA, complete cds
7387	19913	32777	3.25	0.0E+00	AW958603.1	EST_HUMAN	Human P2x1 receptor mRNA, complete cds
7408	19933	32787	1.04	0.0E+00	AF001543.1	EST_HUMAN	EST388573 MAGC resequences, MAGD Homo sapiens cDNA
7408	19933	32788	1.04	0.0E+00	AF001543.1	EST_HUMAN	EST382568 MAGC resequences, MAGA Homo sapiens cDNA
7408	19933	32798	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7425	19949		0.78	0.0E+00	M80354.1	NT	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7426	19950	32815	0.71	0.0E+00	BE408293.1	EST_HUMAN	Human BTF3 protein homologue gene, complete cds
7451	19975		1.16	0.0E+00	R87430.1	EST_HUMAN	601302670F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3837434 5'
7452	19976	32841	2.37	0.0E+00	AW239326.1	EST_HUMAN	ym88h10.r1 Scores adult brain N2b-HB55Y Homo sapiens cDNA clone IMAGE:169051 5'
7488	19980		1.19	0.0E+00	AU117553.1	EST_HUMAN	kb39a05.y1 NCL_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7470	19982	32855	3.61	0.0E+00	11427135	NT	HNF3/FH TRANSCRIPTION FACTOR GENESIS :
7482	20004	32869	0.88	0.0E+00	AA211683.1	EST_HUMAN	AU117663 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7488	20011	32877	0.82	0.0E+00	L32832.1	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7509	20030	32894	0.98	0.0E+00	BF308998.1	EST_HUMAN	zn56f02.r1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7509	20030	32895	0.98	0.0E+00	BF308998.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7517	20037	32905	1.48	0.0E+00	AU118767.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7561	20078	32952	4.63	0.0E+00	AT752561.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
							601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
							AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
							cn17405.r1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17405 random

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7561	20078	32953	4.53	0.0E+00	AJ752591.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7631	20143	33023	1.45	0.0E+00	AF084205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7631	20143	33024	1.45	0.0E+00	AF084205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7639	20151	33035	1.03	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7653	20165	33062	0.87	0.0E+00	BE439545.1	EST_HUMAN	HTMT1-183F1 HTMT1 Homo sapiens cDNA
7654	20166	33053	1.08	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7681	20192	33081	2.91	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7687	20196	33084	1	0.0E+00	N76126.1	EST_HUMAN	z686d05.s1 Soares_fetal_lung_NbHL16W Homo sapiens cDNA clone IMAGE:268458 3'
7691	20200	33087	6.28	0.0E+00	BF217803.1	EST_HUMAN	601895485F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4103729 5'
7699	20208	33095	4.27	0.0E+00	AU126822.1	EST_HUMAN	AU126822 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
7716	24789	33111	1.1	0.0E+00	AW068274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7715	24789	33112	1.1	0.0E+00	AW068274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7718	20226	33114	6.48	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7726	20233	33121	1.01	0.0E+00	AV759487.1	EST_HUMAN	AV759487 BM Homo sapiens cDNA clone BMFBGG05 5'
7726	20234	33122	6.72	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3947365 5'
7726	20234	33123	6.72	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3947365 5'
7727	20235	33124	0.81	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; actinin receptor interacting protein 1 (KIAA0705), mRNA
7727	20235	33125	0.81	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; actinin receptor interacting protein 1 (KIAA0705), mRNA
7728	20236	33126	1.02	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7728	20236	33127	1.02	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7767	20265	33160	1.73	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3884258 5'
7767	20265	33161	1.73	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3884258 5'
7767	20275	33173	0.8	0.0E+00	AW402189.1	EST_HUMAN	UIHF-BKO-eat-c-07-Q-UI.1 NIH_MGC 36 Homo sapiens cDNA clone IMAGE:3054733 5'
7776	20285	33182	0.9	0.0E+00	AW988044.1	EST_HUMAN	EST380119 MAGE resequences, MAGJ Homo sapiens cDNA
7796	20338	33246	1.97	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001607 5'
7840	20382		0.51	0.0E+00	BF217200.1	EST_HUMAN	601895317F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4103693 5'
7853	20395	33300	0.85	0.0E+00	BE313013.1	EST_HUMAN	601150347F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3503050 5'
7884	20406	33313	1.18	0.0E+00	AA149781.1	EST_HUMAN	z601c06.r1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:566410 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7877	20419	33327	0.8	0.0E+00	BF026828.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
7880	20432	33341	0.51	0.0E+00	AA017021.1	EST_HUMAN	z333108.t1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5'
7807	20449	33356	2.32	0.0E+00	BE736048.1	EST_HUMAN	601335668F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3638603 5'
7923	20486	33372	3.32	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7923	20485	33373	3.32	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7953	20495	33404	0.77	0.0E+00	AW874581.1	EST_HUMAN	b334402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O84852 O84852
7953	20496	33405	0.77	0.0E+00	AW874581.1	EST_HUMAN	b334402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O84852 O84852
7860	20502	33411	3.05	0.0E+00	AA397551.1	EST_HUMAN	z81604.t1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
7862	20504	33412	0.83	0.0E+00	AW387131.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
7865	20507		0.83	0.0E+00	AB020691.1	NT	MRO-ST0031-081089-003-a11 ST0031 Homo sapiens cDNA
7866	20508	33414	7.21	0.0E+00	AU142402.1	EST_HUMAN	Homo sapiens mRNA for KIAA0884 protein, partial cds
7970	20512	33418	0.87	0.0E+00	BE388421.1	EST_HUMAN	AU142402 Y78AA1 Homo sapiens cDNA clone Y78AA1000277 5'
7970	20512	33419	0.97	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7985	20527	33433	0.52	0.0E+00	7867276	NT	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7887	20529	33435	0.87	0.0E+00	W95278.1	EST_HUMAN	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
7887	20529	33436	0.87	0.0E+00	W95278.1	EST_HUMAN	z305601.t1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7889	20531		17.03	0.0E+00	BF673096.1	EST_HUMAN	z305601.t1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7883	20535		1.38	0.0E+00	AU134114.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4204128 5'
8007	20549	33453	2.35	0.0E+00	BF525534.1	EST_HUMAN	AU134114 OVARG1 Homo sapiens cDNA clone OVARG1001288 5'
8007	20549	33454	2.35	0.0E+00	BF525534.1	EST_HUMAN	602086632F1 NCJ CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8037	20579	33484	1.88	0.0E+00	AL120124.1	EST_HUMAN	602086632F1 NCJ CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8037	20579	33485	1.88	0.0E+00	AL120124.1	EST_HUMAN	DKFZp781P092.t1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781P092 5'
8077	20819		1.82	0.0E+00	BE877883.1	EST_HUMAN	DKFZp781P092.t1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781P092 5'
8088	20839	33550	2.09	0.0E+00	AW500549.1	EST_HUMAN	DKFZp781P092.t1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781P092 5'
8108	20847	33556	11.19	0.0E+00	AW157233.1	EST_HUMAN	U1HF-BNO-ek4-Q01-QUI.t1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077498 5'
8123	20864	33574	0.65	0.0E+00	AW072395.1	EST_HUMAN	U1HF-BNO-ek4-Q01-QUI.t1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077498 5'
8141	20882	33594	1.05	0.0E+00	11421722	NT	eu63108.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783789 3' similar to
8144	20885	33597	0.75	0.0E+00	W01616.1	EST_HUMAN	TR:O80463 O80463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
							z307d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2587639 3' similar to contains element OFR repetitive element;
							Homo sapiens centrosomal protein 2 (CEP2), mRNA
							z336d05.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294633 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8146	20887	33598	1.55	0.0E+00	BE745597.1	EST_HUMAN	801578195F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928898 5'
8148	20887	33600	1.55	0.0E+00	BE745597.1	EST_HUMAN	801578195F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928898 5'
8158	20889	33613	1.32	0.0E+00	AJ21735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8178	20719	33634	6.51	0.0E+00	D45032.1	NT	Human DNA for ceruloplasmin, exon 6
8198	20739	33651	1.47	0.0E+00	A367350.1	EST_HUMAN	q98612.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:188334 3' similar to TR:Q14873 Q14873
8211	20762	33668	3.14	0.0E+00	BE674157.1	EST_HUMAN	7d76d04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3276882 3' similar to TR:O95793 O95793
8213	20764	33668	1.31	0.0E+00	A885871.1	EST_HUMAN	w60b10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to
8224	20765	33682	1.38	0.0E+00	BE563650.1	EST_HUMAN	SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
8224	20765	33683	1.38	0.0E+00	BE563650.1	EST_HUMAN	801334760F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3888655 5'
8231	20772	33692	1.83	0.0E+00	11427235	NT	801334760F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3888655 5'
8231	20772	33693	1.83	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8233	20774	33695	1.7	0.0E+00	AA403192.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8233	20774	33696	1.7	0.0E+00	AA403192.1	EST_HUMAN	z68602.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to
8275	20816		4.38	0.0E+00	AA398511.1	EST_HUMAN	TR:G1304132 G1304132 TPRD. ;
8283	20824	33745	0.5	0.0E+00	BE637593.1	EST_HUMAN	z68602.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to
8284	20825	33746	1.22	0.0E+00	AW364874.1	EST_HUMAN	z73608.s1 Scores_basile_NHT Homo sapiens cDNA clone IMAGE:727968 3' similar to gb:S85855
8284	20826	33747	1.22	0.0E+00	AW364874.1	EST_HUMAN	PROHIBITIN (HUMAN);
8303	20844	33766	1.24	0.0E+00	BE612586.1	EST_HUMAN	RC2-FN0094-120800-013-h07 FN0094 Homo sapiens cDNA
8303	20844	33767	1.24	0.0E+00	BE612586.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8318	20859	33784	1.28	0.0E+00	AL163209.2	NT	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8318	20859	33785	1.28	0.0E+00	AL163209.2	NT	601452412F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3856179 5'
8326	20867	33790	0.78	0.0E+00	A1884477.1	EST_HUMAN	601452412F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3856179 5'
8333	20874	33796	0.83	0.0E+00	AA502294.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
8338	20879		0.64	0.0E+00	11416799	NT	Homo sapiens chromosome 21 segment HS21C009
8345	20886	33807	1.33	0.0E+00	A1580780.1	EST_HUMAN	wm33a11.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O76457 O76457
8348	20889		1.86	0.0E+00	BE5890787.1	EST_HUMAN	CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ;
							nm32610.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1138434
							G1138434 KIAA0187 PROTEIN ;
							Homo sapiens protocadherin beta 3 (PCDH3), mRNA
							ta04f11.x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
							801431238F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3916569 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8374	20914	33833	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822701.5'
8374	20914	33834	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822701.5'
8375	20916	33835	2.27	0.0E+00	4758696	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8375	20916	33836	2.27	0.0E+00	4758696	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8376	20916	33838	0.6	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8378	20918	33839	0.8	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8443	20883	33868	0.7	0.0E+00	AJ251760.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and Xlaiphas (partial) genes
8448	20888	33904	3.77	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8448	20888	33905	3.77	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8448	20888	33906	3.77	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8463	21003	33920	1.07	0.0E+00	U82978.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8502	21041	33962	0.88	0.0E+00	AF022855.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8502	21041	33963	0.88	0.0E+00	AF022855.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8505	21044	33965	0.89	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016.5'
8520	21059	33982	0.6	0.0E+00	11426572	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8524	21063		1.84	0.0E+00	AW613513.1	EST_HUMAN	xx46e01.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707032.3' similar to gb:M14123_cds4
8526	21065		0.64	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPYRROLINE (HUMAN);
8527	21066	33985	18.45	0.0E+00	D32650.1	EST_HUMAN	601472166F1 NIH_MGC.87 Homo sapiens cDNA clone IMAGE:3874912.6'
8557	21088	34017	3.88	0.0E+00	BE378495.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02
8563	21102	34021	2.84	0.0E+00	AA410545.1	EST_HUMAN	601238488F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3608709.5'
8565	21104		2.44	0.0E+00	BF313946.1	EST_HUMAN	z332e04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724082.5'
8572	21111	34030	0.85	0.0E+00	11424387	NT	601800571F1 NIH_MGC.19 Homo sapiens cDNA clone IMAGE:4128744.5'
8576	21115	34034	1.28	0.0E+00	AW139873.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
8576	21115	34035	1.26	0.0E+00	AW139873.1	EST_HUMAN	UI-H-BI1-adr-12-O-UJ1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687.3'
8581	21120		0.82	0.0E+00	A1840190.1	EST_HUMAN	UI-H-BI1-adr-12-O-UJ1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687.3'
8600	21138	34053	1.78	0.0E+00	BF377697.1	EST_HUMAN	wes30b10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288579.3' similar to TR:O15044
8608	21147	34063	0.55	0.0E+00	AL163301.2	NT	O15044 KIAA0335. ;
8614	21153	34067	2.14	0.0E+00	BE280272.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
8619	21158	34071	2.58	0.0E+00	BF700165.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
8619	21158	34072	2.58	0.0E+00	BF700165.1	EST_HUMAN	601150051F1 NIH_MGC.19 Homo sapiens cDNA clone IMAGE:3502838.5'
8619	21158	34071	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC.56 Homo sapiens cDNA clone IMAGE:4284642.6'
8619	21158	34072	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC.56 Homo sapiens cDNA clone IMAGE:4284642.6'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8818	21158	34073	2.58	0.0E+00	BF700185.1	EST_HUMAN	602127864F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4284542 5'
8833	21172	34080	0.83	0.0E+00	A1488722.1	EST_HUMAN	h3h11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2150949 3'
8860	21188	34117	2.45	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stanley GS) Homo sapiens cDNA
8867	21206	34123	18.43	0.0E+00	AA882527.1	EST_HUMAN	ar80g02.s1 NCI CGAP Lu6 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 50S
8873	21212	34131	4.87	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN);
8873	21212	34132	4.87	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8897	21236	34159	1.28	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8898	21238	34161	1.78	0.0E+00	BE278917.1	EST_HUMAN	601159330F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138734 5'
8708	21247		4.02	0.0E+00	AV1718377.1	EST_HUMAN	AV1718377 FHTB Homo sapiens cDNA clone FHTBAAAF11 5'
8715	21254	34175	3.11	0.0E+00	AW337277.1	EST_HUMAN	hw73c07.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X63587
8721	21260	34180	1.42	0.0E+00	AU124051.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
8798	21335	34280	0.9	0.0E+00	AU140704.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001675 5'
8806	21345	34269	0.54	0.0E+00	AB007823.1	NT	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'
8810	21349	34272	0.8	0.0E+00	R17132.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8810	21349	34273	0.8	0.0E+00	R17132.1	EST_HUMAN	y09e08.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31874 5'
8814	21353	34275	3.85	0.0E+00	AW592233.1	EST_HUMAN	y09e08.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31874 5'
8814	21353	34276	3.85	0.0E+00	AW592233.1	EST_HUMAN	h148a09.x1 Scores NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2835088 3'
8849	21388	34311	0.5	0.0E+00	AU128804.1	EST_HUMAN	h148a09.x1 Scores NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2835088 3'
8859	21398	34321	1.27	0.0E+00	AV714784.1	EST_HUMAN	AU128804 NT2RP2 Homo sapiens cDNA clone NT2RP2004245 5'
8874	21413	34336	2.8	0.0E+00	AL040428.1	EST_HUMAN	AV714784 DCB Homo sapiens cDNA clone DCBAUA08 5'
8880	21418	34342	1.55	0.0E+00	AF133901.1	NT	DKFZp434C1814_s1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C1814 3'
8882	21420	34345	1.68	0.0E+00	AB040945.1	NT	DKFZp434C1814_s1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C1814 3'
8889	21427	34352	0.54	0.0E+00	BF675505.1	EST_HUMAN	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
8891	21428		0.97	0.0E+00	BF058288.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
8921	21458	34377	6.2	0.0E+00	11422857	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8930	21468	34398	1.15	0.0E+00	K01241.1	NT	7k29b03.x1 NCI CGAP OV18 Homo sapiens cDNA clone IMAGE:4274708 6'
8937	21475	34398	4.14	0.0E+00	AB020630.1	NT	Homo sapiens tumor protein p73 (TP73), mRNA
8937	21475	34398	4.14	0.0E+00	AB020630.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
8942	21480	34402	1.81	0.0E+00	AV680739.1	EST_HUMAN	Homo sapiens mRNA for KIAA0823 protein, partial cds
							Homo sapiens mRNA for KIAA0823 protein, partial cds
							AV680739 GLC Homo sapiens cDNA clone GLCGKG12 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8948	21498	34408	3.39	0.0E+00	7706838	NT	Homo sapiens polycystin-L (PKDL), mRNA
8953	21491	34413	2.58	0.0E+00	BE783326.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
8954	21492	34414	0.56	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8954	21492	34415	0.58	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8966	21504		1.07	0.0E+00	H73837.1	EST_HUMAN	y03h08.11 Sources fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:232767 5'
8976	21514	34437	4.52	0.0E+00	BE319402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8976	21514	34438	4.52	0.0E+00	BE319402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8986	21524	34453	0.63	0.0E+00	BE612721.1	EST_HUMAN	601462562F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858100 5'
8986	21524	34454	0.63	0.0E+00	BE612721.1	EST_HUMAN	601462562F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858100 5'
8989	21527		0.58	0.0E+00	M80986.1	NT	Human polymorphic loci in Xq28
8991	21528	34458	1.84	0.0E+00	X14768.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9011	21548	34477	2.5	0.0E+00	A061395.1	EST_HUMAN	en28a04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9016	21553	34481	1.82	0.0E+00	A1854607.1	EST_HUMAN	w344a12.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MGB3_HUMAN
9021	21558	34486	4.57	0.0E+00	9256598	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9031	21568	34497	2.1	0.0E+00	AW958311.1	EST_HUMAN	Homo sapiens proteoglycan alpha 8 (PGDH8), mRNA
9041	21578	34507	2.81	0.0E+00	9835487	NT	EST370381 MAGE resequences, MAGE Homo sapiens cDNA
9056	21593	34523	1.13	0.0E+00	AU142682.1	EST_HUMAN	Human endogenous retrovirus, complete genome
9070	21607	34538	1.25	0.0E+00	11436895	NT	AU142682 Y78AA1 Homo sapiens cDNA clone Y78AA1000878 5'
9071	21608		0.9	0.0E+00	BE410768.1	EST_HUMAN	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9085	21621	34557	1.89	0.0E+00	BF002024.1	EST_HUMAN	601301878F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q8UH82
9096	21635	34573	0.83	0.0E+00	AB011150.1	NT	7q97h12.x1 NCL CGAP_C018 Homo sapiens cDNA clone IMAGE:3943463 5'
9100	21636	34574	7.17	0.0E+00	BE784823.1	EST_HUMAN	Q8UH82 HYPOTHETICAL 42.5 KD PROTEIN. ;
9104	21640	34578	0.52	0.0E+00	BE810292.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9104	21640	34580	0.52	0.0E+00	BE810292.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9107	21643	34583	1.17	0.0E+00	AU136229.1	EST_HUMAN	RC3-PT0151-280600-011-c05 PT0151 Homo sapiens cDNA
9112	21648	34588	1.18	0.0E+00	BE883843.1	EST_HUMAN	RC3-PT0151-280600-011-c05 PT0151 Homo sapiens cDNA
9120	21648	34589	1.18	0.0E+00	BE883843.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9130	21665	34605	0.79	0.0E+00	AB011168.1	NT	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911988 5'
9133	21668	34606	1.64	0.0E+00	AA344801.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911988 5'
9133	21668	34610	1.64	0.0E+00	AA344801.1	EST_HUMAN	Homo sapiens mRNA for KIAA0564 protein, partial cds
							EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
							EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9188	21705	34647	0.85	0.0E+00	AW873469.1	EST_HUMAN	bs54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9188	21705	34848	0.85	0.0E+00	AW673488.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2803367 5' similar to TR:O60276 O60276 KIAA0522 PROTEIN ;
9222	21738	34860	3.48	0.0E+00	BE207083.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9222	21738	34861	3.48	0.0E+00	BE207083.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9233	21955	34864	2.35	0.0E+00	BF348013.1	EST_HUMAN	602023150F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158300 5'
9288	21794	34743	2.8	0.0E+00	BE712616.1	EST_HUMAN	QV2-IT0698-250700-282-508 HT0698 Homo sapiens cDNA
9289	21829	34846	0.88	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3859035 5'
9289	21898	34847	0.88	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3859035 5'
9305	21905	34854	0.53	0.0E+00	AI908351.1	EST_HUMAN	RC-BT108-040390-032 BT108 Homo sapiens cDNA
9308	21908	34856	1.54	0.0E+00	5803088	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9308	21908	34857	1.54	0.0E+00	5803088	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9317	21831	34782	1.86	0.0E+00	AL042278.1	EST_HUMAN	DKFZp344L0120.r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp344L0120 5'
9382	21868	34816	2.17	0.0E+00	AI088043.1	EST_HUMAN	aw60h01.x1 Scara5_NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 KIAA0171 PROTEIN ;
9359	20288	33188	0.83	0.0E+00	BF308982.1	EST_HUMAN	601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138068 5'
9381	20300	33199	2.26	0.0E+00	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9381	20300	33200	2.26	0.0E+00	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9383	20302	33203	18.79	0.0E+00	AI280908.1	EST_HUMAN	qm08a08.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN P28316 60S RIBOSOMAL PROTEIN L23A ;
9383	20302	33204	18.79	0.0E+00	AI280908.1	EST_HUMAN	qm08a08.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN P28316 60S RIBOSOMAL PROTEIN L23A ;
9384	20303	33205	6.56	0.0E+00	AW953936.1	EST_HUMAN	EST368026 MAGC resequences, MAGC Homo sapiens cDNA
9391	21814	34783	3.79	0.0E+00	AF153486.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
9394	21817	34787	0.81	0.0E+00	BE885128.1	EST_HUMAN	601610882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812165 5'
9394	21817	34788	0.81	0.0E+00	BE885128.1	EST_HUMAN	601610882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812165 5'
9403	21912		19.73	0.0E+00	BE255820.1	EST_HUMAN	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9408	21916	34884	1.36	0.0E+00	BE781382.1	EST_HUMAN	601468828F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870007 5'
9408	21916	34884	1.36	0.0E+00	BE781382.1	EST_HUMAN	601468828F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870007 5'
9408	21917	34886	29.88	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:IM36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9428	21937	34986	3	0.0E+00	BE263191.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9448	21972	34922	4.5	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9448	21972	34923	4.5	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9448	21974	34926	2.7	0.0E+00	BE748215.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927648 5'
9458	21984	34936	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	21984	34937	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	21984	34938	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9478	21977	34924	1.89	0.0E+00	BE600549.1	EST_HUMAN	601873425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9498	21986	34952	0.76	0.0E+00	AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 5'
9508	22008	34955	2.38	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9508	22008	34956	2.38	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9540	22040	35001	1.32	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0842-130300-017-g01 BT0842 Homo sapiens cDNA
9559	22059	35021	1.88	0.0E+00	AW500263.1	EST_HUMAN	UI-HF-BN0-akg-b-12-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9559	22059	35022	1.88	0.0E+00	AW500263.1	EST_HUMAN	UI-HF-BN0-akg-b-12-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9568	22068	35028	1.75	0.0E+00	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9568	22068	35028	1.75	0.0E+00	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9570	22070	35030	0.72	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3874037 5'
9570	22070	35031	0.72	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3874037 5'
9578	22078	35043	1.14	0.0E+00	W56629.1	EST_HUMAN	z116e11.r1 Soares_fetal_NBHH18W Homo sapiens cDNA clone IMAGE:340844 5'
9578	22078	35044	1.14	0.0E+00	W56629.1	EST_HUMAN	z116e11.r1 Soares_fetal_NBHH18W Homo sapiens cDNA clone IMAGE:340844 5'
9591	22091	35055	1.05	0.0E+00	AB035356.1	NT	Homo sapiens mRNA for neurixin I-alpha protein, complete cds
9595	22095	35060	0.64	0.0E+00	AI124780.1	EST_HUMAN	em56a11.xt Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9597	22097	35060	2.65	0.0E+00	AW500526.1	EST_HUMAN	UI-HF-BN0-akg-c-07-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9640	22140	35107	1.46	0.0E+00	AF009698.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9668	22165	35138	2.21	0.0E+00	S78486.1	NT	AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9668	22165	35139	2.21	0.0E+00	S78486.1	NT	AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9668	22168	35144	2.54	0.0E+00	BE566320.1	EST_HUMAN	601334903F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689880 5'
9689	22188	35161	1.5	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301189-043-h11 CT0311 Homo sapiens cDNA
9708	22206	35178	0.91	0.0E+00	11436432	NT	Homo sapiens multimarin (MMRN), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9709	22207	35180	0.74	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9718	22216	35190	0.83	0.0E+00	BE208710.1	EST_HUMAN	bb28601.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2884000 3'
9733	22231	35208	2.41	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9733	22231	35209	2.41	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9742	22240	35221	1.45	0.0E+00	AW500938.1	EST_HUMAN	UIHF-BF0p-air-7-05-QUI r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
9748	22246	35227	19.66	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9748	22246	35228	19.66	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9761	22259	35242	2.32	0.0E+00	7682087	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9779	22277	35282	1.98	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0120 5'
9784	22282	35288	0.71	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2416 5'
9794	22282	35275	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9795	22283	35276	2.48	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
9822	22320	35304	2.61	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9822	22320	35305	2.61	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9838	22336	35318	3.23	0.0E+00	BF092898.1	EST_HUMAN	MR4-TN0114-110800-101-404 TN0114 Homo sapiens cDNA
9865	22382	35342	2.74	0.0E+00	BE280780.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
9874	22371	35348	8.19	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9874	22371	35349	8.19	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9883	22380	35355	9.02	0.0E+00	AW236288.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2689977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
9884	22381	35356	0.92	0.0E+00	AA341305.1	EST_HUMAN	EST146740 Fetal kidney II Homo sapiens cDNA 5' end
9893	22390	35368	0.6	0.0E+00	11427236	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9916	22412	35387	0.79	0.0E+00	AW864113.1	EST_HUMAN	EST376180 MAGe resequences, MAGH Homo sapiens cDNA
9926	22425	35398	6.82	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y78AA1002307 5'
9926	22425	35399	6.82	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y78AA1002307 5'
9932	22428	35402	3.44	0.0E+00	AF072406.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9935	22430	35404	2.52	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
9935	22430	35405	2.52	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
9968	22463	35447	3.55	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9968	22463	35448	3.55	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9984	22479	35462	2.1	0.0E+00	AJ293844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
9984	22479	35463	2.1	0.0E+00	AJ293844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
9989	22484	35470	0.82	0.0E+00	AV085712.1	EST_HUMAN	AV085712 GK0 Homo sapiens cDNA clone GKCDX07 5'

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9986	22484	35471	0.82	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKX Homo sapiens cDNA clone GKCDXA07 5'
9985	22480	35478	0.57	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9987	22492	35481	2.78	0.0E+00	AA198387.1	EST_HUMAN	Zp97h11.1r1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:828197 5'
10020	22515	35508	1.81	0.0E+00	AA131248.1	EST_HUMAN	Z31f01.1r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10020	22515	35508	1.81	0.0E+00	AA131248.1	EST_HUMAN	Z31f01.1r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10081	22556	35551	1.58	0.0E+00	AF178308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10102	22587	35560	0.75	0.0E+00	BE880658.1	EST_HUMAN	601491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:383857 5'
10113	22608	35588	11.65	0.0E+00	BE730772.1	EST_HUMAN	60157012F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10113	22608	35588	11.65	0.0E+00	BE730772.1	EST_HUMAN	60157012F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10118	22613	35603	1.05	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10127	22622	35612	0.99	0.0E+00	BE988611.1	EST_HUMAN	601846134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930177 5'
10127	22622	35613	0.89	0.0E+00	BE958511.1	EST_HUMAN	601845134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930177 5'
10142	22637	35628	0.79	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10163	22648	35642	0.78	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10154	22648	35643	0.57	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
10187	22682	35657	0.81	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10170	22685	35680	1.29	0.0E+00	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10178	22674	35686	1.47	0.0E+00	AB028280.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
10180	22875	35687	0.53	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887818 5'
10180	22875	35688	0.83	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887818 5'
10187	22882	35673	6.03	0.0E+00	AB008690.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10187	22882	35674	6.03	0.0E+00	AB008690.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10184	22888	35682	0.57	0.0E+00	AA194770.1	EST_HUMAN	Zq08h11.1r1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:828885 5' similar to TR:G407097
10188	22891	35684	1.18	0.0E+00	AA7044457.1	EST_HUMAN	Z19800.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:U141423_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10188	22893	35685	1.31	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyltransferase mRNA, complete cds
10200	22695	35688	5.5	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184839 5'
10200	22695	35688	5.5	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184839 5'
10227	22722	35713	0.83	0.0E+00	BE697149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10227	22722	35714	0.83	0.0E+00	BE697149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10258	22761	35738	0.53	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DC8 Homo sapiens cDNA clone DC8BDC09 5'
10258	22761	35740	0.53	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DC8 Homo sapiens cDNA clone DC8BDC09 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10285	22780	35770	0.77	0.0E+00	AB01818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
							Q61204 NOTCH2-LIKE;
10285	22780	35771	0.77	0.0E+00	AB01818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10288	22782	35782	1.32	0.0E+00	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3' end
10321	22815	35811	0.83	0.0E+00	AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002369 5'
10348	22842	35838	2.69	0.0E+00	BF438218.1	EST_HUMAN	neb45e12.x1 Scores_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10349	22843		1.61	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'
							xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:IM69086 MOESIN (HUMAN);
10387	22861	35854	3.53	0.0E+00	AW517980.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484703 5'
10371	22866	35858	21.07	0.0E+00	BE49213.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZp781P1010 (DKFZp781P1010), mRNA
10386	22880	35874	0.55	0.0E+00	11438005	NT	H. sapiens mRNA for NK receptor (183 Act)
10410	22804	35901	1.22	0.0E+00	X98893.1	NT	
10411	22905	35902	3	0.0E+00	BE781742.1	EST_HUMAN	601487419F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870700 5'
10430	22924	35929	2.88	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842-150200-012-003 BT0842 Homo sapiens cDNA
10430	22924	35930	2.88	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842-150200-012-003 BT0842 Homo sapiens cDNA
10437	22931	35938	0.6	0.0E+00	YD8032.1	NT	Human endogenous retrovirus-K, LTR U5 end gag gene
10443	22937	35947	0.68	0.0E+00	AI696930.1	EST_HUMAN	tt64607.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2244812 3'
10450	22944	35954	5.48	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
10450	22944	35955	5.48	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
10463	22947	35966	1.83	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845958 3'
10453	22947	35957	1.83	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845958 3'
10458	22952	35960	0.49	0.0E+00	D28954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10458	22952	35961	0.49	0.0E+00	D28954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10474	22968	35977	0.68	0.0E+00	H39805.1	EST_HUMAN	yp01e10.r1 Scores breast 3Nbt-Bst Homo sapiens cDNA clone IMAGE:186138 5'
10487	22981	35989	0.48	0.0E+00	AW748117.1	EST_HUMAN	QV0-BT0107-230789-007-c08 BT0107 Homo sapiens cDNA
10488	22990	35998	1.14	0.0E+00	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10508	23002	36010	0.8	0.0E+00	D28954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10515	23053	36064	2.78	0.0E+00	AV711078.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAGG05 5'
10515	23053	36065	2.78	0.0E+00	AV711078.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAGG05 5'
10517	23055		6.05	0.0E+00	AW813763.1	EST_HUMAN	RC3-ST0197-120200-015-e03 ST0197 Homo sapiens cDNA
10525	23062	36073	7.48	0.0E+00	AW903563.1	EST_HUMAN	EST375638 MAGE repeat, MAGH Homo sapiens cDNA
10538	23075	36086	1.91	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10538	23075	36089	1.91	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10540	23077	38091	1.82	0.0E+00	AW057821.1	EST_HUMAN	w61f05.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2663086 3' similar to TR:Q60586 Q60586 VDX;
10548	23086	38089	2.28	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylar-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
10550	23086	38100	2.73	0.0E+00	AI652239.1	EST_HUMAN	w628a12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2308974 3' similar to contains element MSR1 MSR1 repetitive element;
10550	23088	38101	2.73	0.0E+00	AI652239.1	EST_HUMAN	w628a12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2308974 3' similar to contains element MSR1 MSR1 repetitive element;
10581	23097	38110	4.31	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10581	23097	38111	4.31	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10576	23111	38124	1.88	0.0E+00	AW404795.1	EST_HUMAN	UIHF-BLD-acm-3-04-0-ULF1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058383 5'
10580	23115	38129	5.92	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20076 (FLJ20076), mRNA
10581	23116	38130	10.05	0.0E+00	4504538	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10581	23116	38131	10.05	0.0E+00	4504538	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10582	23117	38132	2.9	0.0E+00	AI981827.1	EST_HUMAN	wu32a06.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
10585	23120	38136	2.57	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906805 5'
10589	23124	38138	15.86	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919838 5'
10591	23128	38139	2.44	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10591	23128	38140	2.44	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10606	23140	38162	6.94	0.0E+00	BE003304.1	EST_HUMAN	601874332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10608	18572	31304	2.31	0.0E+00	AA1898805.1	EST_HUMAN	zp95b11.r1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:627833 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10630	23162	38174	1.99	0.0E+00	AA809080.1	EST_HUMAN	mw17c08.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);
10632	23164	38176	5.44	0.0E+00	BE783488.1	EST_HUMAN	601588828F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843015 5'
10640	23172	38183	19.41	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH08 5'
10640	23172	38184	19.41	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH08 5'
10654	23186	38202	18.4	0.0E+00	AW516055.1	EST_HUMAN	xx04g10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852228 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
10660	23192	38207	3.16	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002704 5'
10665	23197	38210	2.88	0.0E+00	AW583333.1	EST_HUMAN	hg13402.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;
10685	23197	38211	2.88	0.0E+00	AW583333.1	EST_HUMAN	hg13402.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10685	23197	36212	2.88	0.0E+00	AW563333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2846476 3' similar to contains element MSR1 repetitive element;
10687	23196	36213	1.96	0.0E+00	Z34997.1	NT	H sapiens mRNA for H1 histamine receptor
10688	23200	36214	3.18	0.0E+00	F13068.1	EST_HUMAN	HS31C031 normalized infant brain cDNA Homo sapiens cDNA clone o-31c03
10678	23208	36220	3.91	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10679	23211	36222	33.46	0.0E+00	11425570	NT	Homo sapiens ryanodine receptor 1 (skatela) (RYR1), mRNA
10685	23225	36229	3.59	0.0E+00	AW338094.1	EST_HUMAN	xx6860.1x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832685 3' similar to gb.X17116 IG MU CHAIN C REGION (HUMAN);
10696	23226	36240	5.84	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B18-ali-h-9-01-Q-UJ.1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
10698	23228	36241	5.84	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B18-ali-h-9-01-Q-UJ.1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
10698	12891		16.23	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
10701	23230	36243	2.17	0.0E+00	AB014587.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
10714	23242	36269	2.26	0.0E+00	BE288449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028219 5'
10730	23256	36272	1.89	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0645 protein, partial cds
10746	23270	36286	2.18	0.0E+00	BE792155.1	EST_HUMAN	601562046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836539 5'
10747	23271		78.35	0.0E+00	BF684081.1	EST_HUMAN	602141405F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302432 5'
10749	23273	36288	4.68	0.0E+00	AU118358.1	EST_HUMAN	AU118388 HEMBA1 Homo sapiens cDNA clone HEMBA1003488 5'
10760	23274		8.16	0.0E+00	AW236269.1	EST_HUMAN	xt72b01.x1 NCL_CGAP_GML1 Homo sapiens cDNA clone IMAGE:2698977 3' similar to gb.X02162_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10755	23279	36292	7.25	0.0E+00	A1148809.1	EST_HUMAN	q43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'
10755	23279	36293	7.25	0.0E+00	A1148809.1	EST_HUMAN	q43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'
10756	23280	36294	3.47	0.0E+00	AW391937.1	EST_HUMAN	QV4-ST0234-121199-032-506 ST0234 Homo sapiens cDNA
10768	23292		1.54	0.0E+00	AU118608.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
10771	23295	36301	20.95	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
10777	23301	36307	1.89	0.0E+00	AW804516.1	EST_HUMAN	QVQ-UM0093-170400-191-406 UM0093 Homo sapiens cDNA
10777	23301	36308	1.89	0.0E+00	AW804516.1	EST_HUMAN	QVQ-UM0093-170400-191-406 UM0093 Homo sapiens cDNA
10776	23302	36309	2.04	0.0E+00	BF940309.1	EST_HUMAN	602937014F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4184979 5'
10779	23303	36310	39.28	0.0E+00	BE281209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3183310 5'
10790	23313	36321	3.78	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
10794	23317	36326	3.48	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
10794	23317	36327	3.48	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
10816	23337	36350	55.63	0.0E+00	AA740782.1	EST_HUMAN	cd32607.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element;
10822	23343	36358	3.04	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10836	23366	36371	1.92	0.0E+00	BE268478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536887 5'
10835	23366	36372	1.92	0.0E+00	BE268478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536887 5'
10838	23366	36374	6.99	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNAKulture) Homo sapiens cDNA clone 3NHC4817
10845	23366	36382	2.16	0.0E+00	AA746376.1	EST_HUMAN	aa56h0.1.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306009 5'
10845	23366	36383	2.16	0.0E+00	AA746376.1	EST_HUMAN	aa56h0.1.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306009 5'
10856	23377	36395	8.08	0.0E+00	AL157808.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761J2116 5'
10868	23388	36404	12.62	0.0E+00	AU116888.1	EST_HUMAN	AU116888 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
10881	23402	36419	2.07	0.0E+00	AV693656.1	EST_HUMAN	AV693656 GKC Homo sapiens cDNA clone GKCCNC03 5'
10893	23432	36453	3.17	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
10893	23432	36454	3.17	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
10894	23433		1.8	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAAD08 5'
10828	23448	36467	3.19	0.0E+00	BE598423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
10835	23452	36474	1.69	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BNO-akg-4-02-Q-U1.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077019 5'
10835	23452	36475	1.69	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BNO-akg-4-02-Q-U1.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077019 5'
							bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048488 5' similar to gb:Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
10938	23455	36478	6.2	0.0E+00	BE018263.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
10972	23487	36516	5.22	0.0E+00	BE897953.1	EST_HUMAN	ea08g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10973	23488	36517	1.89	0.0E+00	A1456545.1	EST_HUMAN	ea08g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10973	23488	36518	1.89	0.0E+00	A1456545.1	EST_HUMAN	ea08g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10986	23500	36530	1.82	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
11018	23532	36568	3.57	0.0E+00	4758827	NT	Homo sapiens neurodin III (NRDN3) mRNA
11019	23533	36569	8.71	0.0E+00	BF206581.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11023	23537	36573	20.4	0.0E+00	AW207734.1	EST_HUMAN	UI-H-BI2-age-h-01-Q-U1.r1 NCI_CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11028	23542	36577	6.39	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11028	23542	36578	6.39	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11028	23543	36579	3.28	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN.;
11029	23643	36580	3.28	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN.;
11053	23568	36602	2.05	0.0E+00	BF089687.1	EST_HUMAN	QVQ-UM0091-120600-365-b12 UM0091 Homo sapiens cDNA
11054	20011	32877	2.13	0.0E+00	I32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11057	23569	36604	3.38	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-H04 HT0230 Homo sapiens cDNA
11057	23569	36605	3.38	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-H04 HT0230 Homo sapiens cDNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11092	23604	36844	5.37	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-ack-b-10-Q-UI.at1 NC1 CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
11092	23604	36845	5.37	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-ack-b-10-Q-UI.at1 NC1 CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
11101	23611	36851	3.82	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
11105	23615	36855	1.61	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11105	23615	36856	1.61	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11108	23616	36857	8.82	0.0E+00	BE879401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11108	23616	36858	8.82	0.0E+00	BE879401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11113	23623	36864	1.85	0.0E+00	D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11119	23628		5.3	0.0E+00	BF249536.1	EST_HUMAN	601875630F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088710 5'
11132	23640	36860	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11132	23640	36861	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11137	23645	36865	3.57	0.0E+00		NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11137	23645	36866	3.57	0.0E+00	11430888	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11164	23661	36706	9.12	0.0E+00	45039444	NT	Homo sapiens eukaryotic translation initiation factor 6A (EIF6A) mRNA
11165	23669	36714	1.68	0.0E+00	BF576287.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11165	23672	36718	8.44	0.0E+00	AW328173.1	EST_HUMAN	cd0405.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11168	23675		49.81	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11173	23680	36725	5.47	0.0E+00	BF308998.1	EST_HUMAN	601869823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11173	23680	36726	5.47	0.0E+00	BF308998.1	EST_HUMAN	601869823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11180	23688	36733	45.22	0.0E+00	BF362482.1	EST_HUMAN	QV2-NNQ054-230800-333-404 NNQ054 Homo sapiens cDNA
11201	23708	36757	1.89	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11201	23708	36758	1.99	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11205	23710		6.26	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11206	23711		1.61	0.0E+00	45037861	NT	Homo sapiens tyr-related kinase (FRK) mRNA
11217	23720	36774	2.82	0.0E+00	8923688	NT	Homo sapiens golgin-like protein (GLP), mRNA
11218	23722		2.58	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11220	23723		7.59	0.0E+00	BE257744.1	EST_HUMAN	601116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3957384 5'
11233	23764	36820	5.51	0.0E+00	BE206848.1	EST_HUMAN	bsd4407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN.;
11233	23764	36821	5.51	0.0E+00	BE206848.1	EST_HUMAN	bsd4407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN.;
11235	23766	36823	4.68	0.0E+00	AW763028.1	EST_HUMAN	QV0-CT0225-101289-071-508 CT0225 Homo sapiens cDNA
11240	23771		3.42	0.0E+00	AA559707.1	EST_HUMAN	nl42a08.s1 NC1 CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M86176 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11241	18112	30521	6.08	0.0E+00	AI924954.1	EST_HUMAN	wp06g08.x1 NCL_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2484094 3'
11242	23772	36829	9.55	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11260	24801	36847	1.56	0.0E+00	AW292778.1	EST_HUMAN	UI-H-BWO-sj4-07-Q-U1.s1 NCL_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2729509 3'
11266	23004	36812	2.1	0.0E+00	4758827	NT	Homo sapiens neurodin III (NRXN3) mRNA
11274	23727	36781	1.59	0.0E+00	BE965909.2	EST_HUMAN	601859088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11274	23727	36782	1.59	0.0E+00	BE965909.2	EST_HUMAN	601859088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11276	23728	36783	4.55	0.0E+00	BE185656.1	EST_HUMAN	IL5-H10731-020500-077-005 H10731 Homo sapiens cDNA
11286	23740	36786	5.82	0.0E+00	AL048540.1	EST_HUMAN	DKFZp434G178.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G178 5'
11288	23740	36787	5.82	0.0E+00	AL048540.1	EST_HUMAN	DKFZp434G178.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G178 5'
11298	23750	36807	16.85	0.0E+00	AI923116.1	EST_HUMAN	nm3g03.x1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13688
11301	23764	36851	7	0.0E+00	AA760913.1	EST_HUMAN	nm3g03.x1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13688
11301	23764	36852	7	0.0E+00	AA760913.1	EST_HUMAN	Q13688 ALKB HOMOLOG PROTEIN.1
11306	23766	36858	2.02	0.0E+00	BE910546.1	EST_HUMAN	7f27f12.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3902928 5'
11314	23012	36021	7.16	0.0E+00	BE676347.1	EST_HUMAN	CHECKPOINT SUPPRESSOR 1.1
11323	23021	36030	1.69	0.0E+00	AV757420.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11352	23806	36865	3.65	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11352	23806	36866	3.65	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11366	23818	36879	4.02	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLAGE1 Homo sapiens cDNA clone PLAGE1008077 5'
11381	23833	36898	9.87	0.0E+00	BE622317.1	EST_HUMAN	601441098F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11386	23838	36900	11.61	0.0E+00	AI207425.1	EST_HUMAN	HA2767 Human fetal liver cDNA library Homo sapiens cDNA
11386	23838	36901	11.61	0.0E+00	AI207425.1	EST_HUMAN	HA2767 Human fetal liver cDNA library Homo sapiens cDNA
11415	23866	36927	36.86	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:38338012 3'
11415	23866	36928	36.86	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:38338012 3'
11425	23876	36940	2.19	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11425	23876	36941	2.19	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11428	23879	36944	2.52	0.0E+00	AW006022.1	EST_HUMAN	wz91M01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2568225 3' similar to WP:F53H10.2
11431	24902	36947	3.76	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3316689 3' similar to TR:Q13458
11450	23800	36867	3.91	0.0E+00	AW397776.1	EST_HUMAN	MR4-ST0118-281089-012-503 ST0118 Homo sapiens cDNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11450	23900	36968	3.81	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-281098-012-503 ST0118 Homo sapiens cDNA
11458	23909		2.48	0.0E+00	AW803777.1	EST_HUMAN	MR3-SN0010-310300-107-003 SN0010 Homo sapiens cDNA
11471	23921	36960	3.38	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11471	23921	36961	3.38	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11476	23926	36967	7.44	0.0E+00	U38263.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11476	23926	36969	12.8	0.0E+00	BE379254.1	EST_HUMAN	601237081F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609823 5'
11479	23929	37000	12.8	0.0E+00	BE379254.1	EST_HUMAN	601237081F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609823 5'
11482	23941	37012	2.5	0.0E+00	BE784758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11483	23942	37013	115.56	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11507	23956	37026	18.88	0.0E+00	BE409993.1	EST_HUMAN	601268403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11508	23957	37027	1.94	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-180500-011-002 HT0241 Homo sapiens cDNA
11509	23958	37028	3.08	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11509	23958	37029	3.08	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11510	18292	30771	1.77	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11510	18292	30772	1.77	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
11518	23966	37036	2.03	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
11521	23969	37040	4.44	0.0E+00	BE903372.1	EST_HUMAN	601876357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
11533	23981	37051	1.84	0.0E+00	BF312552.1	EST_HUMAN	601897624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11533	23981	37052	1.84	0.0E+00	BF312552.1	EST_HUMAN	601897624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11535	23983	37054	3.01	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11535	23983	37055	3.01	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11544	23992		4.03	0.0E+00	BE908402.1	EST_HUMAN	601498563F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900398 5'
11560	24007	37078	1.74	0.0E+00	9835487	NT	Human endogenous retrovirus, complete genome
11574	24803		23.39	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
11580	24028	37094	55.98	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532888 5'
11589	24032	37102	7.09	0.0E+00	AL040783.1	EST_HUMAN	DKFZp434D0415_J1 434 (synonym: hless3) Homo sapiens cDNA clone DKFZp434D0415 5'
11652	25091	30499	6.23	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
11668	24925		1.78	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11688	24936		8.17	0.0E+00	AL160983.1	EST_HUMAN	qet17b12.x1 Sceres_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
11678	24097		3.67	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-9, complete cds
11686	24112		4.16	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11701	24114		1.35	0.0E+00	AB016195.1	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
11708	24120		3.59	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11728	24134		6.98	0.0E+00	5802873	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11783	24897	30711	1.49	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11774	24908		4.78	0.0E+00	AL041831.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434K0819 5'
11803	25058		4.26	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
11812	24184		11.28	0.0E+00	AL048544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434G218 5'
11824	24941		2.82	0.0E+00	AI003497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
11882	25079		2.35	0.0E+00	N54484.1	EST_HUMAN	y40e08.at Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL. POLYPROTEIN;
11877	24227		4.72	0.0E+00	AF106658.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
11880	13460	26007	6.48	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11880	13460	26008	5.46	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11889	24945		2.49	0.0E+00	10092687	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
11917	13204		3.24	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
11955	24720	30870	4.32	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12017	24871	30708	24.36	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
12028	24928		1.5	0.0E+00	BE090210.1	EST_HUMAN	RC8-BT0711-280300-011-D05 BT0711 Homo sapiens cDNA
12073	24838		2	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12112	24373		4.16	0.0E+00	8635487	NT	Human endogenous retrovirus, complete genome
12155	24831		1.93	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12189	24927		1.52	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12244	14314	26855	4.92	0.0E+00	H30132.1	EST_HUMAN	yc58e08.r1 Soares breast 3Nbh8at Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
12244	14314	26859	4.92	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12258	24468		33.19	0.0E+00	D50859.1	NT	yc58e08.r1 Soares breast 3Nbh8at Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
12269	24469	30928	3.51	0.0E+00	11418189	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 6 PRECURSOR (HUMAN);
12259	24469	30928	3.51	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACT GP9) pseudogene
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12278	14717	27289	1.42	0.0E+00	4759489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12318	24508		1.61	0.0E+00	AW684688.1	EST_HUMAN	h188a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879154 3'
12401	15863	28440	5.09	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12409	18031	30492	2.86	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12412	24586		2.65	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for carboxylate sulfotransferase, exon 1, 2, 3, 4, 5
12453	24587	30917	1.67	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 180kD subunit (CPSF1), mRNA
12491	25102		2.92	0.0E+00	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C048
12488	13277	25754	2.02	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12573	24870	30876	1.66	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12576	24872		2.54	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P20M, complete cds
12580	24876		4.31	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
12600	24898		2.35	0.0E+00	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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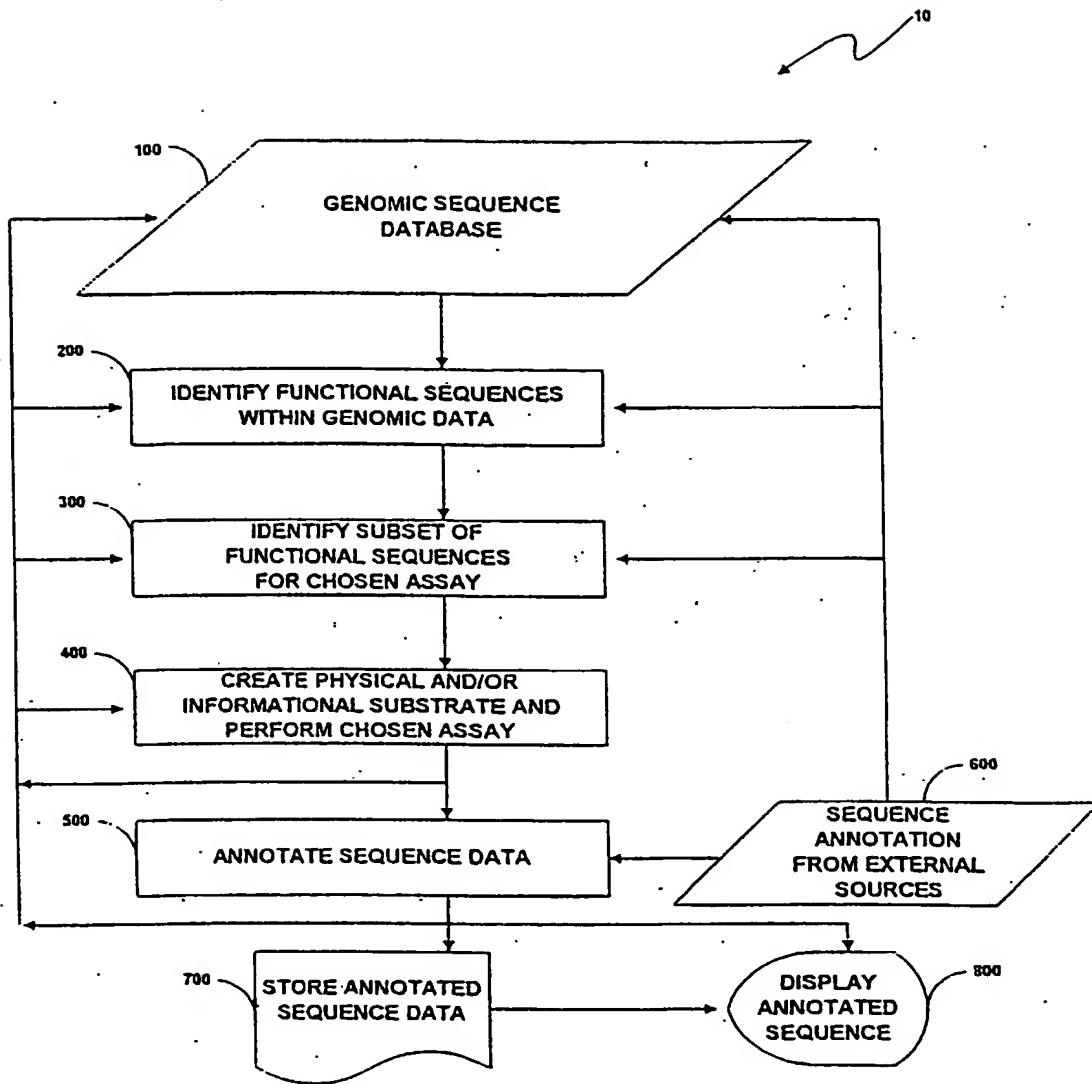


Fig. 1

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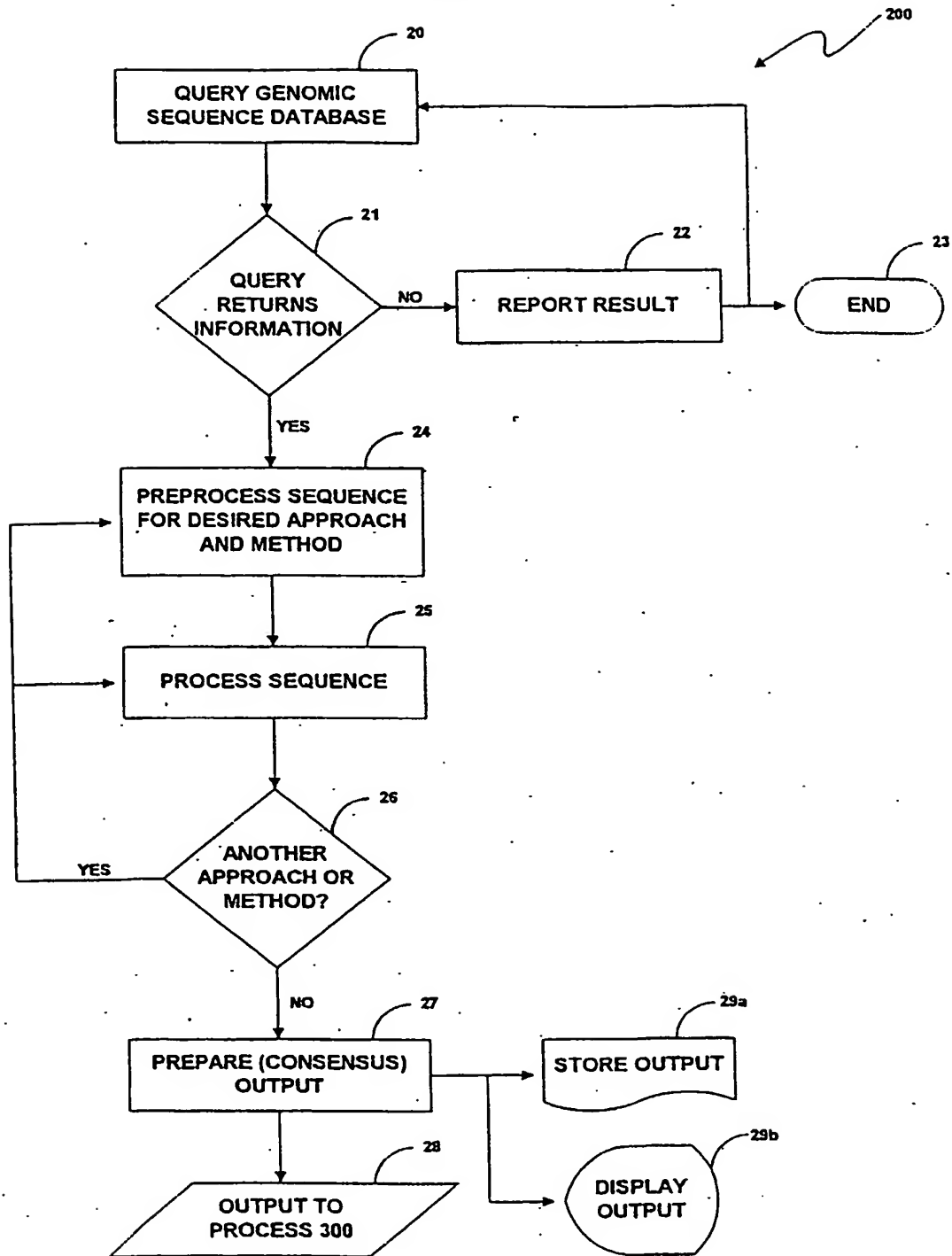


Fig. 2

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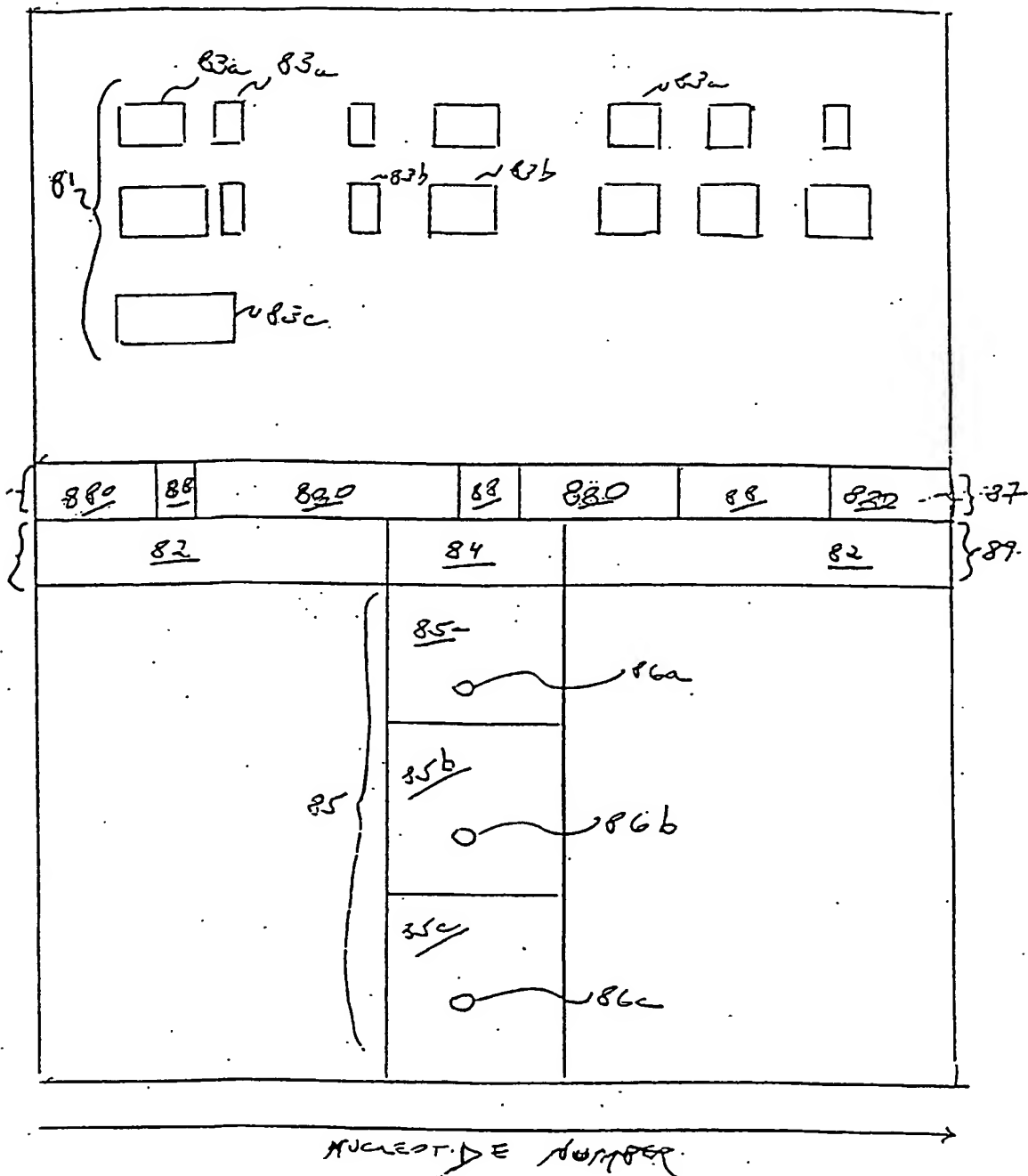


Fig. 3

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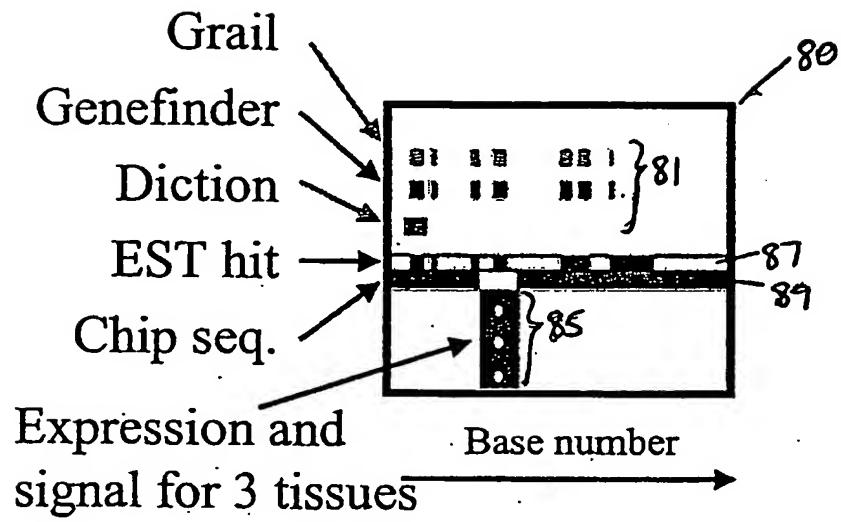


Fig. 4

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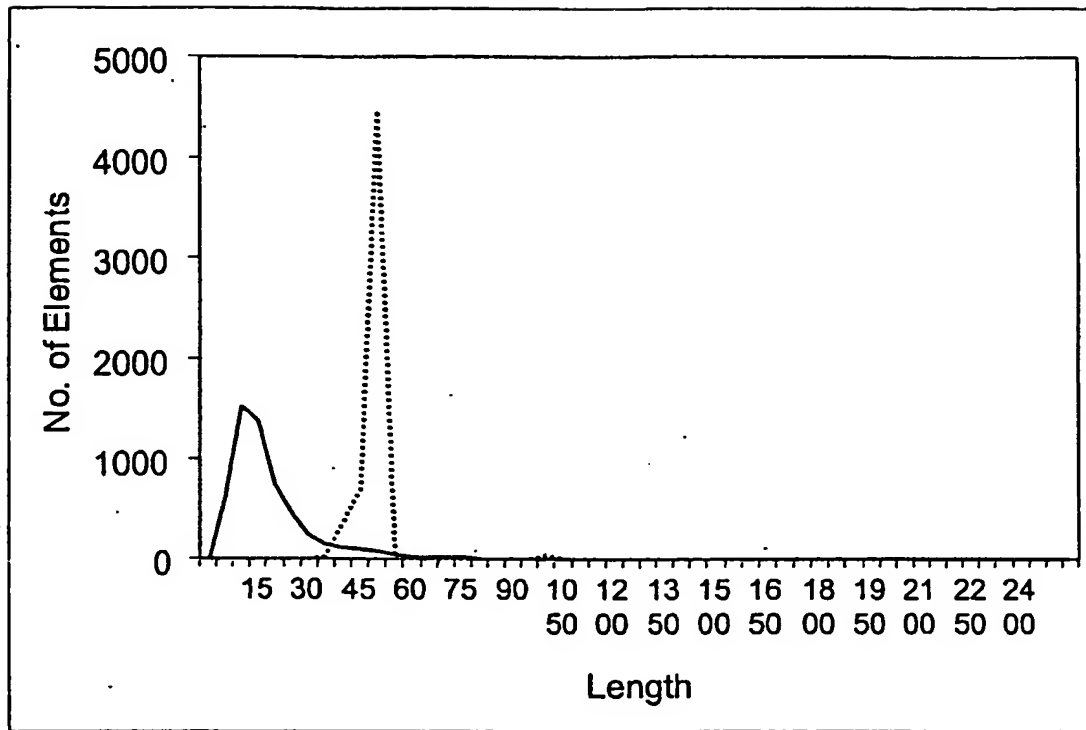


Fig. 5

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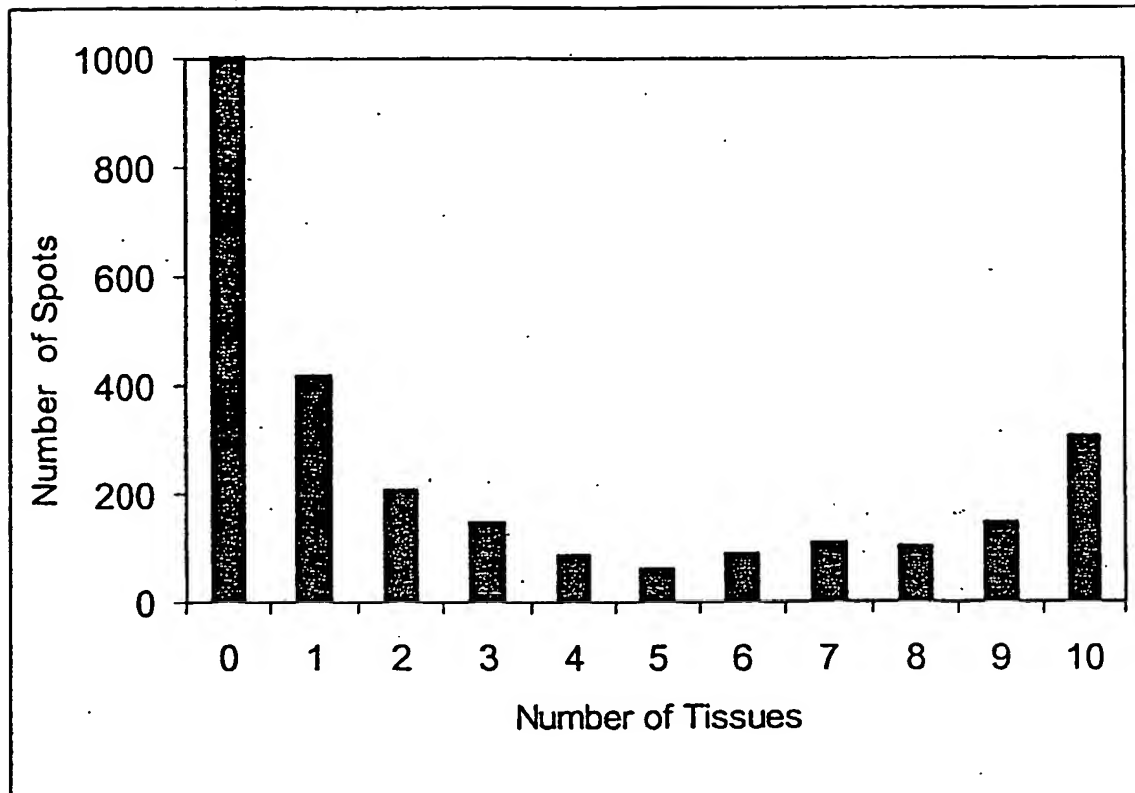


Fig. 6

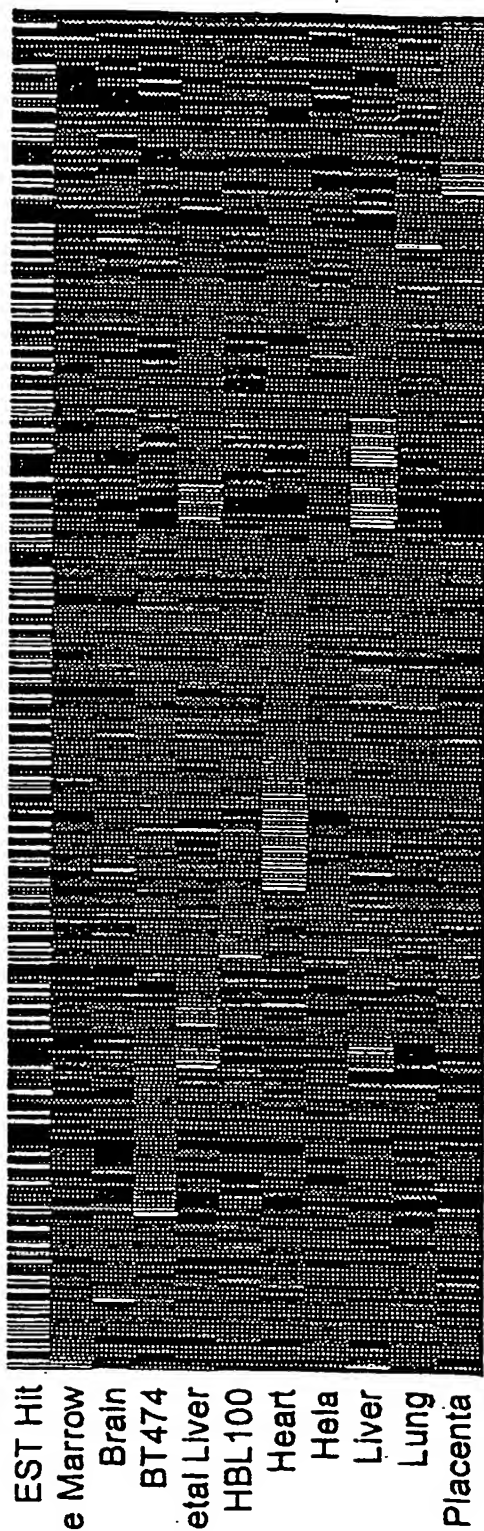


Fig. 7a

ratio legend

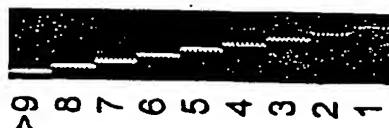


Fig. 7b

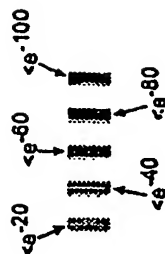


Fig. 7c

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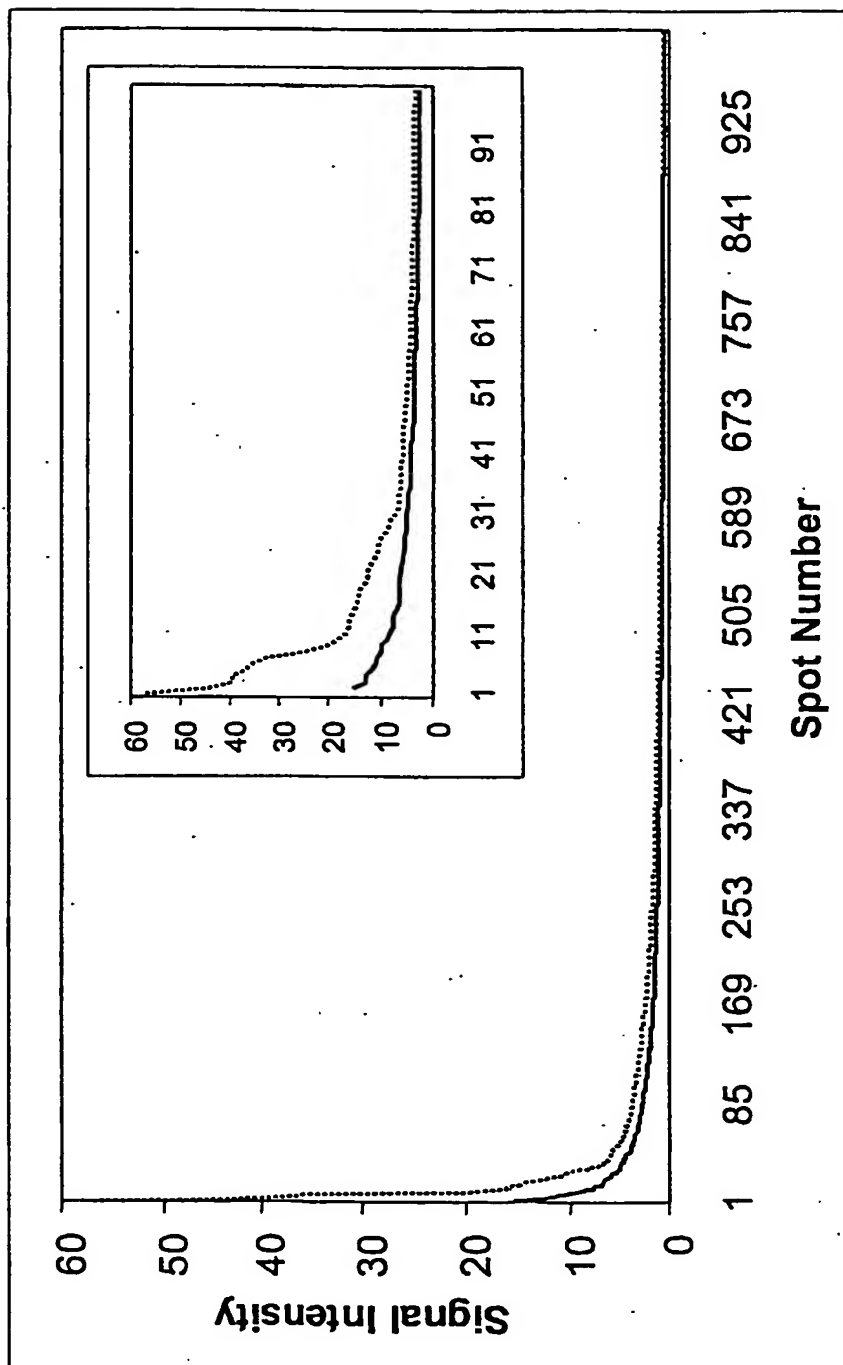


Fig. 8

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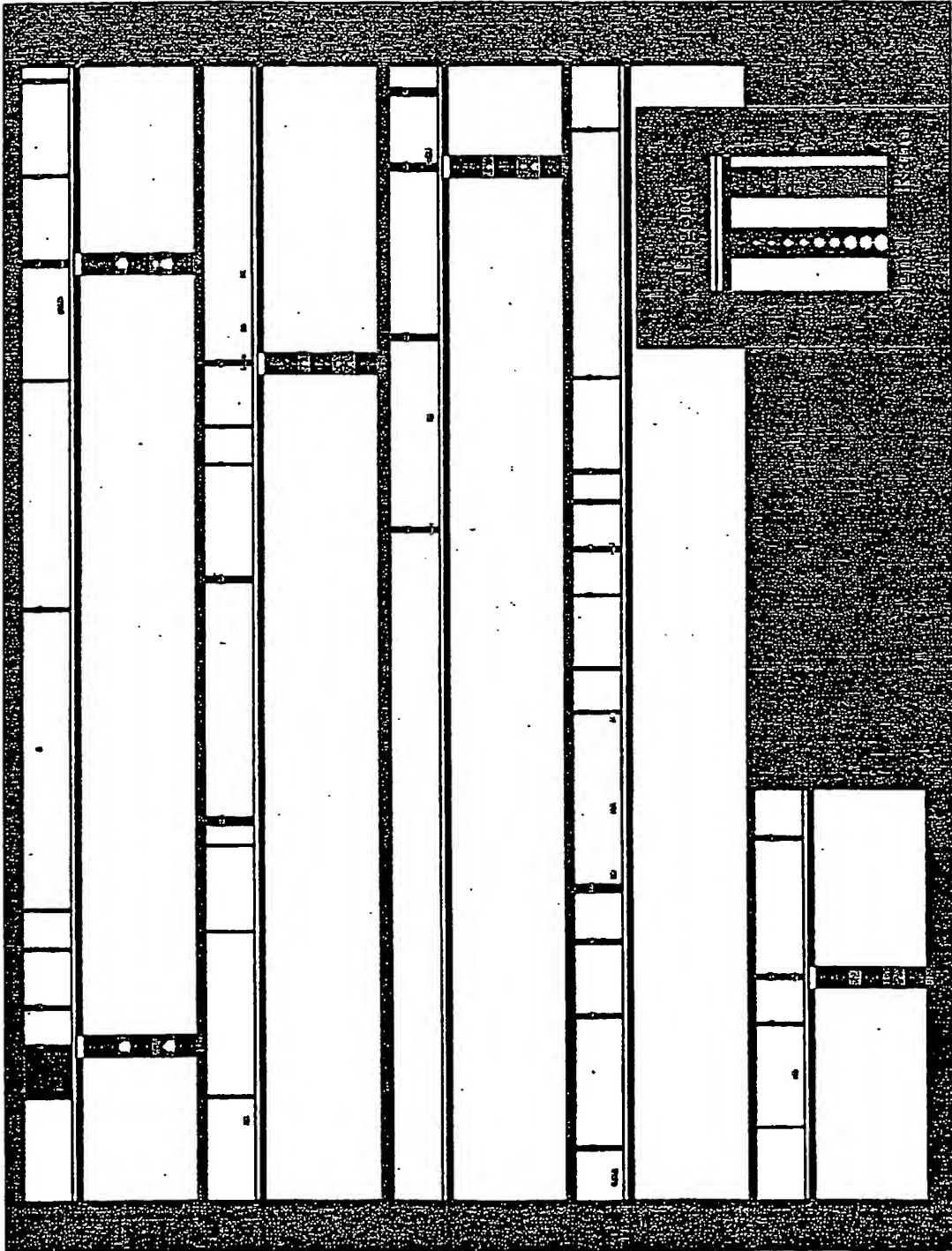


Fig. 9

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Fig. 10

